

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:05:49 ; Search time 23.1073 Seconds

(without alignments)
3605.942 Million cell updates/sec

Title: US-10-817-423-2

Perfect score: 4491
Sequence: 1 MRNGKSGVVRLPNDLEDL.....LCDGQWHSVAVSIKQRIHL 866

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: Dir1:*
2: Dir2:*
3: Dir3:*
4: Dir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3560.5	79.3	1713	2 A55347	adhesive ligand ep
2	1190	26.5	1816	1 S68960	laminin alpha-4 ch
3	948	21.1	3635	2 T10053	laminin alpha 5 ch
4	636.5	14.2	3712	2 S18253	laminin alpha-1 ch
5	600.5	13.4	3672	2 T23433	hypothetical prote
6	579.5	12.9	3704	2 T37316	probable laminin a
7	545	12.1	3084	1 MMMSA	laminin alpha-1 ch
8	531.5	11.8	1751	1 MMHDM	laminin alpha-2 ch
9	529.5	11.5	3075	1 S14458	laminin alpha-1 ch
10	516.5	11.5	3106	1 S53868	laminin alpha-2 ch
11	358.5	8.0	3102	2 T43281	laminin alpha ch
12	321.5	7.2	1530	2 I45944	neurexin I-alpha
13	320	7.1	1507	2 A40228	neurexin I-alpha
14	301.5	6.7	1438	2 A48216	neurexin III-alpha
15	301.5	6.7	1471	2 B48218	neurexin III-alpha
16	301.5	6.7	1578	2 I48216	neurexin III-alpha
17	288	6.4	1715	2 C40228	neurexin II-alpha
18	261	5.8	1283	2 T13799	neurexin IV - trui
19	222.5	5.0	2823	2 F87908	protein T22A3.8 [i
20	222.5	5.0	2823	2 T23064	hypothetical prote
21	211.5	4.7	1264	2 T19545	hypothetical prote
22	195.5	4.4	3707	2 S18252	heparan sulfate pr
23	188	4.2	1722	2 B89753	protein FltC7.4 [i
24	183	4.1	1385	2 T14158	neurexin IV - mous
25	183	4.1	4391	2 A58056	perlecan precursor
26	179.5	4.0	3097	2 T00021	DN-cadherin - trui
27	174	3.9	1381	2 T31083	parandolin - rat
28	169.5	3.8	3375	2 T19821	hypothetical prote
29	168.5	3.8	882	2 A39030	androgen-binding p

30	165.5	3.7	5147	1 IJFPTM	cadherin-related c
31	164.5	3.7	402	1 BOHUS	sex steroid-binding
32	163	3.6	403	2 A26371	sex steroid-binding
33	163	3.6	3034	2 T14119	seven-pass transme
34	161	3.6	1959	1 AGRT	agrin - rat
35	160	3.6	2325	2 A61208	chondroitin sulfat
36	156	3.5	1193	2 T21133	hypothetical prote
37	155	3.5	1955	1 AGCH	agrin precursor
38	154.5	3.4	357	2 A34436	sex steroid-binding
39	149	3.3	1328	2 T43060	agrin - electric r
40	148	3.3	281	2 T33466	hypothetical prote
41	146	3.3	757	2 T34362	hypothetical prote
42	146	3.3	4307	2 T20721	hypothetical prote
43	142	3.2	1523	2 T13953	MEGF5 protein - ra
44	140	3.1	2610	2 T20968	hypothetical prote
45	138	3.1	1025	2 T42626	secreted leucine-r

ALIGNMENTS

RESULT 1

A55347
adhesive ligand epiligrin, alpha-3 chain form A precursor - human
C:Species: Homo sapiens (man)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C/Accession: A55347
R:Ryan, M.C.; Tizard, R.; Vandevanter, D.R.; Carter, W.G.
J. Biol. Chem. 269, 22779-22787, 1994
A/Title: Cloning of the lam3 gene encoding the alpha3 chain of the adhesive ligand epi
A/Reference number: A55347; PMID:94357926; PMID:8077230
A/Accession: A55347
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1713 <RVA>
A/Cross-references: UNIPROT:Q16787; GB:U34155; NID:9551596; PID:9551597
C/Superfamily: laminin alpha-4 chain; laminin G repeat homology; laminin-type EGF-like
C/Keywords: alternative splicing
F/67-114/Domain: laminin-type EGF-like homology <LE2>
F/192-1534/Domain: laminin G repeat homology <LG4>

Query Match	Score	79.3%	Score	3560.5	DB 2	Length	1713
Best Local Similarity	78.4%	Pred. No.	1.1e-239				
Matches	680	Conservative	86	Mismatches	98	Indels	3
							Gaps 2
QY	1	MRNGKSGVVRLPNDLEDLKGYSLSLFLQPDLENGSTEDMFWYTLGNKDSKDYIG	60				
DB	771	MRNGKSGVVRLPNDLEDLKGYSLSLFLQPDLENGSTEDMFWYTLGNKDSKDYIG	830				
QY	61	MAVVDGQLTCVNMIGDREAVQIDVLTSESQBAVMDRKYRQRIYOPALNTYKATSN	120				
DB	831	MAVVDGQLTCVNMIGDREAVQIDVLTSESQBAVMDRKYRQRIYOPALNTYKATSN	890				
QY	121	KPRAPAVYDLEGGSSNTLNLDPEDAVFYGVGPDPDELRSRLRPPYKCIELDDNEN	180				
DB	891	KPRAPAVYDLEGGSSNTLNLDPEDAVFYGVGPDPDELRSRLRPPYKCIELDDNEN	950				
QY	181	VLSTLYNFKTFNLTTEVEBCRRRKRKESDKNVEGTEGYARIPTQPNAPFNFITQITTV	240				
DB	951	VLSTLYNFKTFNLTTEVEBCRRRKRKESDKNVEGTEGYAVPQPHAPITFGQITQTV	1010				
QY	241	DRGLLPPAENQDNFISLNTIDGMLVRYKANSPEPKGRIPTDINDGKHSILITTKLQ	300				
DB	1011	DRGLLPPAENQDNFISLNTIDGMLVRYKANSPEPKGRIPTDINDGKHSILITTKLQ	1070				
QY	301	KRAMINNVERSVRIEIEIPFSTYVGLGIPAIAREFNISTPAFOGCMKUKTSGVRL	360				
DB	1071	KRAMINNVQNTIITIDGVPFSTYVGLGIPAIAREFNISTPAFOGCMKUKTSGVRL	1130				
QY	361	NDTVGVTKKCSSEDKLVRTASFSRGGQMSFTNLDPSTDFQUSFGQTFQPSGTLINHQ	420				
DB	1131	NDTVGVTKKCSSEDKLVRTASFSRGGQMSFTNLDPSTDFQUSFGQTFQPSGTLINHQ	1190				

Qy	421	TRTSLSLWTEDEGHEIESTRSDNIPFSPGPMWGDLLHHYSVSDPSGRLILDDOVR	480
Dd	1191	TWTNKLQVTLDEGDIETELSTSDSGPFIKSPQTYMDGLAHVSVSDNSGLRLIDDQULR	1250
Qy	481	RNORLPFSFNAQOSLRLOGGHEGICISNVLYQRFOSQSEPVJDLBASKTYKDASLGGCSLN	540
Dd	1251	NSKELKHISSRQSIIRLGSSNFEQICISNVFYQRLSPREVJDLTNSIKRDVLSGGCSLN	1310
Qy	541	KPEPLMLFKSKRPFKGRIFVWNOUMODAPQAT-RSTFANWDDGSLCPLPLNTAKSHALQ	599
Dd	1311	KPEPLMLKSGSTRFNFKTKYTRINOLQDTVPASPSVAVWVD--ACSELPPTYQANHGLQ	1368
Qy	600	FGDSEPTSHLLKLPOEELKPRSOESFLDIQTSPKGLVFACTQKOSPLALVYAADRVFVAL	659
Dd	1369	FGDLPPTHLLPKLPOEELKPRSQFPAVMDQITSSKGLVHYHTITKNSFMALYLSKRLVFPAL	1428
Qy	660	GAGGKCLRLSKERKHYHDKMTVVYFGLNGSKARLYVVDGLRAQESLPGNSTISPREOYLL	719
Dd	1429	GTDEKCKRLKSKERKNDKMTVVYFGHDEBGRRLVVDGLRARRESLPGNSTISRAPVYL	1488
Qy	720	GLPLSRPKRKSPLPOHSFVGLCLRDPOLNSKPLDPSPARFVSPVSCLGSGLEKGIYFSQGGHV	779
Dd	1489	GSPSGRKRKSLPNTSPVGCCLKNFQDLSKPLVYTPSSSFVSSCLGGPLKEKGIYFSBEGHV	1548
Qy	780	ILANSVSLGPELKLTPSIRPRSLTGVLILHVGSOQSGORLSVYMEAGKVTTSVSDAGSVT	839
Dd	1549	VLAHSVLLGPPEFKLVFSIRPRSLTGILIHIGSQPOKHLCVYLBNQKVTASMDSGAGGTST	1608
Qy	840	SITPKQOSICDQOMSVANSIKORILHL	866
Dd	1609	SITPKQOSICDQOMSVAVTIKOHILHL	1635

RESULT 2

laminin alpha-chain precursor - human
N:Alternate names: laminin Ab
C:Species: Homo sapiens (man)
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C:Accession: S68960, S65926, S49149, S40150, I53516
R:Richards, A., Al-Imara, L., Pope, F.M.,
Bur, J., Blochem, 238, 813-821, 1996
A:Title: The complete cDNA sequence of laminin alpha-4 and its relationship to the other
A:Reference number: S68960, MUID:96300249, PMID:8706685
A:Accession: S68960
A:Molecule type: mRNA
A:Residues: 1-1816 <R1>
A:Cross-references: UNIPROT:Q16363, UNIPROT:Q14731, EMBL:X91171, NID:g1212962, PIDN:CAA6
A:Experimental source: tissue: tissue type heart
R:Riivaniemi, A., Salnio, K., Sariola, H., Tyysvaasen, K.
FEBS Lett. 365, 183-188, 1995
A:Title: Primary structure and expression of a novel human laminin alpha-4 chain.
A:Reference number: I53516, MUID:95300971, PMID:7781776
A:Accession: S65926
A:Molecule type: mRNA
A:Residues: 1-142, 'P', 144-177, 'P', 179-490, 'Y', 492-1056, 'P', 1058-1816 <R1V>
A:Cross-references: EMBL:S78569, NID:g1042081, PIDN:AB34635.1, PID:g1042082
R:Richards, A.J., Al-Imara, L., Carter, N., Levarsha, M., Lloyd, J.C., Pope, F.M.
submitted to the EMBL Data library, December 1993
A:Description: Localisation of the gene (LAMA4) to chromosome 6q21 and isolation of a pa
A:Reference number: S49149
A:Accession: S49149
A:Molecule type: mRNA
A:Residues: 236-1816 <R1>
A:Cross-references: EMBL:X76939, NID:g509805, PIDN:CAA54258.1, PID:g509806
R:Richards, A.J., Al-Imara, L., Carter, N., Lloyd, J.C., Pope, F.M.
submitted to the EMBL Data library, February 1993
A:Description: Isolation of a partial cDNA encoding a protein homologous to laminin A. A
A:Reference number: S40150
A:Accession: S40150
A:Molecule type: mRNA
A:Residues: 1403-1541, 'S', 1543-1816 <R1>
A:Cross-references: EMBL:X70904, NID:g437804, PIDN:CAA50261.1, PID:g437805

C:Genetics:
A:Gene: GDB:LAMA4; LAMA3
A:Cross-references: GDB:203904; OMIM:600133
A:Map position: 6q21-6q21
C:Complex: laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
A:Description:
A:Interact: Interact with cells and with other basement membrane proteins to promote C5superfamily: laminin alpha-4 chain; laminin G repeat homology; laminin-type Egf-like R C:Keywords: basement membrane; cell binding; coiled coil; extracellular matrix; glycoprotein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-1816/Product: laminin alpha-4 chain #status predicted <MAT>
F:82-129/Domain: laminin-type EGF-like homology <LE1>
F:153-164/Domain: laminin-type EGF-like homology <LE2>
F:187-228/Domain: laminin-type EGF-like homology <LE3>
F:241-265/Domain: laminin-type EGF-like homology #status atypical <LE4>
F:717-719/Region: cell attachment (R-G-D) motif
F:862-1031/Domain: laminin G repeat homology <LG1>
F:1068-1223/Domain: laminin G repeat homology <LG2>
F:1252-1398/Domain: laminin G repeat homology <LG3>
F:1488-1636/Domain: laminin G repeat homology <LG4>
F:1665-1816/Domain: laminin G repeat homology <LG5>
F:1108, 215, 308, 458, 524, 550, 571, 574, 631, 633, 735, 751, 754, 780, 803, 1086, 1281, 1359, 1411/Bindin
F:266, 269/Dsulfide bonds: interchain #status predicted

Query Match

Best Local Similarity 33.2%; Pred. No. 3.6e-74;
Matches 310; Conservative 161; Mismatches 372; Indels 90; Gaps 27

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0Y 1 MRPNKSGVETRLNPNLEDDIKGYTSLFLP-----QRDLNENGSTBEMPMWYLGNDKASK 56
Db 829 MMEFGQSAVEHASTSHDDLKAFSLSLYMKPPRYKRELTE--TADQFLYLSLSSKNACK 885
0Y 57 DYIGMAVVDGQJTCVNIJGDBREAEVQJDOVLTESBSQEAWMRYKFORIYQFANKLTYKE 116
Db 886 EYMGLAIKNDLVVYVNIJTKDVEIPLDS--KPVSSWPAFYSIKIERVGHGKVFILTP 943
0Y 117 ATSKRPAPAVYDLEGGSSNTLNLDBEDAVFYVGGYPRPBELPSRLRPPRYGCIELDD 176
Db 944 SLSTAEKRLPKGEPFGSDSLDLDBEDVIFYGVSPNFKPLPTSLNLGQFGCLBLAT 1003
0Y 177 LNEVVLISYNEKTYNLTTEVEBCEPRK-----EESBDKNYFEGTGVA--RIPTQPN--A 227
Db 1004 LNDVIGLNYNPKHLYNMDPSTSVPCARDKLAFQTSRAASYFFPDSGAVYAVRDITRRKFG 1063
0Y 228 PFPNFQIOTQTYDRCGLLFPARENODNFIISNIEDGNLMRY-----KLNSEPKKXGI 280
Db 1064 QVTFPDIIEVRTPANGIILLMVNGSMFRLKEMRGYLAVFYDDPFGSGRHYLBPTLKA-- 1122
0Y 281 RDTLNDGKHSILTTIGKLOKMMINVERSVRI---EGELPDSYTYLGGIP-----I 331
Db 1123 --QINDAKYHEIST-IYHNDKMKLLVDRRHVYSMDNEKKKIPTDIIYIGAPBEIIOSR 1179
0Y 332 AIRERFNIISTPAPQCKMNL---KKTSGVYRLNDTVGVTKKCSBDMVLVITASFSRGOM 388
Db 1180 ALRAHLPLDI-NFGCKMKGFQFKCDENLLEQTETLIVGVGCPEDSILSRAYFN--GQS 1236
0Y 389 SFTMLD-VPSIDRQQLSFGQTPQPSGTLNHOQRTSSLVLTLEDGHIELSTBNSNPIR 447
Db 1237 FIASIQKISFPDGEEGGNFRTLOPNGLIFYYASGSUVFISISLNGVIMDVK--GIKVO 1294
0Y 448 KSPSTYMDGLLHHYSVIDSITSGLR--LLID-DQVLRNRQRLPSPSNQAQSLR--LGS-- 499
Db 1295 SVDMQYNDGLSHF--VLSVSPTREYELIVDKSRGSGNPKRGKIEQQAQBKKRYFEGGSP 1352
0Y 500 -----GHPEGCTISAVLVORFSQSPYVLDLASKSTKQDASIGGCSLNKPPMLFKSPKRF 554
Db 1353 ISAGYANFTGICISNAVETFRVDREVEDFORYTEKVTSLYBCEPIESSPLFLMKKAKNL 1412
0Y 555 NKGRIFPNVNO--LMQDAPQATRSTEAMQDGRSCPLNT-----KASHRLQOF 600
Db 1413 SKPQASQNKKGKSKDAP-----SMDPVALKLPERKNTPRNSCHLSNSPRALIEAHQY 1465
0Y 601 GDSPTSHLLKLQGBLLKPSRQSLDIQTTSPKGLVFEYAGTKD--SFLALVYVADGRVVA 658

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Db      1466 GGTANRQREPEHLKQDREGAKSOSIRARTSSHGMIFFYVDQDENDMTLFLAHGRLYVM 1525
Qy      659 LGAGKKLRKSRERHDKMTHTVVPGLNGKARLVVDGIRPAQEGSI--PQNSTISPREQV 717
Db      1526 FNVGHKKLKRISQEKYNDGLMHVDVIFRERSGGLVLDGLRVLEESLPTEATWIKIGPFI 1585
Qy      718 YLGLPLSRKPSLPQ-----HSPVGLADPQLNKGKLDPSARGVSPCLDGLSLEKGIYFS 773
Db      1586 YLDGVAPEGKAVKAVQVINSIYFSGCLSNQLQNGASTSASQTSVTECFEGEMETGIYFS 1645
Qy      774 QGGGHTLVANSVSLPELKTFSIRPSRLTGVLIVHVSQSGORLSVYMEAGKVTTSVSD 833
Db      1646 TBGGYVVLDSFNIQLKFEIAPFRPRSSSGTLVHGSVNGEYLVAMKMGQVIVKKNNG 1705
Qy      834 AGGSVTSITPKQSLCDGQMSHVAVSIRKRIHL 866
Db      1706 IRDFTSVTEPKQSLCDGRMHRITVIRDSNVQL 1738

RESULT 3
T10053
laminin alpha 5 chain - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T10053
R/Miner, J.H.; Lewis, R.M.; Sanez, J.R.
submitted to the EMBL Data Library, November 1997
A/Reference number: Z16923
A/Accession: T10053
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-3635 <MIN>
A/Cross-references: UNIPROT:Q61001; EMBL:U37501; NID:G2599231; PID:G2599232
C/Genetics:
A/Gene: lamas
C/Keywords: basement membrane; cell binding; extracellular matrix
F/1888-1939/Domain: laminin-type EGF-like homology <LBS>
F/1942-1970/Domain: EGF homology <EGF>

Query Match      21.1%; Score 948; DB 2; Length 3635;
Best Local Similarity 30.6%; Pred. No. 8.9e-57;
Matches 285; Conservative 167; Mismatches 360; Indels 120; Gaps 37;

Qy      1 MRNKGSGVRLPNDLEDLKGYTSLFLQRPDLRNGG--TEDMFVMTLGNKDAKDY 58
Db      2656 MKEFGSGVRLPRLDIALAAYALFKHIQSPPADPEPKTGDHFLVYMGSRQATGQDY 2715
Qy      59 IGMAVVDGQLTCVYNTLGDRL--BAVQIDQVLTSSSQSAVMDRVKFORITVPKLTNTKKA 117
Db      2716 MGVSRLRQKQVHWYRLKAGPTTISIDENIGEQ-----PAVSIIDTLPQGHNSVTVL- 2768
Qy      118 TSNPKAPAVYDLEGSS-----SNTLNLDPEDAVFYGVYPPDELPRLSPFPYKGCIE 173
Db      2769 -----KQMHKIKGDIIVAGSBSGLNLHDPDVFYVGGYPSNTPPBPRLFPDYLGIE 2822
Qy      174 LDDINENVLSLYNFKTTFNLTTEVEBCRRRKEE-----SDKNYFEGTGARLPTQPNAP 228
Db      2823 METLNEVSLVYNEQTFMLDITAVDKCARSKATGDPMLTGDGYLDSGFAISFEKQ-- 2880
Qy      229 FPN---FLOTITQTVDDGLFLFRANQNFISINLEDNLMRYTLNS-----EPPK- 276
Db      2881 FSNKRRDQELRLVSYNGIIFFLQESQFLCLAVQEGTLVLFYDFGSLKKADFLQPPQA 2940
Qy      277 -----EKGIPTINDGKHSILITIGKQKRMVWNSVRIEGLIFDFTYVYLGIT--- 329
Db      2941 LTAASKAIQVFLAAGNRKRVLV---RYBRATVFSVDQNMU---EMAD--AYVIGVPPR 2992
Qy      330 --PLAIBERNISTPAPQGCCKNIK---KTSGVVLADPTGVTKKCSBDMKLVTPASPSR 384
Db      2993 QLPSTLRLQLP--SGSGVSGIKGKALKGVYDLKRLN--TIGISFGCTADLLVGRTWTFHG 3050
Qy      385 GGGGSPFNLDV--PSTDFQLSFGHQTQPSGTLNLHQRTSSLLVTLIEDHIELSTDSN 443

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Db      3051 HGFPLALPDVAITVWVSGFGRGTQDNNLLYRTSPDGPYQVSLREGHTVLRMNQOE 3110
Qy      444 IPIFKPPTMGLLHHVSIPTSGRLIID--QVLRNQQLPFSNMQ-----QSLRL 497
Db      3111 V---ETQRFADAPFVAVFYSNVTVQVLDQQLVSHKHTTPTMLQLEPSPRLTL 3167
Qy      498 GG-----GHFPGCISNVLYVQFSSPEVLDLASKTKKDAISGCSLKNPPLMFKS 550
Db      3168 GGLPVSGTFNPSGCLSNVFPVQRLRGPRVFDLHQMGSVNVSV--GCT-----PAQLIETS 3222
Qy      551 PKRPNKRIFFNVNQLMDAPQATSTSEAW-----QDGRCLPPLNTKASHRALQF--GDSP 604
Db      3223 RATAQK-----VRRSRQSPQDLACTTPMLPGTIQAVQGGPLPS-----YLQFVGI 3272
Qy      605 TSHLLKLPOELKPKPSQPSLDIQTTPSKGLVYVYAGTKSFLALYADGENVFALAGKR 664
Db      3273 SHNRRLHLSM--LVRFPAASQGLLSTAP-----MSGRSPS--LVLFNHHGFVPAQTEGPGP 3325
Qy      665 KLRLSKERYHDKMHTVVPGLNGKARLVVDGLRA--QEGSLPQNSTISPREQVYL---- 719
Db      3326 RLQVQSRQHSRACQMRHVSYRWGMQQLQLVVDGSSQTMSCALMHRVPRARPPITLSVG 3385
Qy      720 GLPLSRKPKSLP--QHSFVGLARDFOULNSKPLDPSARFVSPCLGSLKGIYFSQGGH 778
Db      3386 GLPASVSSSLPVSVGSGCLKTLQDKQPLRTPTQVGVTPCVSGPLBEGDLPFGSGV 3445
Qy      779 VILANSVSLPELKTFSIRPSRLTGVLIVHVSQSGORLSV--YMEAGKVTTSV---SSDA 834
Db      3446 VTLELPKAKPVPVLEIEMRPLAAGLIFHL-----GQALATPYMQLKVLTEQVLLQAND 3501
Qy      835 GGSVTSITPKQSLCDGQMSHVAVSIRKRIHL 866
Db      3502 AGSFTWVTPYKLCDRMHRVAVIMGDTURL 3533

RESULT 4
S18253
laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C/Accession: S28399; S18253
R/Kinsche-Gullberg, M.; Garrison, K.; Mackrell, A.J.; Fessler, J.H.
EMBO J. 11, 4519-4527, 1992
A/Title: Laminin A chain: expression during Drosophila development and genomic sequence
A/Reference number: S28399; NMID:93049203; PMID:1425386
A/Accession: S28399
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-3712 <KUS>
A/Cross-references: UNIPROT:Q00174; GB:M96388; NID:G157799; PID:AAA28662.1; PID:G15780
R/Garrison, K.; Mackrell, A.J.; Fessler, J.H.
J. Biol. Chem. 266, 22899-22904, 1991
A/Title: Drosophila laminin A chain sequence, interspecies comparison, and domain struc
A/Reference number: S18253; NMID:92078147; PMID:1744083
A/Accession: S18253
A/Molecule type: mRNA
A/Residues: 1762-3712 <GAR>
A/Cross-references: EMBL:M75882; NID:G157797; PID:AAA28661.1; PID:G157798
C/Genetics:
A/Gene: FlyBase:lama
A/Cross-references: FlyBase:FBgn0002526
C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
C/Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular
F/273-330/Domain: laminin-type EGF-like homology <LEG>
F/333-400/Domain: laminin-type EGF-like homology <LEG2>
F/541-584/Domain: laminin-type EGF-like homology <LEG3>
F/1176-2115/Domain: III <DOM3>
F/1176-1806/Domain: laminin-type EGF-like homology #status atypical <LE1>
F/1809-1856/Domain: laminin-type EGF-like homology <LE2>
F/1859-1914/Domain: laminin-type EGF-like homology <LE3>
F/1917-1967/Domain: laminin-type EGF-like homology <LE4>
F/1970-2014/Domain: laminin-type EGF-like homology <LE5>

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QY 498 GGCH-----PEGCISNVLVORFSGSPVFLVLAASKSTKDAISGCSL 539
 DB 3184 DQSNPDASFLSAFPGKSGEFTVGCIGDVTL-----NGKLDLPAN-SKIKELISLNGCSL 3237
 QY 540 ---NKPEFLMLFKSPKRFKRGRI FVNVQIMODAPQATST-----EAMQDGRSCL 586
 DB 3238 SDDENISTTTTAAKPTDDSDVAVLPIDEEBSSTTTTTTTTTTEPTEBPAPADGHCSTL 3297
 QY 587 P--PLATKASHRLAQGDSTSHLLKLPOELLKPSQSFLDQTSPPKLVYAGTK-D 643
 DB 3298 PEDPMVQFEDAEFGNSQOYSRIEYDILPEALDKSGEFTFKRPTSDNIIPIANTKRT 3357
 QY 644 SFPLAVYADGRVVEALGAGGKRLRSKERYHDGKMTVVGANGKARLVV-DGLRAOE 702
 DB 3358 DHIAVLEHGRVVFYTDGSGQVYIKSDKSIDGRMHTIKVSRGSAHLIVDNGSYESE 3417
 QY 703 GSLPGN-STISPREQVTLG---LPLSRKPKSL---PQHSFVGCILDFOLNSKPLDPSPAR 755
 DB 3418 GAANNQMBDLIETQPPFYVGVADLAGFARNLVVGRSQSGCIKDFKNGKSLDN-GKE 3476
 QY 756 FGVSPLCGSLERGIYFSGGGHVLANSVSLPELKLTFSLRSLTGLVLIHVGSQSG 815
 DB 3477 FGTEOCQSFS-BEGMYFGKDGAYAIQDYEVGLTGLLEVEMRPMKNGILFEGVGLV--E 3533
 QY 816 RLSTVYBAGKVTTSVSDAGSVTSITP--KQSLCDGQMSVAVSIKORIL 864
 DB 3534 YITVEFVNGSITKTVESGGBELMHHPDIENQYCDGQMSFKISKRNLL 3584

RESULT 6

T37316
 probable laminin alpha chain - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T37316
 R/Joh, K.; Zhu, K.; Hedgecock, E.M.; Inoue, T.; Horii, K.
 submitted to the EMBL data library, August 1998
 A/Description: Laminin alpha chain gene in the nematode C. elegans.
 A/Reference number: Z21681
 A/Accession: T37316
 A/Molecule type: DNA
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A:Cross-references: UNIPROT:P91904; EMBL:AB016806; PDB:BAJ2347.1
 A:Experimental source: strain N2
 C:Gene: epi-1
 A:Map position: IV
 A:Introns: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 3
 C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 12.9%; Score 579.5; DB 2; Length 3704;
 Best Local Similarity 23.7%; Pred. No. 4.9e-31;
 Matches 237; Conservative 155; Mismatches 388; Indels 215; Gaps 40;
 QY 3 FNGKSGVRLPNDLBDLKYSLSLFLQRPDLRENGTGEDMFVYIGKDA-----54
 DB 2696 FERKSSLDLNIIPORVTRSAHADISFYRTE-QEHS-----IPLFGNEETAVGSRAPV 2748
 QY 55 SKYIIGAVVDGQLTCVYNIGDRBAVQIDOVLTSSQSAWMDRVFQCIYQPAKLANTY 114
 DB 2749 TADYVALEIYEGPKITVDJADPAVAKD-----TPVNGILMRRLIERI-----GKT 2797
 QY 115 KEATSNKPKAPAVYDLE---GGSSNTLNLNDPREDAVFYVGGYPPDELPRLRPPYKGC 171
 DB 2798 VSTYTLAKPNSVETAEKSSVAGNGKSVTLNNOQISRLFVGGVPTSAISIDLYNRDPVD 2857
 QY 172 IEDDLLENVLSLYNFTTNLNTTEVEPRKREEDKAY--FEGGYA-----R 220
 DB 2858 IESLKHGEPICIGMNSREKNTVNGAKKPKITDNDABELVSLDGGYTSYKPSHMPR 2917
 QY 221 IPIQNPAPFNFIQTQITVDRLGLPAENQDNPISINIDGMVYKXLSNPBPKKGI 280

DB 2918 KATKISLSEFLT-----SPHGLFVYGKDFMALBELSDGKVLVDLGS-----GV 2964
 QY 281 RDTI-----NGKHSILITIGKIQKRMIVNNSVNIIEGI-----EDFSF---YVLG 327
 DB 2965 GQWTESSNVNDGKMT--VSTVREKHVKIMIDGETEVLGEGVGPCKDSMSTEBFLYLG 3022
 QY 328 GPIAIRRBNISTPAFQCGMKNLKKTSGVRLND---TVGVKKCSMDKLVRTASF-S 383
 DB 3023 GTPSGLSVTTI--VLRLCISKVLGSDNVLDLSHAKGVRSQC--PLHSRTVYSFLS 3078
 QY 384 RGGQMSFTNLDPVSTDRFQLSFEGPOT--FQPSGTLNLHQTSTSLVTL-EDGHELEST 439
 DB 3079 DRTTASFNNAATERSED-VSGTFKFKTRSIROPSSLFTVNDDEDSVLSVINEGDLITVS 3137
 QY 440 RD--SNIPFKSPGTYMDGLHVSISTPSGLRLIDQVLRNRRLSFSMAQSL 497
 DB 3138 GEDIAETLELAASP---DEKMHVSTIRKTYIIRIDADD-----SFSNVARAKHA 3183
 QY 498 GGCH-----PEGCISNVLVORFSGSPVFLVLAASKSTKDAISGCSL 539
 DB 3184 DQSNPDASFLSAFPGKSGEFTVGCIGDVTL-----NGKLDLPAN-SKIKELISLNGCSL 3237
 QY 540 N-----KPPFLML 547
 DB 3238 SDDENISTTTTAAKPTDDSDVAVLPIDEEBSSTTTTTTTTTTEPTEBPAPADGHCSTL 3297
 QY 548 -----FKSPKRNKGRIFVNVQIMODAPQATSTEAQDGRSCLP--PLNTQASHR 586
 DB 3298 NAKRBSSTPEEPEDHP-----ESVLSAPRDPGHCSPLEDPVQFEDAE 3341
 QY 597 ALQFGDSPSHLLKLPOELLKPSQSFLDQTSPPKLVYAGTK-DSPLAVYADGRV 655
 DB 3342 GNFPSQOYSRIEYDILPEALDKSGEFTFKRPTSDNIIPIANTKRTDHIAVLEHGRV 3401
 QY 656 VFALGAGKRLRSKERYHDGKMTVVGANGKARLVV-DGLRAQSGSLPGN-STISF 713
 DB 3402 VFYTDGSGQVYIKSDKSIDGRMHTIKVSRGSAHLIVDNGSYSEGAANNQMBDLIET 3461
 QY 714 REQVTLG---LPLSRKPKSL---PQHSFVGCILDFOLNSKPLDPSPARFVSGSLG 767
 DB 3462 QPFFYVGVADLAGFARNLVVGRSQSGCIKDFKNGKSLDN-GKEFTEOCQSFS-E 3519
 QY 768 KGIYFSGGGHVLANSVSLPELKLTFSLRSLTGLVLIHVGSQSGORLSTVYBAGKVT 827
 DB 3520 PGMYFGKDGAYAIQDYEVGLTGLLEVEMRPMKNGILFEGVGLV--EYITVEFVNGS 3577
 QY 828 TVSSSDAGSVTSITP--KQSLCDGQMSVAVSIKORIL 864
 DB 3578 TVYSSGGBELMHHPDIENQYCDGQMSFKISKRNLL 3616

RESULT 7

MMMSA
 laminin alpha-1 chain precursor - mouse
 N/Alternate names: laminin chain A1
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
 C/Accession: A31771; A30449; S00624; A30450; S08895; S02678; S01790; A30451; S14670
 J/Sasaki, M.; Kleinman, H.K.; Huber, H.; Deutzmann, R.; Yamada, Y.
 J. Biol. Chem. 263, 16536-16544, 1988
 A/Title: Laminin, a multidomain protein. The A chain has a unique globular domain and h
 A/Reference number: A31771; M01D:89034134; EMD:3182802
 A/Accession: A31771
 A/Molecule type: mRNA
 A:Residues: 1-3084 <SAS>
 A:Cross-references: UNIPROT:P91937; EMBL:J04064; NID:G309419; PDB:AAA39410.1; PDB:G309
 A/Molecule type: protein
 A:Residues: 183-195;570-571,'A',573-586;596-612,'X',614-617,'EMK',630-646;1217-1222,'YF
 2486;2624-2639;2818-2843;3009-3033,'V',3035 <SAS>
 R/Harti, L.; Oberhaeumer, I.; Deutzmann, R.
 Eur. J. Biochem. 173, 629-635, 1988
 A/Title: The N terminus of laminin A chain is homologous to the B chains.

A:Reference number: S00624; MWID:88225080; PMID:3267223
A:Accession: S00624
A:Molecule type: mRNA
A:Residues: 1-208, 'T', 210-334 <HAR>
A:Cross-references: EMBL:X0737; NID:952857; PIDN:CAA30561.1; PID:952858
A:Accession: A30450
A:Molecule type: protein
A:Residues: 311-335, 'N', 337-339, 630-642, 'D', 644, 692-734, 737-748, 'X', 750-760, 'G', 762-763, 3-1389, 1449-1459 <H2>
A:Note: the sequence from Fig. 7 is inconsistent with that from Fig. 5 in having 209-116
R:Manu, J. Biochem. 178, 71-80, 1988
A:Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th
A:Reference number: S08895; MWID:89078415; PMID:2462498
A:Accession: S08895
A:Molecule type: protein
A:Residues: 153-169 <MAN>
R:Fujiwara, S.; Shikai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
Biochem. J. 252, 453-461, 1988
A:Title: Structure and distribution of N-linked oligosaccharide chains on various domain
A:Reference number: S02678; MWID:88326259; PMID:2458101
A:Accession: S02678
A:Molecule type: protein
A:Residues: 630-642, 'D', 644, 2690-2704 <FUS>
R:Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberhauser, I.; Hartl, L.
Eur. J. Biochem. 177, 35-45, 1988
A:Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te
A:Accession: S01790; MWID:89030693; PMID:3181157
A:Reference number: S01790
A:Molecule type: mRNA
A:Residues: 2538-3084 <DEU>
A:Cross-references: EMBL:X13459; NID:955499; PIDN:CAA31807.1; PID:9818014
A:Accession: A30451
A:Molecule type: protein
A:Residues: 1911-1997, 1997-2006, 2033-2045, 'X', 2047-2054, 'X', 2056-2066, 'X', 2068-2105, 2120
470; 2487-2499; 2502-2525, 2528-2557, 2561-2591, 'X', 2593-2594, 2600-2610, 2616-2645, 2648-2655;
93; 2998-3005, 'A', 3007-3033, 'V', 3035, 3068-3083 <BE2>
A:Note: 2256-Val was also found
R:Olson, D.; Nagayoshi, T.; Pazio, M.; Peltonen, J.; Uakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A:Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A:Reference number: A34961; MWID:89280632; PMID:2733383
A:Accession: S14670
A:Molecule type: protein
A:Residues: 2424-2436; 2440-2451; 2461-2467; 2487-2525; 2550-2557; 2561-2593; 2600-2610; 2616-2
-2942, 'T', 2944-2964; 2969-2976; 2980-2993; 2998-3000, 'I', 3002-3018, 'V', 3020-3034; 3068-3083
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C:Function:
A:Description: interact with cells and with other basement membrane proteins to promote
C:Superfamily: laminin alpha-1 chain; laminin & repeat homology; laminin-type EGF-like h
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-3084/Product: laminin alpha-1 chain #status predicted <MAT>
F:25-277/Domain: VI <DOM6>
F:227-333/Domain: laminin-type EGF-like homology <LE01>
F:278-519/Domain: V <DOM5>
F:324-401/Domain: laminin-type EGF-like homology <LE02>
F:404-458/Domain: laminin-type EGF-like homology <LE03>
F:461-507/Domain: laminin-type EGF-like homology <LE04>
F:510-519/Domain: laminin-type EGF-like homology <LE05>
F:520-715/Domain: IVD <DO4B>
F:716-1166/Domain: IIID <DO3B>
F:716-746/Domain: laminin-type EGF-like homology #status atypical <LE06>
F:749-795/Domain: laminin-type EGF-like homology <LE07>
F:798-853/Domain: laminin-type EGF-like homology <LE08>
F:830-834/Region: cell adhesion #status predicted
F:856-906/Domain: laminin-type EGF-like homology <LE09>
F:909-955/Domain: laminin-type EGF-like homology <LE10>
F:958-1002/Domain: laminin-type EGF-like homology <LE11>
F:1005-1048/Domain: laminin-type EGF-like homology <LE12>
F:1051-1094/Domain: laminin-type EGF-like homology <LE13>
F:1097-1116/Domain: laminin-type EGF-like homology #status atypical <LE14>
F:1118-1154/Domain: laminin-type EGF-like homology #status atypical <LE15>

[illegible]

Db 2695 -----GELPPEPPTLPQPELCAVD-----TAPGVYGAH---QFGLSQNSHLVLEPQ 2739
 Qy 615 ELKPSQPSLDIQTSPPKLVYAGTKD--SFALVYADGRVVPALGAGKGLRLRSKE 672
 Db 2740 SDVRKRLQVQLSIRTFSSGLIYVHAQNMQDVATQLQGRHFMFDLKGRTKXSHPA 2799
 Qy 673 RYHDKKHTVFPGLNGKALVVDGLAQSGLPQN-STISPREQVLT-GLPLSRKPKSL 730
 Db 2800 LLSDKKHTVETRYRKAKMTVDQSSPSVTVGNATLIDVERKTLGLPSHYRANKI 2859
 Qy 731 P--QHSFVGLRDFOLNSKEPLDS--PSAPGVSPCLGSLKGIYPSQGGHVLANSVS 786
 Db 2860 GTTHSIPACIGIMVNGQQLDKDRPLASAVDRCVVA-QEGTFEFGSVYALVKGK 2918
 Qy 787 LGELKLTFSIRPSRLTGVLIHVSQSGQLSYMEAGKTTVSISDAGSVTSITPK-- 844
 Db 2919 VRDLNLTTEFRRTSKRGVLLGISAKVDAILGEIVDGKVLPHVNGAGRTIATYQPRAA 2978
 Qy 845 QSLCDGQWHSV-AVSIKORIL 864
 Db 2979 RALCDGKMTLQAHKSKHRIV 2999

RESULT 8

MATHUM
 laminin alpha-2 chain - human (fragment)
 N/Alternate names: laminin W chain; merosin heavy chain
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1991 #sequence, revision 21-Aug-1998 #text_change 09-Jul-2004
 C/Accession: PX0082; A35899; A38970; S14461
 R/Hori, H.; Kanamori, T.; Mizuta, T.; Yamaguchi, N.; Liu, Y.; Nagai, Y.
 J. Biochem. 116, 1212-1219, 1994
 A>Title: Human laminin W chain: Epitope analysis of its monoclonal antibodies by immunoblot
 A/Reference number: PX0082; MUID:95221315; PMID:753762
 A/Accession: PX0082
 A/Molecule type: mRNA
 A/Residues: 1-1751 <HOR>
 A/Cross-references: UNIPROT:P24043
 A/Experimental source: Placenta
 R/Shiriy, K.; Lelvo, I.; Argyres, W.S.; Ruoslahti, E.; Engvall, E.
 Proc. Natl. Acad. Sci. U.S.A. 87, 3264-3268, 1990
 A>Title: Merosin, a tissue-specific basement membrane protein, is a laminin-like protein
 A/Reference number: A35899; MUID:90238994; PMID:2185464
 A/Accession: A35899
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 'V', 623-1751 <EHR1>
 A/Cross-references: EMBL:M59832
 A/Accession: A38970
 A/Molecule type: protein
 A/Residues: 1368-1384, 1389-1406, 1593-1607 <EHR2>
 A/Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in lacking 1599-V
 R/Shiriy, K.; Lelvo, I.; Argyres, S.W.; Ruoslahti, E.; Engvall, E.
 Submitted to the EMBL Data Library, December 1990
 A/Description: The tissue-specific basement membrane protein merosin is a laminin-like protein
 A/Reference number: S14461
 A/Accession: S14461
 A/Molecule type: mRNA
 A/Residues: 'V', 623-1264, 'R', 1266-1751 <LEI>
 A/Cross-references: EMBL:M59832; NID:G187520; PIDN:AA63215.1; PID:G187521
 C/Comment: This protein is a prominent component of the basement membrane that mediates cell-cell interactions
 C/Genetics:
 A/Gene: GDB:LAMA2; LAMM
 A/Cross-references: GDB:133362; OMIM:156225
 A/Map position: 6q22-6q23
 C/Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
 C/Function:
 A/Description: Interact with cells and with other basement membrane proteins to promote cell adhesion
 C/Superfamily: laminin alpha-1 chain; laminin G repeat; laminin-type EGF-like domain
 C/Keywords: basement membrane; calcium binding; coiled coil; extracellular matrix; glycoprotein
 F/21-58/Domain: laminin-type EGF-like homology #status atypical <LE01>
 F/61-107/Domain: laminin-type EGF-like homology <LE02>
 F/110-165/Domain: laminin-type EGF-like homology <LE03>

I/168-212/Domain: laminin-type EGF-like homology <LE04>
 P/527-567, 1071-1300/Region: 3DM and 2D9 binding
 P/811-972/Domain: laminin G repeat homology <LG1>
 P/1005-1165/Domain: laminin G repeat homology <LG2>
 P/1191-1354/Domain: laminin G repeat homology <LG3>
 P/1430-1578/Domain: laminin G repeat homology <LG4>
 P/1605-1751/Domain: laminin G repeat homology <LG5>
 P/120, 238, 255, 341, 451, 542, 557, 561, 658, 669, 686, 767, 881, 1001, 1076, 1119, 1192, 1199, 1289, 1350
 Query Match 11.8%, Score 531.5, DB 1, Length 1751,
 Best Local Similarity 24.1%, Pred. No. 3, 1e-28;
 Matches 225; Conservative 161; Mismatches 360; Indels 187; Gaps 44;
 43 DMFVTLKNDKNDK--DYIGMAVVDGQLTCVNVLGPRLREAVQV--DQVLTSSQGEAVMDR 99
 Db 821 DNLFFYLQ--SKAFIDPLAIEKRRKVSGLMVGSGVGRVEYDPLTIDISTYRIVASR 877
 Qy 100 VKFQRIYQPAKINLTREKATSNKPKA--PAVVDLEGSSNTLINDPEDAVYGVYPPD 156
 Db 878 TGRNGTISVAL-----DGPKASIVPSTHSTSPPGYTLIDVD-ANAMLVFGGLTGK 928
 Qy 157 FELPSRLRPPPYKCIETLDLNNVSLNFKTTFNLTTEVPCRRKESDKN--YF 213
 Db 929 LKKADAVRVTFTFGCGKRTYFDNKPICLNNFRE--KSGDCKGTVSPQVEDSEGTIOF 984
 Qy 214 EGTGYARIPQPAAPPNPQIT-----QTVDRGLLFPANOD--NPSINIDGNLMVR 267
 Db 985 DGEGLYLV--SRPLRWPN--ISTVMFKRFTSSGALLMTYATRLDRFMSVELTDGHLKVS 1042
 Qy 268 YKNSBPPEKGIKIDT-----NDGKHSHLITGLQKRWVNVNRSVRIGEIFDFS 322
 Db 1043 YDLGS-----GMAVSVMNNDGKMKK--FTLSHIOQANISYIDIDNQNENATSS 1094
 Qy 323 T-----YLLGIP--IAIRRFNISTPAPQCKNL--KRTSGVVRAND 362
 Db 1095 SGNNFGDLKADDKITFGGLPTLRNLSMKARPEVNLKTKSGCLXIDISRTPNILSSPD 1154
 Qy 363 TVGVYTKKSGEDMKLVYTAASRSG--QMSFTNLDVSTDRFQSLRFQGTQPSGTL-- 417
 Db 1155 YGVATYGCQ--LENVYTVSPKPKGPELSPVPIDVGT--EINLSTNREGDITLLGS 1208
 Qy 418 -----NHQTRSSLLVLTEDGIR--LST--RDSNPYFSPGTYMGLLHVS 462
 Db 1209 GGTAPAPRRKRRKRTGQAYVYIILNRGLVHLSTGARTRKTYIRREPNI.FHGRHSVA 1268
 Qy 463 VISDTSGRLLLIDQVLRNRQLPSFSNQ--QSLRLGG-----HFGCISN 508
 Db 1269 V-ERTGIFVYQVDERRMYQNLTVEQPLEVKTLFVGAPPEFQSPPLRNI.PPFGCIWN 1327
 Qy 509 VLVQPSQSPRYVDLASKTKKQDASLGGCSLNK-----PPPLML-----FKS 550
 Db 1328 LVINSVP-----MDFARPSPFNKADIGRCHQGRDEBDGAAAEIVTOPEPVPAPPT 1382
 Qy 551 PKRPNKGRIFNVNQLQDAPQATRSTEAQDGRSCPLPLNTKASHALQSPDSTHLL 610
 Db 1383 P-----TPVLTGHCALAESSEPLLIG-----SKQGLSRNSHIAI 1417
 Qy 611 KLPELILKPSQPSLDIQTSPPKLVYAG--TKDSFLALVYADGRVVA--LGAGKGL 666
 Db 1418 APDPTVNRKRLTLELVRTEASGLLFYMARINHADPAVQLANGLPYFEGYDGSDDTH 1477
 Qy 667 RLRSKRRYHDKKHTVFPGLNGKALVVDGLAQSGLPQNSTISPRE-----QVY 718
 Db 1478 MIPTK--INDGQNHKKIKMSKQEGILYVDG-----ASNNTISPKKADILDVGMLY 1527
 Qy 719 L-GLPLSRKPKSL--POHSFVGLRDFOLNSKE--LDSPEARGVSPCLGSLKGIYFS 773
 Db 1528 VGLPLPNTYTRRIGPTTYISIDGCVRYLMAHAPADLQPTSSHYGTCFANA-QRGTYF- 1585
 Qy 774 QGGGHVILANSVSLGELKLTFSIRPSRLTGVLIHVSQSGQLSYMEAGKTTVSISD 833
 Db 1586 DGTGPAKAVAGFVAGDLIVFEFFRTTGTGVLGISQMDMGIEMLIDKLMFHVNDG 1645

QY 834 AG--GSVSTITPKQSLCDGQWHSV-AVSTKORI 863
 DB 1646 AGRFAYVDAGVPGHLCDSQMHKVTANKIKHRI 1678

RESULT 9

114458 laminin alpha-1 chain precursor - human
 C|Species: Homo sapiens (man)
 C|Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #ext_change 09-Jul-2004
 C|Accession: S14458; S14663; A34961
 R|Haaparaanta, T.; Uitto, J.; Ruoslahti, E.; Engvall, E.
 Matrix 11, 151-160, 1991
 A|Title: Molecular cloning of the cDNA encoding human laminin A chain.
 A|Reference number: S14458; MUID:91333420; PMID:1714537
 A|Accession: S14458
 A|Status: not compared with conceptual translation
 A|Molecule type: mRNA
 A|Residues: 1-3075 <HAA>
 A|Cross-references: UNIPROT:P25391
 R|Nielsen, M.; Vuolteenaho, R.; Booc-Handford, R.; Kallunki, P.; Tryggvason, K.
 Biochem. J. 276, 369-379, 1991
 A|Title: Primary structure of the human laminin A chain. Limited expression in human tis
 A|Reference number: S14663; MUID:91264789; PMID:2049067
 A|Accession: S14663
 A|Molecule type: mRNA
 A|Residues: 1-227, 'RE', 230-251, 'MLP', 255-418, 'E', 420-518, 'L', 520-1022, 'V', 1024-1074, 'V',
 A|Cross-references: EMBL:X58531; NID:934225; PID:CA41418.1; PID:934226
 R|Olson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
 Lab. Invest. 60, 772-782, 1989
 A|Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
 A|Reference number: A34961; MUID:89280632; PMID:2733383
 A|Accession: A34961
 A|Status: not compared with conceptual translation
 A|Molecule type: mRNA
 A|Residues: 'W', 2397-2745, 'L', 2747-3053, 'L', 3055-3072, 'PSG', 'OLS>
 A|Note: the authors translated the codon AGA for residue 2692 as Pro
 C|Genetics:
 A|Gene: GDB:LAMA1; LAMA
 A|Cross-references: GDB:120135; OMIM:150320
 A|Map position: 18p11.32-18p11.22
 C|Superfamily: laminin alpha-1 chain, laminin G repeat homology; laminin-type EGF-like h
 F|1-17/Domain: signal sequence #calcium binding; cell binding; coiled coil; disulfide bon
 F|18-3075/Product: laminin alpha-1 chain #status predicted <MAT>
 F|18-269/Domain: VI <DOM6>
 F|18-269/Domain: V <DOM5>
 F|270-516/Domain: V <DOM5>
 F|270-324/Domain: laminin-type EGF-like homology <LE1>
 F|327-394/Domain: laminin-type EGF-like homology <LE2>
 F|397-451/Domain: laminin-type EGF-like homology <LE3>
 F|454-500/Domain: laminin-type EGF-like homology <LE4>
 F|503-512/Domain: laminin-type EGF-like homology #status atypical <LE5>
 F|517-708/Domain: IYB <DOA8>
 F|709-1159/Domain: IYB <DOA8>
 F|709-739/Domain: laminin-type EGF-like homology #status atypical <LE6>
 F|742-788/Domain: laminin-type EGF-like homology <LE7>
 F|791-846/Domain: laminin-type EGF-like homology <LE8>
 F|849-899/Domain: laminin-type EGF-like homology <LE9>
 F|902-948/Domain: laminin-type EGF-like homology <LE10>
 F|951-995/Domain: laminin-type EGF-like homology <LE11>
 F|998-1041/Domain: laminin-type EGF-like homology <LE12>
 F|1044-1087/Domain: laminin-type EGF-like homology <LE13>
 F|1090-1109/Domain: laminin-type EGF-like homology #status atypical <LE14>
 F|1111-1147/Domain: laminin-type EGF-like homology #status atypical <LE15>
 F|1150-1159/Domain: laminin-type EGF-like homology #status atypical <LE16>
 F|1160-1361/Domain: IYA <DOA4>
 F|1362-1553/Domain: IYA <DOA4>
 F|1362-1553/Domain: laminin-type EGF-like homology #status atypical <LE17>
 F|1403-1449/Domain: laminin-type EGF-like homology <LE18>
 F|1452-1506/Domain: laminin-type EGF-like homology <LE19>
 F|1509-1553/Domain: laminin-type EGF-like homology <LE20>
 F|1554-2125/Domain: I/YI, heptad repeats <DOM2>
 F|2116-2120/Region: cell adhesion #status predicted

F|2126-3075/Domain: G <DOM>
 F|2142-2300/Domain: laminin G repeat homology <LG1>
 F|2329-2484/Domain: laminin G repeat homology <LG2>
 F|2510-2676/Domain: laminin G repeat homology <LG3>
 F|2534-2536/Region: cell attachment (R-G-D) motif
 F|2739-2888/Domain: laminin G repeat homology <LG4>
 F|2916-3073/Domain: laminin G repeat homology <LG5>
 F|318,164,555,665,763,801,838,926,952,1045,1407,1579,1596,1678,1689,1698,1717,1804,1894,1
 rate (Asn) (covalent) #status predicted
 F|297-305/Disulfide bonds: #status predicted

Query Match 11.8%; Score 529.5; DB 2; Length 3075;
 Best Local Similarity 22.4%; Pred. No. 1,1e-27;
 Matches 211; Conservative 175; Mismatches 403; Indels 155; Gaps 36;

7 SCGEVRLPNDLEDEGY-----TSLSLFQRPDLRENGSTEDMFVYLGKPKAS 55
 DB 2114 ASIKYAVGADRDICAIYQPOISSTYNTLTIAVKTQEP-----DNLFYLGSSIRAS 2164
 QY 56 KDYIGMAVVDGQLTCVNLGDBAEVQIDQVLTSESQEAVMWRVKFQRIYQPAKLN--Y 113
 DB 2165 -DFLAVEMRRGRVAFELMDLGSSTRLBPDPDIDNRWHSI-----HVAREFGNIGSL 2216
 QY 114 TTEATSNPKAPAVVDLEGSSNTL-LNLDBEDAFVYGYVPDPELRSRLRPFYKKCI 172
 DB 2217 VEMSSNQ-KSPETKTSKSPGTANVLVN--NSTLMFVGJGGQYKSPAVKVFHKQCL 2272
 QY 173 ELDDLENVLSYNFKTFFNLNTTEV-PCR-----RRKEESDKYFEGTGARIPTQDNA 227
 DB 2273 GSAFLNGSIGLWNY-----IREBKCKCPSSQNEBDSHFHDSGYSVVEKSLPA 2324
 QY 228 PEPNFIQTITQTVDRGLLEF--AENQDNFSLNTEEDGMVRYKLNSEPEKGIQDTIN 285
 DB 2325 TVYQILMFNTPSPNGLLLYLGSYGTQFLSTELPRGVKWTDLGSGPITLLTDR--RYN 2383
 QY 286 DQKHSILITTKLOKRWI-----NVNRSVRISEI-----PFSTYTGIGIPIA 332
 DB 2384 NGTWYKILFQNRKRGVLAVIDAYNTSNKER-QGETPGASDLNRLKDPILYVGLSPRS 2442
 QY 333 IBERNISTPAPFGCMKUL-KTSGVNLNDTVGTYKKCEDMKLVTRASFSGQMSFT 391
 DB 2443 RYVREGVTTKSVGCIKNLEISRTFDLRNSYGRKGL--LEIRSVSPFKSGYIELP 2500
 QY 392 NLDPVSTRFQLSFGFTQFPESGTL-----NHQRTSSLVLTLEDGIELEST 439
 DB 2501 PKSLPSESEWLTFA--FTNSGIIILALGQVDERGRDEAHVPEFSVMLIGNIEVHY 2558
 QY 440 RDSN-----IPFKSP-GTYMDGLAHVSVISDTSGALLDDQ--VLRRQRLPSFN 490
 DB 2559 NRGDTGRLKALHAPGTGCSGQASHSLVNRRIITVQDENNVEMKGLTIVESRTI 2618
 QY 491 AQSRLTGG-----GHPEGCSNVLVORFQSPFVLLDASKSTKQDASLGCC 537
 DB 2619 NVSNLYVGGIPREGGTSILIMRBSFHGCIKNLIF-----NLELIPNSAVHGQVDLDIC 2673
 QY 538 SLNKPPFL-----MLFKSPRRFNKGRIFVYNQLMODAPQATRSTEAQODGRSCLPPLN 590
 DB 2674 WLSERPKLPADABDSKTLREPRAPPEQC--VDALLEVYPGA----- 2713
 QY 591 TQASHRALQFGSPSHLLKLQELKRPSPFSIDITQTSKGLVFPAGTGD--SFLAL 648
 DB 2714 ---H---QFGTQNSHPLTFPNQSAVRKQSVESIRTPASSGLIYMAHQADYAVL 2766
 QY 649 VYADRVVVALDAGGKCLRSEKERYHOGKMTTVFGLNGGARLVVQGLRQESLPLPN 708
 DB 2767 QLHGGRHMFPLGKGRTVSHPALSDSKMTVKTVDYVKKGFITVDGRESPMYTVGD 2826
 QY 709 STSPREQVYL--GLPLSRKPKSLPQ--HSFVGLCRLDPQLNSKPL--DPSPARFGVSPCL 762
 DB 2827 GMLDVBEGFLYGLGSPQYQARKIGNITHSPACIGDVTVNSKQDQKPSVSAFVYNNRY 2886
 QY 763 GGSLEKGIYSGGGGHVILANSVSLGPELKLTFSTRPSLTVGLIHVGSQSQRLSYVKE 822

Db 2887 AVA-QEGTVPDGSGYALVKEGVKQSDVNITLFRTSSQNGVLLGISTAKVDALIGELV 2945

QY 823 AGKVTTSVSDAGSGVSTITPKOS--LCDQGMHSV-AVSIKORI 863

Db 2946 DGRVLPFVNNAGRIPTAPEKATVLCDEKMHITLQANKSKHRI 2989

RESULT 10

laminin alpha-2 chain precursor - mouse

N/Alternate names: laminin M chain; merosin heavy chain

C/Species: Mus musculus (house mouse)

C/Date: 21-Aug-1998 #sequence revision 21-Aug-1998 #text_change 09-Jul-2004

C/Accession: I49077; S50829; T48655; S31576; S53866

R/Berrier, S.M.; Uchida, A.; Sugiyama, S.; Doi, T.; Polistina, C.; Yamada, Y.

Matrix Biol. 14, 447-455, 1995

A/Title: Cloning and expression of laminin alpha 2 chain (M-chain) in the mouse.

A/Reference number: I49077; MUID:95316259; PMID:7795883

A/Accession: I49077

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-3106 <RES>

A/Cross-references: UNIPROT:Q60675; EMBL:U12147; NID:9699109; PIDN:AAC52165.1; PID:9699109

R/Xu, H.; Wu, X.R.; Wewer, U.M.; Engvall, E.

Nature Genet. 8, 297-302, 1994

A/Title: Murine muscular dystrophy caused by a mutation in the laminin alpha-2 (lam2) g

A/Reference number: S50829; MUID:95179178; PMID:7874173

A/Accession: S50829

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 64-281 <XUH>

A/Cross-references: GB:S75315; NID:9833929; PIDN:AAB3573.1; PID:9833930

R/Chang, A.C.; Madsworth, S.; Colligan, J.E.

J. Immunol. 151, 1789-1801, 1993

A/Title: Expression of merosin in the thymus and its interaction with thymocytes.

A/Reference number: I48655; MUID:93346725; PMID:8345183

A/Accession: I48655

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 2162-2204, 'D', 2206-2213, 'EY', 2216-2279 <RB2>

A/Cross-references: EMBL:X69869; NID:953055; PIDN:CAA9502.1; PID:953056

C/Complex: laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C/Function: interact with cells and with other basement membrane proteins to promote

C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

C/Keywords: basement membrane; calcium binding; coiled coil; extracellular matrix; glyco

F/1-22/Domain: signal sequence #status predicted <SIG>

F/23-3106/Product: laminin alpha-2 chain #status predicted <MAT>

F/283-337/Domain: laminin-type EGF-like homology <LE01>

F/340-407/Domain: laminin-type EGF-like homology <LE02>

F/410-462/Domain: laminin-type EGF-like homology <LE03>

F/465-511/Domain: laminin-type EGF-like homology <LE04>

F/514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>

F/720-750/Domain: laminin-type EGF-like homology <LE06>

F/753-800/Domain: laminin-type EGF-like homology <LE07>

F/803-858/Domain: laminin-type EGF-like homology <LE08>

F/861-911/Domain: laminin-type EGF-like homology <LE09>

F/914-960/Domain: laminin-type EGF-like homology <LE10>

F/963-1007/Domain: laminin-type EGF-like homology <LE11>

F/1010-1053/Domain: laminin-type EGF-like homology <LE12>

F/1056-1099/Domain: laminin-type EGF-like homology <LE13>

F/1102-1121/Domain: laminin-type EGF-like homology #status atypical <LE14>

F/1123-1159/Domain: laminin-type EGF-like homology #status atypical <LE15>

F/1162-1171/Domain: laminin-type EGF-like homology #status atypical <LE16>

F/1176-1413/Domain: laminin-type EGF-like homology #status atypical <LE17>

F/1416-1469/Domain: laminin-type EGF-like homology <LE18>

F/1465-1520/Domain: laminin-type EGF-like homology <LE19>

F/1523-1567/Domain: laminin-type EGF-like homology <LE20>

F/2166-2327/Domain: laminin G repeat homology <LG1>

F/2360-2520/Domain: laminin G repeat homology <LG2>

F/2546-2709/Domain: laminin G repeat homology <LG3>

F/2785-2933/Domain: laminin G repeat homology <LG4>

F/2960-3106/Domain: laminin G repeat homology <LG5>

Query Match 11.5%; Score 516.5; DB 1; Length 3106;

Best Local Similarity 23.2%; Pred. No. 9.1e-27;

Matches 220; Conservative 169; Mismatches 375; Indels 183; Gaps 46;

32 RPDIRENG-----GTEDMFVMTLGNKASK--DYIGMAVVDGQLTCVYNLGDREA 79

Db 2155 RPEIKKGSYNNIVVHKVAVADNLLFLYG---SAKIDFLAIBRKGVFLWVSGVG 2211

QY 80 EVOIDOVLTESSEQEAVMORVKFORIYQPAKNTYTBASNKRA--PAVYDEGSSN 136

Db 2212 RVGFPLTLID---DSYWRFEASRGRMSISV---RALDGKASWVSTYHSVSPGY 2264

QY 137 TLINLDEDAVFYGVGPPDFELPSRLRPPEYGCIELDNINNVSLVFKTPMLNT 196

Db 2265 TLIDVD-ANMLFVGGJTGKIKADAVRYTFTGCMGETYFDKPFGLMNFRE---KSG 2319

QY 197 EVFPCRRRKESDKN---YEGTGVARIPTPNAPPPPIQTI---QTVDRGLLFFAE 249

Db 2320 DCKGCTVSPQVDSBGTIQFDGGLV-SRPLRWPN-ISTVMFKRFTSSSALLMYLA 2377

QY 250 NQD-NFISLNIEDGNLWRYKLNSEPPKEGIRDTI---NDGKHSLITIGLQKR 302

Db 2378 TRDLKDFMSVELSDGHVKSVDLGS-----GMTSVSNQNHNDGKKA--FTLSRIQK 2429

QY 303 MNTNV-----NRSVRIBEIRDF-----STYLIGIP-----IAIRRFNISTPAFQ 345

Db 2430 ANISTVIDNSQENAVATSSGNNFGDLKADKITYFGPTLRNLSMKRPEVNVKYS 2489

QY 346 GCMKNTL---KTSGVRLNDVTGVTKKCSSEDMKLVRTASPRGG--QMSFTNLDVSTDR 400

Db 2490 GCLNDKIBSKTPNLSPPYGVYTKCS--LENNVTSPPKGFVLAVALSIDVG--- 2544

QY 401 FQSPFGQTFQPSGTL-----NQRTSSLLVTLBDG---HIELSTRD-S 442

Db 2545 -EINLSFTNBSGIILLGSGTLTPRRKRQQTQAYVAIFLNGRLVHLSSGTRMR 2603

QY 443 NIPFSPGYTMNGLHNSVIDTSGRLILDDOVLRRQRPLSPENAO-QSLRLDGG- 500

Db 2604 KIVKEPMLFHGRHSVAV-BRTGIFVQIDEBRHLQNTLEQPIEVKLLFVGAP 2662

QY 501 -----HFGCISNVLFQRFSPSEVDLASKSTKQDASLGGCLNPPMLF 548

Db 2663 PERQSPRLRTPAFQGCWMLVINSIP-----NDPAQPLAFKADIGCTYQF 2711

QY 549 KSPKRFNKGRIFFVNOQLMDAPATRSSTEAMDGRECLP-PLNTKA-----SHRAL- 598

Db 2712 ---REDESAVPAEVIQ--PQSVPT-----PAFPPVPTWVHGPCVASEPALLT 2757

QY 599 ---QFGDSPSHLLKLPQELKPRSQFSLDIOTTSPEKLVFYAG--TKDSFLALYADG 653

Db 2758 GSKQFGLSRNSHAIAYDDTKVKNRLLTELEVTEBSGLLFYMGRLNHADFVGVQIRNG 2817

QY 654 RVVFLGAGGKRLRSKERYHDKMHTVYFGLNGGKARLVQDLRAQBSLPGNSTSP 713

Db 2818 PPFSTYDLSSGSTRMIPTKINDGWMKIKIVAVKQEGILYVDASQ-----TISP 2869

QY 714 REQVYL-----GLPSRKPKSL--PQHSFVGLRLDQLNSKP--LDPSARFGVSP 760

Db 2870 KKADILLDVGGLLVVGGFLPNTTTRRIGPVYISLDGCCRNLHMQAPVDLDQPTSSFHVGT 2929

QY 761 CLGGSLEKGIYSGGGGHTVANSVSLGPELKLTFSTRPSLSLGVLIHVSQSGQRSLSV 820

Db 2930 CFPANA-BSGTYF-DGTFGKAVAGFVGLDLVAFEFRTTRPGLVGLGISQKDDGIR 2987

QY 821 MEAGKVTTSVSDAGSGVSTITPKO--SLCDQGMHSV-AVSIKORI 863

Db 2988 MIDBKLMFAYDNGA-GRFTAIYDAEIPGHMCNQMYVTYAKIKRNL 3033

RESULT 11

T43291

laminin alpha chain - Caenorhabditis elegans


```

Db      925 IADPVTF-----KTKSSVALATLQAYTS 949
Qy      607 -HLLKLQPELAKPRSPSIDIOTSPKGLVFF-AGTKDSFLALVYADG--RVVPALGAG 662
Db      950 MHLFFQ-----FKTSLDGLILYNSGGDNFIIVELVKGLHYVFDLGNG 994
Qy      663 GKRLRLSKERYDGHKWHVFGANGKARLVVDGLRAQSGSLPGNSTISPREQVYGLP 722
Db      995 ANLIKSSNKPLNDNQHNMVISHDTSNLTATVKTIDTKITQITAGARNLNLKSDLYIGV 1054
Qy      723 LSRKPKSLP-----QHSFVGCCLDFOLNSKPLDSPARFVSPCL--GGSLEKG----- 769
Db      1055 AKETVYKSLPFLVNAKEGFQCCLASVDLNGRLPDL-----ISDALFCNGQIERGCEGPT 1108
Qy      770 -----IYPSQGGGHVYL----- 781
Db      1109 TCOEDSCSNQGVCLQOWDGISCDOSMTSPFSGPLCNDPGTTYIIFSKGGQITTYKMPNDRP 1168
Qy      782 ---ANSVSLGPELKLTPSIRPSRLTGYLHVGSQS--GQRLSYVMEAGKTTYSVSDAGG 836
Db      1169 STRADRIATG-----FSTVQKE--AVLVKRVDSSSGLGDTLELHIHQKI--GVKENVGT 1218
Qy      837 SVTSITPKOSLC-DGQWHSV 855
Db      1219 DDIAIESNNAINDGKHVV 1238

```

RESULT 13

```

A40228
neurexin I-alpha precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: A40228; S27884
R/Unkaryov, Y.A.; Petrenko, A.G.; Geppert, M.; Suedhof, T.C.
Science 257, 50-56, 1992
A/Title: Neurexins: synaptic cell surface proteins related to the alpha-latrotoxin recep
A/Reference number: A40228; MUID:92320296; PMID:1621094
A/Accession: A40228
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-1507 <USH>
A/Cross-references: UNIPROT:Q63372; GB:M6374; NID:G205710; PIDN:AAA41704.1; PID:G205711
C/Superfamily: neurexin; EGF homology
C/Keywords: alternative splicing; transmembrane protein
F/1-30/Domain: signal sequence #status predicted <SIG>
F/31-1507/Product: neurexin I-alpha #status predicted <MAT>
F/580-712/Domain: EGF homology <EGF>
F/1087-1119/Domain: EGF homology <EGF1>

```

Query Match 7.1%; Score 320; DB 2; Length 1507;
 Best Local Similarity 19.5%; Pred. No. 1.4e-13;
 Matches 201; Conservative 134; Mismatches 354; Indels 344; Gaps 45;

```

Qy      35 LRENGGTEDMFVNYLGNKASKOYIGMAVVDGULTVYVNGDRRAVQIDQVLTSESSE 94
Db      315 LQKRG-----LMATGK---SADVNLALKNAGVSLVINGSGAFALVPEV--NGKFN 364
Qy      95 AVMDRVFQR-IYQFAKLTNTKEATSNKPRAPAVYDLEGSSNTLNLADBEDAVFYGY 153
Db      365 NAMHDVAVTNLNLGSHSIGAMWTIS--VDGILTTGYTQEDYTMLGSDD--FFYVGS 419
Qy      154 PPDEFLPSRLRPFPYKCIELDLNENVLNFKTTFNLTATEVEPCRRKRESDKNYF 213
Db      420 PSTADLPGSPVSNFMGCLK-----EYVYKNDVLELISRLAKQGDPPKMI 465
Qy      214 EGT-----GYARIPQPNAPFPNFITQITQTVDRGLLPPAENOD- 252
Db      466 HGVAFAKCEVAVTADPTTTPESPFSISLPKMAKKTGISPDFTITPPNGLIFSHKPR 525
Qy      253 -----NFISLNEEDGNLWRYKLNSPPEKGIKRTINDGKSHLITITGKL 299
Db      526 HOKDAKHPQMIKVDFAIEMLDGHLVLLDMGSGTIIKILQKKVNDG----- 574

```

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Qy      300 OKRMWNV-----NERSVRI-----EGEIPDF-STYLLGIGIPIAIRERNIS 341
Db      575 ----WYHVDQDRGRGRTISVNTLRTPTYPAPGESEILDDDELYLGLP---ENKAGIV 627
Qy      342 P-----AFQGMKRL-----KTSGVRLNDVYGVTKKSEB 373
Db      628 PTEVMTALNVYGVGCIKDLFDIGQSKDIRQMAEIOSTGAVKSCSRETAQCLSNPCKN 687
Qy      374 -----WK-----LVPTAS-----PSRGQMSFTNLDV---STDFFQLSFG 407
Db      688 NEMCRDGMWRYVCDSCGTGLGSCREAVTSLYDSM-FMKQLPVVMTTEADVSLRP 746
Qy      408 QTFQPSGTLNHOFTS--SLVTLLEDGHIELSTRDSNPI-----FKSPQTYM-----D 455
Db      747 RSGRAVGIIMATTSRDSDTLRIELDAGKVLTVNIDCIRINSSKGPETLPAGYNLD 806
Qy      456 GLAHVSVISDPSGLRLIDDOVLARNORLPSFSNAQSLRLQGGH---FEECISNVLV 511
Db      807 NEMHTVAVVRGKSLKLVDDQAMTQ-----MAGDTRLFEFNIETGIT 853
Qy      512 QR--FSQSPF-----VLDLASKSTKQDASLGCSLN-KPPFLMLFKSPKR 553
Db      854 ERYVLSVSPSNFGLHLSLTFNGMAYIDL-----KNGDIDYCELMARQFPMIADPV 908
Qy      554 FNGKRIFNVNQLMQDAPQATRSTEAWQDGRSLPPLNTKASHRALQFDSPTS-HLLKL 612
Db      909 F-----KTKSSVALATLQAYTSMHLFFQ- 932
Qy      613 PQLAKPRSQPSIDITQTPKGLVFF-AGTKDSFLALVYADG--RVVPALGAGKRLRL 669
Db      933 -----FKTSLDGLILYNSGGDNFIIVELVKGLHYVFDLGANGANLIKGS 978
Qy      670 SKERYDGHKWHVFGANGKARLVVDGLRAQSGSLPGNSTISPREQVYGLP LSRKPKS 729
Db      979 SNPLNDNQHNMVISHDTSNLTATVKTIDTKITQITAGARNLNLKSDLYIGVAKETYS 1038
Qy      730 LP-----QHSFVGCCLDFOLNSKPLDSPARFVSPCL--GGSLEKG----- 769
Db      1039 LPLVNAKEGFQCCLASVDLNGRLPDL-----ISDALFCNGQIERGCEGPTTCQEDSC 1092
Qy      770 -----IYPSQGGGHV-----ILANSV 785
Db      1093 SNOGVCLQOWDGRSCDCSMTSPFSGPLCNDPGTTYIIFSKGGQITTYKMPNDRPSTADRL 1152
Qy      786 SLGPELKLTPSIRPSRLTGYLHVGSQS--GQRLSYVMEAGKTTYSVSDAGSVTSITP 843
Db      1153 AIG-----FSTVQKE--AVLVKRVDSSSGLGDTLELHIHQKI--GVKENVGTDDIAIEB 1202
Qy      844 KOSLC-DGQWHSV 855
Db      1203 SMAINDGKHVV 1215

```

RESULT 14

```

A48216
neurexin III-alpha secreted type 1 precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Dec-2002
C/Accession: A48216; B48216
R/Unkaryov, Y.A.; Suedhof, T.C.
Proc. Natl. Acad. Sci. U.S.A. 90, 6410-6414, 1993
A/Title: Neurexin IIIalpha: extensive alternative splicing generates membrane-bound and
A/Reference number: A48216; MUID:93342001; PMID:8341647
A/Accession: A48216
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1438 <USH>
A/Cross-references: GB:I14851
A/Accession: B48216
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1368,1372-1438 <US2>
A/Cross-references: GB:I14851

```


C:Genetics:
 A:introns: 1372/1
 C:Superfamily: neuexin; EGF homology
 C:Keywords: alternative splicing; brain; cell surface component; duplication; extracellular
 F:1-27/Domain: signal sequence #status predicted <Sig>
 F:202-234/Domain: EGF homology <EGF>
 F:651-683/Domain: EGF homology <EGF1>

Query Match 6.7%; Score 301.5; DB 2; Length 1438;
 Best Local Similarity 19.8%; Pred. No. 2,6e-12;
 Matches 204; Conservative 135; Mismatches 342; Indels 349; Gaps 49;

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QY 36 RENGTEDEMFVMTLGNKSKDYIGMAVVDGQLTCVYNIAD----- 76
DB 295 QKNG-----LILHTGK---SADYVNLALDKGAVSLVINLDSGAFPAIVEPVNGKFNNDAM 346
QY 77 -----REAEVQIDQVLTSESGEAVMDRVKFORIYQFALNTKRTSKPKAPAV 127
DB 347 HDVKVTRNLKQVTVISVDGILTTT-----GYQE----- 374
QY 128 YDLEGGSSNTLLNLDEPDVAVFYGYPPDFELPSRLRFPYKGCIE----- 173
DB 375 -----DYTMLG---SDDFYVGGSPSTADLPGSFVSNMFMCKLEGVYKXNDIRLELS 424
QY 174 -LDDLNEVNLSTYN---FKTFNLNTVEBPCRRKESDKNYEGTGARIPQPNAPF 229
DB 425 RLARIIDGTMKIKYGEVVFKE---NVATLDPI-----NFEPEAYISLPKNTKEM 472
QY 230 PNFIQTIQTTVDGILFFA-----ENOD-----NFSINLBDGNLMVRKLNSEBP 275
DB 473 GSISDFPRTTEBNGILFTHGKPOERKDVRSQKNTKVDFAVAILDGNLYLLDWSGTT 532
QY 276 KEGKIRDTINDGKHSILITITGKLOKRMIVNERSVRI---EGEIPDF-STYLLGGLP 330
DB 533 KYKATQKKNDEGMYH--VDIQDGRSGTISVNSRRTPTFASGESILDLBGMVYLGILP 590
QY 331 IAIREFPNISTP-----AFQGMKNL-----KKTSGVRLNDVTGVTKCS-- 371
DB 591 ---ENRAGILPTELTMTAMLNKGYGICIRDLFIDGRSKNIRQLAEQNAAGVSCSRMS 647
QY 372 -----EDMK-----LVRTAS--FSRGGMSFTNLDPV--- 396
DB 648 AKQCDYPCKNNAVCCKGMNRFICDCTGTGYMGRTERESILSYDGSN--YMKVIMPMVM 706
QY 397 STDREFSGFQTFQPSGTLNMQRTS--SLVTFEDGHIESTDSNIPi-----FKSP 450
DB 707 HTEAEVSVRRMGOBAYGLLVATTSRDSADTLRLBEDGGRVYKMLWMLDCIRINCSSKEP 766
QY 451 GTYM-----DGLLHVSVISDTSGRLRLIDQV---LRRNQRLPSFSNAQOQLRLG 499
DB 767 ETLYAGQKLNDEMHVTRVVRGKSLKLVDDOVAEGTVMGDHTRL--EPFINIRGTIMTEK 825
QY 500 -----GHFEGCISNVLYQRFQSPBEVLDLASKYTKKASLGGCSLKNPPLMLP 548
DB 826 RYTSVPSSTFGLQSLMFGLL-----YIDLC-----KXGDDIDYCEL----- 863
QY 549 KSEKRFNKGRIFFVNOILMODAPQATRSTEAMQDGRSCLPPLNTKASHRALQFQDSPTS--H 607
DB 864 -----KAR--FGLRNLIADP-----VTFKTKSSYLTIATIGATTSNH 898
QY 608 LILKLPOELIKPRSQSLDIQTTSPIYG--LVFVAGTKDSFIALLYVADGRV--VFALGAGK 664
DB 899 LFPQ-----FKTISADGFIIFNSGDGNDFAIVELVNGYIHYVDDLGNPN 943
QY 665 KILRLKERYHDKMHTVVFGLNGKARLVVDGLRAQEGSLPENSITISPEQYLL--GLP-- 722
DB 944 VINGSDRPLNDQMHVNVITRDNSTHSLKVDTKVTVYINGAKMLDLGDLVYMGALQ 1003
QY 723 --LSRRKSLP--POHSFVGLRDLQNLSPLD-----SPSARFVSPCL 762
DB 1004 GMYSNLPKLVASADGQGLASVYDNGRLPDLINDALHRSQGLDRGCEGSPITTCQEDSC-- 1062
QY 763 GGSLEKGI-----YFSQGGGHVILANSVSLGP----- 789

```

```

DB 1063 ---ANQGVMOQWEGFTDCSMTSYSQNCNDPGATYIFKSGGILTYTPANRPSYRS 1119
QY 790 -ELKLTFSIRPSRLTGLVLIHNGSQS--GQRLSVMEAKTQTSVSSDGSVSTTPROS 846
DB 1120 DRLAVGFSFTYVD--GLIVRIDSPADGLDFQLHTBOGT--GVFNIGTVDISIKBERT 1175
QY 847 -LCDGQMHV 855
DB 1176 PUNDKHYV 1185

```

RESULT 15

B48218
 neuexin III-alpha membrane-bound type 3 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Dec-2002
 C:Accession: B48218; C48218
 R:ushkaryov, Y.A.; Suedhof, T.C.
 Proc. Natl. Acad. Sci. U.S.A. 90, 6410-6414, 1993
 A:Title: Neuexin IIIalpha: extensive alternative splicing generates membrane-bound and
 A:Reference number: A48216; MUID:93342001; PMID:8341647
 A:Accession: B48218
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1471 <USH>
 A:Cross-references: GB:L14851
 A:Accession: C48218
 A:Molecule type: mRNA
 A:Residues: 1-1368,1372-1471 <US2>
 A:Cross-references: GB:L14851
 C:Genetics:
 A:introns: 1372/1
 C:Superfamily: neuexin; EGF homology
 C:Keywords: alternative splicing; brain; cell surface component; duplication; receptor;
 F:1-27/Domain: signal sequence #status predicted <Sig>
 F:202-234/Domain: EGF homology <EGF>
 F:651-683/Domain: EGF homology <EGF1>

Query Match 6.7%; Score 301.5; DB 2; Length 1471;
 Best Local Similarity 19.8%; Pred. No. 2,7e-12;
 Matches 204; Conservative 135; Mismatches 342; Indels 349; Gaps 49;

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QY 36 RENGTEDEMFVMTLGNKSKDYIGMAVVDGQLTCVYNIAD----- 76
DB 295 QKNG-----LILHTGK---SADYVNLALDKGAVSLVINLDSGAFPAIVEPVNGKFNNDAM 346
QY 77 -----REAEVQIDQVLTSESGEAVMDRVKFORIYQFALNTKRTSKPKAPAV 127
DB 347 HDVKVTRNLKQVTVISVDGILTTT-----GYQE----- 374
QY 128 YDLEGGSSNTLLNLDEPDVAVFYGYPPDFELPSRLRFPYKGCIE----- 173
DB 375 -----DYTMLG---SDDFYVGGSPSTADLPGSFVSNMFMCKLEGVYKXNDIRLELS 424
QY 174 -LDDLNEVNLSTYN---FKTFNLNTVEBPCRRKESDKNYEGTGARIPQPNAPF 229
DB 425 RLARIIDGTMKIKYGEVVFKE---NVATLDPI-----NFEPEAYISLPKNTKEM 472
QY 230 PNFIQTIQTTVDGILFFA-----ENOD-----NFSINLBDGNLMVRKLNSEBP 275
DB 473 GSISDFPRTTEBNGILFTHGKPOERKDVRSQKNTKVDFAVAILDGNLYLLDWSGTT 532
QY 276 KEGKIRDTINDGKHSILITITGKLOKRMIVNERSVRI---EGEIPDF-STYLLGGLP 330
DB 533 KYKATQKKNDEGMYH--VDIQDGRSGTISVNSRRTPTFASGESILDLBGMVYLGILP 590
QY 331 IAIREFPNISTP-----AFQGMKNL-----KKTSGVRLNDVTGVTKCS-- 371
DB 591 ---ENRAGILPTELTMTAMLNKGYGICIRDLFIDGRSKNIRQLAEQNAAGVSCSRMS 647
QY 372 -----EDMK-----LVRTAS--FSRGGMSFTNLDPV--- 396

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Db 648 AKGCDSPCKNNNAVCDDGNRFICDCTGTGWTGRTCEAREASILSYDSM-YMKVIMPMW 706
QY 397 STDRLPQSPGQTFQPSGTLNHOQRTS--SLVLTEDGHELESTRDSNIPi---FKSP 450
Db 707 HTAEADVSPFRMSQRAYGLLVATTSRDSADTLRLIEDGGRVKLMVNDICIRINSSKGP 766
QY 451 GTM-----DGLHVSYSIDTSGRLIDDOY-----LRBNQRLPSFSAOQSLRGG 499
Db 767 ETLVACQKNDNEMHTVVRVRKSKLTVDDVABGTWGDHTRL-BFNHIEGTINTEK 825
QY 500 -----GHFEGCISNVLVORFQSPPEVLDLASKSTKXOASLGGCSLNKPPFLMLF 548
Db 826 RYISVVPSSPIGHLQSLMFGLL-----YIDL-----KNGDIDYCEL----- 863
QY 549 KSPKRFNKGRIFENVNOLMODAPQATRSTEAMQDGRSCLPPLNTKASHRALQFSDSPTS-H 607
Db 864 -----KAR-FGLRNTIADP-----VFKTSSYLTLATLQAYTSMH 898
QY 608 LLLKLQELKPKRSQPSLDIQTSPIKG-LVFYAGTKDSPLALYVADGRV--VPALGAGK 664
Db 899 LFPQ-----FKTTSADGFILFNSGDGNDFLAVELVKGYIHVFDLGNGPN 943
QY 665 KLRLSKERYHDGKMTVVFGLNGKARLVVDGLRAQEGSLPGNSTISPREOYVL-GLP- 722
Db 944 VIKGNSDRPLANDQNMHNVTTRDNSNTHSLKVDTKVTVYINGAKNLDLKGDLYMAGLAQ 1003
QY 723 --LSRRPKSL-PQHSFVGCRLRDPQLNSKPLD-----SPSARFVSPCL 762
Db 1004 GWYSNLPKLVASRDGFGCLASVDLNGRLPDLINDALHRSQIDRCCEGSPSTCQEDSC- 1062
QY 763 GGSLEKGI-----YFSQGGHVTILANSVSLGP----- 789
Db 1063 ---ANQGVCMQWEGFTCDCSMTSYSGNQCNDPGATYIFKSGGLIITYWPANDRPESTRS 1119
QY 790 -ELKLPFSIRPSLSLTVLHVGSOS--GQRLSVYMEAGKYTTSVSDAGSVTSITPKOS 846
Db 1120 DRLAVGFSTTVKD--GILVRIDAPGLGDFLQHLIEQKI--GVFNIGTVVDISIKEERT 1175
QY 847 -LCDGQWHSY 855
Db 1176 PVNDGKYHV 1185
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Search completed: February 22, 2005, 08:19:35
Job time : 29.1073 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:07:29 ; Search time 146.522 Seconds

(without alignments)
3026.590 Million cell updates/sec

Title: US-10-817-423-2

Perfect score: 4491
Sequence: 1 MRFNGSGVFRVLPNDLEDKGYTSLFLFQRPDLRENGGTEPMFVYLGAKKASQYIG 60

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4491	100.0	1725	2 P70570	P70570 ratius norv
2	4043	90.0	3333	1 LMA3 MOUSE	O61789 mus musculu
3	3562.5	79.3	1668	2 O6VU69	O6VU67 homo sapien
4	3562.5	79.3	3327	2 O6VU67	O6VU68 homo sapien
5	3562.5	79.3	3333	2 O6VU68	O6VU67 homo sapien
6	3560.5	79.3	1713	1 LMA3 HUMAN	O16787 homo sapien
7	3560.5	79.3	1806	2 O96TGO	O96TGO homo sapien
8	3560.5	79.3	3333	2 O76E14	O76E14 homo sapien
9	3331	74.2	1725	2 O867A1	O867A1 canis fami
10	1190	26.5	1816	1 LMA4 HUMAN	O16363 homo sapien
11	1185	26.4	1816	2 O91VVO	O91VVO mus musculu
12	1185	26.4	1816	1 LMA4 MOUSE	P97927 mus musculu
13	1042.5	23.2	3695	1 LMA5 HUMAN	O15230 homo sapien
14	1042.5	23.2	3695	2 O8TDF8	O8TDF8 homo sapien
15	950	21.2	1524	2 O6ZQA1	O6ZQA1 mus musculu
16	948	21.1	3718	1 LMA5 MOUSE	O61001 mus musculu
17	636.5	14.2	3712	1 LMA5 DROME	O60174 drosophila
18	636.5	14.2	3712	2 O9VTR0	O9VTR0 drosophila
19	629	14.0	3616	2 O7PPE9	O7PPE9 anopheles g
20	625	13.9	670	2 O9BFT3	O9BFT3 homo sapien
21	600.5	13.4	3672	1 LML2 CAEEL	O21313 caenorhabdi
22	594	13.2	794	2 O8R3Y7	O8R3Y7 mus musculu
23	579.5	12.9	1518	2 O21442	O21442 caenorhabdi
24	579.5	12.9	3704	2 P91904	P91904 caenorhabdi
25	545	12.1	3084	1 LMA1 MOUSE	P19137 mus musculu
26	529.5	11.8	3075	1 LMA1 HUMAN	P25391 homo sapien
27	526.5	11.7	3110	1 LMA2 HUMAN	P24043 homo sapien
28	523.5	11.7	414	2 O14731	O14731 homo sapien
29	516.5	11.5	3106	1 LMA2 MOUSE	O60675 mus musculu
30	514	11.4	354	2 O91YGB	O91YGB mus musculu
31	510	11.4	858	2 O8R145	O8R145 mus musculu

32	442	9.8	3375	2 O8IP51	O8IP51 drosophila
33	425	9.5	3367	2 O9XZC9	O9XZC9 drosophila
34	422.5	9.4	747	2 O7Z5W6	O7Z5W6 homo sapien
35	398	8.9	659	2 O7RQ19	O7RQ19 mus musculu
36	374	8.3	3170	2 O7P880	O7P880 anopheles g
37	358.5	8.0	3102	2 O45614	O45614 caenorhabdi
38	335	7.5	559	2 O6PED3	O6PED3 homo sapien
39	332.5	7.4	1363	1 NX1A CHICK	O9dd0 gallus gall
40	325.5	7.2	1514	1 NX1A RAT	O63372 ratius norv
41	322	7.2	1553	2 O8CH66	O8CH66 mus musculu
42	321.5	7.2	1530	1 NX1A BOVIN	O28166 bos taurus
43	320	7.1	1176	2 O80Y87	O80Y87 mus musculu
44	318	7.1	1477	1 NX1A HUMAN	O9UB1 homo sapien
45	316	7.0	1392	2 O81UE3	O81UE3 homo sapien

ALIGNMENTS

RESULT 1	PRELIMINARY	PRT, 1725 AA.
ID P70570		
AC P70570		
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DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)		
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
OS Rattus norvegicus (Rat).		
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX NCBI_TaxID=10116;		
RN [1]		
RP SEQUENCE FROM N.A.		
RA MEDLINE=97081969; PubMed=8923212;		
RA Baker S.B., Hopkinson S.B., Fitchman M., Andreason G.L., Fraser F.,		
RA Plopper G., Quaranta V., Jones J.C.R.;		
RT "Laminin-5 and hemidesmosomes: role of the alpha 3 chain subunit in		
RT hemidesmosome stability and assembly.";		
RL J. Cell Sci. 109:2509-2520 (1996).		
DR EMBL; U61261; AAB17053.1; -.		
DR HSSP; P35070; 11P0.		
DR GO; GO:0005606; C:laminin-1; IEA.		
DR GO; GO:0005102; F:receptor binding; IEA.		
DR GO; GO:0005198; F:structural molecule activity; IEA.		
DR GO; GO:0030155; P:regulation of cell adhesion; IEA.		
DR GO; GO:0030334; P:regulation of cell migration; IEA.		
DR GO; GO:0045995; P:regulation of embryonic development; IEA.		
DR InterPro; IPR008985; ConA like_1ec_g1.		
DR InterPro; IPR006209; EGF like.		
DR InterPro; IPR002049; Laminin_EGF.		
DR InterPro; IPR001791; Laminin_G.		
DR InterPro; IPR009254; Laminin_I.		
DR InterPro; IPR010307; Laminin_II.		
DR InterPro; IPR003129; TSP N.		
DR Pfam; PR00053; Laminin_EGF; 2.		
DR Pfam; PF02210; Laminin_G_2; 4.		
DR Pfam; PF06008; Laminin_I; 1.		
DR Pfam; PF06009; Laminin_II; 1.		
DR SMART; SM00180; EGF_Lam; 2.		
DR SMART; SM00282; LamG; 5.		
DR PROSITE; PS00022; EGF_1; 1.		
DR PROSITE; PS01186; EGF_2; 1.		
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 2.		
DR PROSITE; PS00025; LAM_G_DOMAIN; 5.		
KW Laminin EGF-like domain.		
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Query Match	100.0%;	Score 4491; DB 2; Length 1725;
Best Local Similarity	100.0%;	Pred. No. 5e-293;
Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
1 MRFNGSGVFRVLPNDLEDKGYTSLFLFQRPDLRENGGTEPMFVYLGAKKASQYIG 60		

Db 782 MFENKSGVEVRLPNDLEDLKGYSLSLFLQREPLEENGTEDEMFVYLGNDAKDYIG 841
 QY 61 MAVVDGOLTCVYNIAGREAEVQIDQVLTSESESOEAVMDRKFORIYQPAKNTYKATSN 120
 Db 842 MAVVDGOLTCVYNIAGREAEVQIDQVLTSESESOEAVMDRKFORIYQPAKNTYKATSN 901
 QY 121 KKAAPAVYDLSEGGSSNTLLNLPEDAVFYVGGYPPDFELPSRLRPYPYKCIELDLNEN 180
 Db 902 KKAAPAVYDLSEGGSSNTLLNLPEDAVFYVGGYPPDFELPSRLRPYPYKCIELDLNEN 961
 QY 181 VLSIVNFKTTFNLTNTEVPCRRRKEESDNKPYEGGYARIPIQNPAPPPNFIQTITV 240
 Db 962 VLSIVNFKTTFNLTNTEVPCRRRKEESDNKPYEGGYARIPIQNPAPPPNFIQTITV 1021
 QY 241 DGLLFFAENQDNFISLNIENEDGNLAMYRYKLNSEPPKRGKIRDTINGKHSIIITIGKQ 300
 Db 1022 DGLLFFAENQDNFISLNIENEDGNLAMYRYKLNSEPPKRGKIRDTINGKHSIIITIGKQ 1081
 QY 301 KKMWINNERSVRIEGEIPDFSTYYIGIPIAIRERFNI STPAFOGCMKRLKKTSGVRL 360
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 QY 361 NDTVGTCKCSBDMKLVRTASFGGQMSPTNLDVSTDRFQUSRFGPTPOBGTILNQ 420
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 Db 1202 TTSLSLVLTLEDGHIESTRDSNIPIFKSPGYMDGLNHSVYSIPTSGLRLIIDQVLR 1261
 QY 481 RNQRLPSFSAQSLRLGGHFEGCISNVLVQRFSGSPVLDLASKTKKDSLGGCSLN 540
 Db 1262 RNQRLPSFSAQSLRLGGHFEGCISNVLVQRFSGSPVLDLASKTKKDSLGGCSLN 1321
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 Db 1322 KPEPFLMFPSPKRFNKGRI FNNVQIMQDAPQARTSTREANODGSCIPPLNTAKSHALQF 1381
 QY 601 GDSPTSHLLKLPQELIKPSPQSLDIQTTS PKGLFYVATKDSFLALVYADGRVFPALG 660
 Db 1382 GDSPTSHLLKLPQELIKPSPQSLDIQTTS PKGLFYVATKDSFLALVYADGRVFPALG 1441
 QY 661 AGGKRLRLSKERYHDGKMTVVFGINGKARLVVDGLRAQEGSLFGNSTISREQVYIG 720
 Db 1442 AGGKRLRLSKERYHDGKMTVVFGINGKARLVVDGLRAQEGSLFGNSTISREQVYIG 1501
 QY 721 LPLSRPKSLPQHSFVGCARDPOLNKNPLDSPARFVSPCLGSLFKGIYFQGGGHYI 780
 Db 1502 LPLSRPKSLPQHSFVGCARDPOLNKNPLDSPARFVSPCLGSLFKGIYFQGGGHYI 1561
 QY 781 LANSVSLGPELKLTFGIRPSRLNGVLVHVSOGSGRLSYVMEAGKTTVSVDAGGSVTS 840
 Db 1562 LANSVSLGPELKLTFGIRPSRLNGVLVHVSOGSGRLSYVMEAGKTTVSVDAGGSVTS 1621
 QY 841 ITPKQSLCDGQWHSVAVSIXORILHL 866
 Db 1622 ITPKQSLCDGQWHSVAVSIXORILHL 1647
 RESULT 2
 LMA3 MOUSE STANDARD; PRT; 3333 AA.
 ID LMA3 MOUSE 061789; 061788; 061966; 090H07;
 AC 061789; 061788; 061966; 090H07;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 GN Laminin alpha-3 chain precursor (Nuclein alpha subunit).
 DN Name=Lama3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]

RP SEQUENCE OF 1-58 FROM N.A., AND SEQUENCE OF 32-38.
 RX MEDLINE=21818471; PubMed=11829758; DOI=10.1042/0264-6021.3620213;
 RA Garbe J.H., Gehring W., Mann K., Timpl R., Sasaki T.;
 RT "Complete sequence, recombinant analysis and binding to laminins and
 RT sulphated ligands of the N-terminal domains of laminin alpha3B and
 RT alpha5 chains.";
 RL Biochem. J. 362:213-221 (2002).
 RN [2]
 RP SEQUENCE OF 1-726 FROM N.A.
 RC STRAIN=ICR;
 RX MEDLINE=97296337; PubMed=9151674; DOI=10.1083/jcb.137.3.685;
 RA Miner J.H., Patton B.L., Lentz S.T., Gilbert D.C., Snider W.D.,
 RA Jenkins N.A., Copeland N.G., Sane J.R.;
 RT "The laminin alpha chains: expression, developmental transitions, and
 RT chromosomal locations of alpha1-5. Identification of heterotrimeric
 RT laminins 8-11, and cloning of a novel alpha3 isoform.";
 RL J. Cell Biol. 137:685-701 (1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM A), AND SEQUENCE OF 716-3284 FROM N.A.
 RP (ISOFORM B).
 RC STRAIN=BALB/c; TISSUE=Lung;
 RX MEDLINE=95394948; PubMed=7655604; DOI=10.1074/jbc.270.37.21820;
 RA Galliano M.-F., Aberdam D., Aguzzi A., Ortonne J.-P., Meneguzzi G.;
 RT "Cloning and complete primary structure of the mouse laminin alpha 3
 RT chain. Distinct expression pattern of the laminin alpha 3A and alpha
 RT 3B chain isoforms.";
 RL J. Biol. Chem. 270:21820-21826 (1995).
 RN [4]
 RP REVISIONS.
 RA Aberdam D.;
 RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1767-2485 FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=94281750; PubMed=8012114;
 RA Aberdam D., Galliano M.-F., Mattei M.-G., Pisani-Spadefora A.,
 RA Ortonne J.-P., Meneguzzi G.;
 RT "Assignment of mouse niclein genes to chromosomes 1 and 18.";
 RL Mamm. Genome 5:229-233 (1994).
 RN [6]
 RP SEQUENCE OF 1767-2485 FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=94363405; PubMed=8081888;
 RA Aberdam D., Aguzzi A., Baudoin C., Galliano M.-F., Ortonne J.-P.,
 RA Meneguzzi G.;
 RT "Developmental expression of niclein adhesion protein (laminin-5)
 RT subunits suggests multiple morphogenic roles.";
 RL Cell Adhes. Commun. 2:115-129 (1994).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
 CC via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-
 CC 6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
 CC phosphorylation of p125-FAK and p80, (3) differentiation of
 CC keratinocytes (by similarity).
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end. The alpha-3 chain is a subunit of laminin-5
 CC (epiligrin/kalinin/niclein), and possibly also a component of
 CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=B;
 CC IsoId=Q61789-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=Q61789-2; Sequence=VSP_003038, VSP_003039;
 CC -1- TISSUE SPECIFICITY: Basal membrane of the upper alimentary tract

and urinary and nasal epithelia, salivary glands and teeth (booth variants). Isoform A is predominantly expressed in skin, hair follicles and developing neurons of the trigeminal ganglion. Isoform B was found in bronchi, alveoli, stomach, intestinal crypts, whisker pads, CNS, telencephalic neuroectoderm, thalamus, Rathke's pouch and periventricular subependymal germinal layer.

-1- DOMAIN: The alpha-helical domains I and II are thought to interact with other laminin chains to form a coiled coil structure.

-1- DOMAIN: Domain IV and G are globular.

-1- SIMILARITY: Contains 15 laminin EGF-like domains.

-1- SIMILARITY: Contains 5 laminin G-like domains.

-1- SIMILARITY: Contains 1 laminin IV domain.

-1- SIMILARITY: Contains 1 laminin N-terminal domain.

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EMBL; AJ293592; CAB9254.2; -

EMBL; U88353; AAC5179.1; -

EMBL; X84014; CA58837.1; -

EMBL; X84013; CA58836.1; ALT_FRAME.

EMBL; L20478; AAA6809.1; -

HSSP; P02468; INPE.

MGI; 99909; Lama3.

GO; GO:0005604; C:basement membrane; IDA.

InterPro: IPR008985; Consilium; IEC_g1.

InterPro: IPR006209; EGF_Like.

InterPro: IPR008979; Gal_bind_Like.

InterPro: IPR009030; Grow_fac_recept.

InterPro: IPR008212; Lam_N2.

InterPro: IPR000034; Laminin_B.

InterPro: IPR002049; Laminin_EGF.

InterPro: IPR001791; Laminin_G.

InterPro: IPR009254; Laminin_I.

InterPro: IPR010307; Laminin_II.

InterPro: IPR008211; Laminin_N.

InterPro: IPR003129; TSP_N.

Pfam; PF00052; Laminin_B_1.

Pfam; PF00053; Laminin_EGF_10.

Pfam; PF00054; Laminin_G_3.

Pfam; PF06008; Laminin_I_1.

Pfam; PF06009; Laminin_II_1.

Pfam; PF00055; Laminin_N_1.

PRINTS; PR00011; EGF_LAMININ.

ProDom; PD003031; Laminin_B_1.

PROSITE; PS00022; EGF_1; 10.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS00025; LAM_G_DOMAIN; 5.

PROSITE; PS01248; LAMININ_TYPE_EGF; 10.

Alternative splicing; Basement membrane; Cell adhesion; Coiled coil; Direct protein sequencing; Extracellular matrix; Glycoprotein; Laminin EGF-like domain; Repeat; Signal.

FT SIGNAL 1 31

FT CHAIN 32 333 Laminin alpha-3 chain.

FT DOMAIN 32 294 Laminin N-terminal (domain VI).

FT FT 295 725 Domain V.

FT DOMAIN 296 350 Laminin EGF-like 1.

FT DOMAIN 353 420 Laminin EGF-like 2.

FT DOMAIN 423 464 Laminin EGF-like 3.

FT DOMAIN 488 530 Laminin EGF-like 4.

FT DOMAIN 533 576 Laminin EGF-like 5.

FT DOMAIN 582 625 Laminin EGF-like 6.

FT DOMAIN 628 678 Laminin EGF-like 7.

FT DOMAIN 681 725 Laminin EGF-like 8.

FT DOMAIN 725 1262 Laminin domain IV 1 (domain IV B).

FT DOMAIN 1263 1464 Domain III B.

FT DOMAIN 1310 1353 Laminin EGF-like 9.

FT DOMAIN 1354 1403 Laminin EGF-like 10.

FT DOMAIN 1404 1454 Laminin EGF-like 11.

FT DOMAIN 1455 1464 Laminin EGF-like 12 (N-terminal).

FT DOMAIN 1465 1653 Laminin domain IV (domain IV A).

FT DOMAIN 1654 1821 Domain III A.

FT DOMAIN 1654 1686 Laminin EGF-like 12 (C-terminal).

FT DOMAIN 1687 1733 Laminin EGF-like 13.

FT DOMAIN 1734 1786 Laminin EGF-like 14.

FT DOMAIN 1787 1821 Laminin EGF-like 15 (incomplete).

FT DOMAIN 1822 2388 Domain II and I.

FT DOMAIN 2389 2590 Laminin G-like 1.

FT DOMAIN 2597 2759 Laminin G-like 2.

FT DOMAIN 2766 2926 Laminin G-like 3.

FT DOMAIN 2986 3150 Laminin G-like 4.

FT DOMAIN 3157 3330 Laminin G-like 5.

FT DOMAIN 1854 1983 Coiled coil (Potential).

FT DOMAIN 2015 2060 Coiled coil (Potential).

FT DOMAIN 2091 2168 Coiled coil (Potential).

FT DOMAIN 2214 2241 Coiled coil (Potential).

FT DOMAIN 2321 2386 Coiled coil (Potential).

FT SITE 2277 2279 Cell attachment site (potential).

FT DISULFID 1310 1317 By similarity.

FT DISULFID 1312 1324 By similarity.

FT DISULFID 1326 1335 By similarity.

FT DISULFID 1338 1351 By similarity.

FT DISULFID 1354 1369 By similarity.

FT DISULFID 1356 1376 By similarity.

FT DISULFID 1378 1387 By similarity.

FT DISULFID 1390 1401 By similarity.

FT DISULFID 1404 1416 By similarity.

FT DISULFID 1406 1423 By similarity.

FT DISULFID 1425 1434 By similarity.

FT DISULFID 1437 1452 By similarity.

FT DISULFID 1467 1496 By similarity.

FT DISULFID 1689 1703 By similarity.

FT DISULFID 1706 1715 By similarity.

FT DISULFID 1718 1731 By similarity.

FT DISULFID 1734 1746 By similarity.

FT DISULFID 1736 1755 By similarity.

FT DISULFID 1757 1766 By similarity.

FT DISULFID 1769 1784 By similarity.

FT DISULFID 1822 1822 Interchain (probable).

FT DISULFID 1825 1825 Interchain (probable).

Query Match 90.0%; Score 4043; DB 1; Length 3333;
Best Local Similarity 89.6%; Pred. No. 2e-262;
Matches 776; Conservative 38; Mismatches 52; Indels 0; Gaps 0;

QY 1 MRFNGSGVVRPLPNDLEDKGYTSLFQRPDLRNGSTEDMFVYLGAKDASROYIG 60
|||||

DB 2390 MRFNGSGVVRPLPNDLEDKGYTSLFQRPDLRNGSTEDMFVYLGAKDASROYIG 2449
|||||

QY 61 MAVVDGQLTCVNIAGDRBAEVQIDVLTSESGEAVMDRYKFORIQPAKANTTKATSN 120
|||||

DB 2450 MAVVDGQLTCVNIAGDRBAEVQIDVLTSESGEAVMDRYKFORIQPAKANTTKATSN 2509
|||||

QY 121 KPRAPAVYDIEGSSNTLNLDPEDAVFYTGYPDFELPSRLRPFPYKGCISLDNLNEN 180
|||||

DB 2510 KPRAPAVYDIEGSSNTLNLDPEDAVFYTGYPDFELPSRLRPFPYKGCISLDNLNEN 2569
|||||

QY 181 VLSVNPKTFFNLTTEVEPCRRKESDNGYEGGVYAIPTQPNAPPNFIQTQTV 240
|||||

DB 2570 VLSVNPKTFFNLTTEVEPCRRKESDNGYEGGVYAIPTQPNAPPNFIQTQTV 2629
|||||

QY 241 DRGLLPAENQDNFISLINEDGNLMVRYKLNSPEPKGIRDTINDGKHSILITTKLQ 300
|||||

DB 2630 DRGLLPAENQDNFISLINEDGNLMVRYKLNSPEPKGIRDTINDGKHSILITTKLQ 2689
|||||

QY 301 KRWIVNERSVAILIEGIFPFTYTGITAIARERNITPAFGCKMKLTKTSSGVRL 360
|||||

DB 2690 KRWIVNERSVAILIEGIFPFTYTGITAIARERNITPAFGCKMKLTKTSSGVRL 2749
|||||

QY 361 NDTVGYTKCSBDMKLVRTASPSRGOMSFNTLDVSTDFQSFSGFQTPQSGTLLNHQ 420
|||||

Db 2750 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDPVSLDRFQLSFGPQTPOPSGTLNLHQ 2809
 QY 421 TTTSSLVLTLEBDGIELSTRDSNIP1FKSPGYMDGLHHVSYISPTSGRLIIDQVLR 480
 Db 2810 TTTSSLVLTLEBDGIELSTRDSNIP1FKSPGYMDGLHHVSYISPTSGRLIIDQVLR 2869
 QY 481 RNQRLPSFNAOQSLRLGGGHEFGCISNVLVQRFSGSPRYVLDAKSTTKDASLGCCSLN 540
 Db 2870 RNQRLPSFNAOQSLRLGGGHEFGCISNVLVQRFSGSPRYVLDAKSTTKDASLGCCSLN 2929
 QY 541 KPPFLMLFKSPKRFNKGRIFFNNQMODAPQATRTSTEAANDGSCPLPLNTKASHRALQ 600
 Db 2930 KPPFLMLFKSPKRFNKGRIFFNNQMODAPQATRTSTEAANDGSCPLPLNTKASHRALQ 2989
 QY 601 GDSPTSHLLKLPQELLKPRSGPSLDIQTSFGKLVFYATGKDSPLALVYADGRVVFALG 660
 Db 2990 GDSPTSHLLKLPQELLKPRSGPSLDIQTSFGKLVFYATGKDSPLALVYADGRVVFALG 3049
 QY 661 AGGKTLRLSKERYHDKMHTVFGNLNGKARLVVDGLRAOEGSLPQNSTISPREQVYLQ 720
 Db 3050 AGGKTLRLSKERYHDKMHTVFGNLNGKARLVVDGLRAOEGSLPQNSTISPREQVYLQ 3109
 QY 721 LPLSRPKSP1PQHSFPGCLRLDPOLNKP1DPSBAPRGVSPCLGSLKGIYFGGGGHY 780
 Db 3110 LPLSRPKSP1PQHSFPGCLRLDPOLNKP1DPSBAPRGVSPCLGSLKGIYFGGGGHY 3169
 QY 781 LANSVLELPELKTLPFIRPSRLTGVLHVHVSOGQRLSVYMBAGKYTTSVSDAGSPTS 840
 Db 3170 LANSVLELPELKTLPFIRPSRLTGVLHVHVSOGQRLSVYMBAGKYTTSVSDAGSPTS 3229
 QY 841 ITPKQSLCDGQMSHVAVSIRKRIHL 866
 Db 3230 ITPKQSLCDGQMSHVAVSIRKRIHL 3255

RESULT 3

Q6VU69 PRELIMINARY; PRT; 1668 AA.

ID Q6VU69
 AC Q6VU69;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Laminin alpha 3 splice variant a.
 GN Name=LAM3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_taxid=9606;
 RX MEDLINE=2893568; Pubmed=12915477; DOI=10.1093/hmg/ddg234;
 RA McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
 RA Dopping-Hepenstall P.J., Bady R.A., Jamil T., Phillips R.J.,
 RA Shabli S.G., Haroon T.S., Khurshid K., Moore J.B., Page B.,
 RA Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
 RA McGrath J.A.;
 RT "An unusual N-terminal deletion of the laminin (alpha)3 isoform leads
 RT to the chronic granulation tissue disorder laryngo-onycho-cutaneous
 RT syndrome";
 RT Hum. Mol. Genet. 12:2395-2409(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA McLean W.H.I.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY327114; AAQ72569.1; -.
 DR GO; GO:0005606; C:laminin-1; IEA.
 DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0030345; P:regulation of cell adhesion; IEA.
 DR GO; GO:0030344; P:regulation of cell migration; IEA.
 DR GO; GO:0045995; P:regulation of embryonic development; IEA.
 DR InterPro; IPR001844; Chaprinin_Cpn60.

DR InterPro; IPR008985; Cona_like_jec_g1.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR009254; Laminin_I.
 DR InterPro; IPR010307; Laminin_II.
 DR InterPro; IPR003129; TSP_N.
 DR Pfam; PF00053; Laminin_EGF_1.
 DR Pfam; PF02210; Laminin_G_2; 4.
 DR Pfam; PF06008; Laminin_I_1.
 DR Pfam; PF06009; Laminin_II_1.
 DR SMART; SM00180; EGF_Lam; 2.
 DR SMART; SM00282; LamG; 5.
 DR PROSITE; PS00296; CHAPERONIN_CPN60; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01248; LAMININ_TYPR_EGF; 2.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
 KW Laminin_EGF-like domain.
 SQ SEQUENCE 1668 AA; 184053 MW; 9EBF5FC45637645C CRC64;

Query Match 79.3%; Score 3562.5; DB 2; Length 1668;

Best Local Similarity 78.4%; Pred. No. 1.6e-230; Indels 3; Gaps 2;

Matches 680; Conservative 86; Mismatches 98;

QY 1 MRFNKGSGVEVRLPNDLEDKGYTSLSLFLQRPDLRENGTEDEMFVMTLAKNDASKDYIG 60
 Db 726 MRFNKGSGVEVRLPNDLEDKGYTSLSLFLQRPDRNGRNGTEENMFVMTLAKNDASRDYIG 785
 QY 61 MAVVDGQLTCVYNLGDREABVQIDQVLTRESBQAVMDRVYKFORLYQAKLNTYTEASLN 120
 Db 786 MAVVDGQLTCVYNLGDREABVQIDQVLTRESBQAVMDRVYKFORLYQAKLNTYTEASLN 845
 QY 121 KKPAAVVDLEGGSSNTLNDPEDAVYVYGGYPDPFELPSRLRPPPKGCTELDLNEN 180
 Db 846 KKPAAVVDLEGGSSNTLNDPEDAVYVYGGYPDPFELPSRLRPPPKGCTELDLNEN 905
 QY 181 VLSLYNFKTTFNTLNTTEVEPCRRKESDKVYFSGTYARLPTQPNAPFPNFIQTITTV 240
 Db 906 VLSLYNFKTTFNTLNTTEVEPCRRKESDKVYFSGTYARLPTQPNAPFPNFIQTITTV 965
 QY 241 DRGLLPFAENQDPISLNIEDGNLNVRYKLNSEPPKRGIRDTINDGKHSLITTYGKLQ 300
 Db 966 DRGLLPFAENQDPISLNIEDGNLNVRYKLNSEPPKRGIRDTINDGKHSLITTYGKLQ 1025
 QY 301 KKMWNVNRSRIRIGKLPDSTVYLGIPAIRERFNISTPAFGCKMKNLKKTSQVRL 360
 Db 1026 KKMWNVNRSRIRIGKLPDSTVYLGIPAIRERFNISTPAFGCKMKNLKKTSQVRL 1085
 QY 361 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDPVSLDRFQLSFGPQTPOPSGTLNLHQ 420
 Db 1086 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDPVSLDRFQLSFGPQTPOPSGTLNLHQ 1145
 QY 421 TTTSSLVLTLEBDGIELSTRDSNIP1FKSPGYMDGLHHVSYISPTSGRLIIDQVLR 480
 Db 1146 TTTSSLVLTLEBDGIELSTRDSNIP1FKSPGYMDGLHHVSYISPTSGRLIIDQVLR 1205
 QY 481 RNQRLPSFNAOQSLRLGGGHEFGCISNVLVQRFSGSPRYVLDAKSTTKDASLGCCSLN 540
 Db 1206 RNQRLPSFNAOQSLRLGGGHEFGCISNVLVQRFSGSPRYVLDAKSTTKDASLGCCSLN 1265
 QY 541 KPPFLMLFKSPKRFNKGRIFFNNQMODAPQAT-RSTEAMODGRSCLPLNTKASHRALQ 599
 Db 1266 KPPFLMLFKSPKRFNKGRIFFNNQMODAPQAT-RSTEAMODGRSCLPLNTKASHRALQ 1323
 QY 600 GDSPTSHLLKLPQELLKPRSGPSLDIQTSFGKLVFYATGKDSPLALVYADGRVVFALG 659
 Db 1324 GDSPTSHLLKLPQELLKPRSGPSLDIQTSFGKLVFYATGKDSPLALVYADGRVVFALG 1383
 QY 660 AGGKTLRLSKERYHDKMHTVFGNLNGKARLVVDGLRAOEGSLPQNSTISPREQVYL 719
 Db 1384 AGGKTLRLSKERYHDKMHTVFGNLNGKARLVVDGLRAOEGSLPQNSTISPREQVYL 1443

QY 720 GLPLSRKPKSLPOHSFVGCILRDPLQNSKPLDPSAPRGVSPCLGSLKGIYFSOGGSHV 779
 DB 1444 GSPSPGKPKSLPTNSFVGCILRDPLQNSKPLDPSAPRGVSPCLGSLKGIYFSOGGSHV 1503
 QY 780 ILANSVSLGPELKLTPSIRPRSLTGVLIVHVSQSGQRLSYMEAGKTYTSVSDAGGSVT 839
 DB 1504 VLAHSVSLGPEFLVFSIRPRSLTGVLIVHVSQSGQRLCYLLEAGKTYTASMDSGAGGTST 1563
 QY 840 SITPKOSLCDQWHSAVSIKORILH 866
 DB 1564 SITPKOSLCDQWHSAVSIKORILH 1590

RESULT 4
 ID 06VU67 PRELIMINARY; PRT; 3277 AA.
 AC 06VU67;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Laminin alpha 3 splice variant D2.
 OS Homo sapiens (Human).
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22835568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
 RA McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Mellerio J.B., Ashton G.S.,
 RA Dopping-Hepenstal P.J., Bady R.A., Jamil T., Phillips R.J.,
 RA Shabir S.G., Haroon T.S., Knutshild K., Moore J.E., Page B.,
 RA Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
 RA McGee J.A.;
 RT "An unusual N-terminal deletion of the laminin (alpha)3a isoform leads
 RT to the chronic granulation tissue disorder laryngo-oncho-cutaneous
 RT syndrome".
 RT Hum. Mol. Genet. 12:2395-2409(2003).
 RL [2]
 RN SEQUENCE FROM N.A.
 RA McLean W.H.I.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DB EMBL: AY327116; AA072571.1; -
 DB GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DB GO: GO:0005506; C:laminin-1; IEA.
 DB GO: GO:0005102; F:receptor binding; IEA.
 DB GO: GO:0005198; F:regulation of cell adhesion; IEA.
 DB GO: GO:0030155; F:regulation of cell migration; IEA.
 DB GO: GO:0030334; P:regulation of cell adhesion; IEA.
 DB GO: GO:0045995; P:regulation of embryonic development; IEA.
 DB InterPro: IPR001844; Chapman Cpn60.
 DB InterPro: IPR008985; Cona like_1ec_g1.
 DB InterPro: IPR006209; BGF like.
 DB InterPro: IPR008978; Gal_bind_like.
 DB InterPro: IPR006210; IEGF.
 DB InterPro: IPR000034; Laminin_B.
 DB InterPro: IPR002049; Laminin_EGF.
 DB InterPro: IPR001791; Laminin_G.
 DB InterPro: IPR009254; Laminin_I.
 DB InterPro: IPR010307; Laminin_II.
 DB InterPro: IPR008211; Laminin_N.
 DB InterPro: IPR003129; TSP_N.
 DB Pfam: PF00052; Laminin_B_1.
 DB Pfam: PF00210; Laminin_EGF_8.
 DB Pfam: PF02210; Laminin_G_2; 4.
 DB Pfam: PF06008; Laminin_I_1.
 DB Pfam: PF06009; Laminin_II_1.
 DB Pfam: PF00055; Laminin_N_1.
 DB PRINTS: PR00011; EGF_LAMININ.
 DB ProDom: PD003031; Laminin_B_1.
 DB SMART: SM00181; EGF_8.
 DB SMART: SM00180; EGF_Lam; 14.

DR SMART: SM00281; Lam; 1.
 DR SMART: SM00282; Lam; 5.
 DR SMART: SM00136; Lam; 1.
 DR PROSITE: PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; 12.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01248; LAMININ TYPE EGF; 13.
 DR PROSITE: PS00025; LAM_G_DOMAIN; 5.
 KW Laminin EGF-like domain.
 SQ SEQUENCE 3277 AA; 360209 MW; 3ACFE9983571222 CRC64;

Query Match 79.3%; Score 3562.5; DB 2; Length 3277;
 Best local Similarity 78.4%; Pred. No. 4.6e-230;
 Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRNKGSGVEVRLPNDLBDLKGYSLSLFLQRLDENGSTDMFYVYLGAKNDKSDYIG 60
 DB MRNKGSGVEVRLPNDLBDLKGYSLSLFLQRLDENGSTDMFYVYLGAKNDKSDYIG 2394
 QY 61 MAVVDQQLTCVNLGSRKAEVQIDVLTSESGQAVMDRKRFORIYQFALNTYTKATSN 120
 DB MAVVDQQLTCVNLGSRKAEVQIDVLTSESGQAVMDRKRFORIYQFALNTYTKATSN 2454
 QY 121 KPRAPAVYDLGSSNTLNLDPEDAVFYVGYPPDFELPSRLFPYKGCIELDLNEN 180
 DB KPRAPAVYDLGSSNTLNLDPEDAVFYVGYPPDFELPSRLFPYKGCIELDLNEN 2514
 QY 245 KPEITPGVYDMGDSNTLNLDPENVFYVGYPPDFELPSRLFPYKGCIELDLNEN 2514
 DB VLSLYNPKTTFNLNTTEVEBCRRKESDKNVEGTYARIPTQNPAPNPNTQITQTV 240
 QY 181 VLSLYNPKTTFNLNTTEVEBCRRKESDKNVEGTYARIPTQNPAPNPNTQITQTV 240
 DB VLSLYNPKTTFNLNTTEVEBCRRKESDKNVEGTYARIPTQNPAPNPNTQITQTV 2574
 QY 241 DRGLTFPAENQDPLSLNTEDEGNTLRYKLSNPPKKEKGRDITNOKHSILITTKQ 300
 DB DRGLTFPAENQDPLSLNTEDEGNTLRYKLSNPPKKEKGRDITNOKHSILITTKQ 2634
 QY 2575 DRGLTFPAENQDPLSLNTEDEGNTLRYKLSNPPKKEKGRDITNOKHSILITTKQ 2634
 DB DRGLTFPAENQDPLSLNTEDEGNTLRYKLSNPPKKEKGRDITNOKHSILITTKQ 2634
 QY 301 KRMWVNVNRSVYIEGIFDFTYVYGGIPIALREPNISPAFOGCMKUKKTSVGVRL 360
 DB KRMWVNVNRSVYIEGIFDFTYVYGGIPIALREPNISPAFOGCMKUKKTSVGVRL 2634
 QY 2635 KRMWVNVNRSVYIEGIFDFTYVYGGIPIALREPNISPAFOGCMKUKKTSVGVRL 2634
 DB KRMWVNVNRSVYIEGIFDFTYVYGGIPIALREPNISPAFOGCMKUKKTSVGVRL 2754
 QY 361 NDTFVGYTKKSEDMKLVRTASFSRGGQMSFTNLDPSTDRFQSPGFQFQPSGTLNMQ 420
 DB NDTFVGYTKKSEDMKLVRTASFSRGGQMSFTNLDPSTDRFQSPGFQFQPSGTLNMQ 2754
 QY 2695 NDTFVGYTKKSEDMKLVRTASFSRGGQMSFTNLDPSTDRFQSPGFQFQPSGTLNMQ 2754
 DB NDTFVGYTKKSEDMKLVRTASFSRGGQMSFTNLDPSTDRFQSPGFQFQPSGTLNMQ 2814
 QY 421 TRTSLSLVTEDEGHILSTRDSNIPPKSGCTYMDGLHNVSYISDTSGRLILDOVLR 480
 DB TRTSLSLVTEDEGHILSTRDSNIPPKSGCTYMDGLHNVSYISDTSGRLILDOVLR 2814
 QY 2755 TWTRNLQVLEDEYIEILSTSDSSPIFKSPQTYMDGLHNVSYISDTSGRLILDOVLR 2814
 DB TWTRNLQVLEDEYIEILSTSDSSPIFKSPQTYMDGLHNVSYISDTSGRLILDOVLR 2814
 QY 481 RNORLPSFSAQOSLFLGGHPEGICISNLYVORFSSQSPVYLDLASXTKQDASLGCSLN 540
 DB RNORLPSFSAQOSLFLGGHPEGICISNLYVORFSSQSPVYLDLASXTKQDASLGCSLN 2814
 QY 2815 NSKRLNHISRSKSLNLGSSNFBGCTISNVFQRLSPVYLDLASXTKQDASLGCSLN 2814
 DB NSKRLNHISRSKSLNLGSSNFBGCTISNVFQRLSPVYLDLASXTKQDASLGCSLN 2814
 QY 541 KPEPLMLFSPKPKFNKRIETVNVQMLQDAPOAT-RSTEAWQDRSCPLPLNTKASHRALQ 599
 DB KPEPLMLFSPKPKFNKRIETVNVQMLQDAPOAT-RSTEAWQDRSCPLPLNTKASHRALQ 2814
 QY 2875 KPEPLMLFSPKPKFNKRIETVNVQMLQDAPOAT-RSTEAWQDRSCPLPLNTKASHRALQ 2932
 DB KPEPLMLFSPKPKFNKRIETVNVQMLQDAPOAT-RSTEAWQDRSCPLPLNTKASHRALQ 2932
 QY 600 FGDSPYSHLLKLPQELIKRSPSLDIQTSFKGLVFYAGTYOSPLIAYVADGRVVAL 659
 DB FGDSPYSHLLKLPQELIKRSPSLDIQTSFKGLVFYAGTYOSPLIAYVADGRVVAL 2932
 QY 2933 FGDIPYSHLLKLPQELIKRSPSLDIQTSFKGLVFYAGTYOSPLIAYVADGRVVAL 2932
 DB FGDIPYSHLLKLPQELIKRSPSLDIQTSFKGLVFYAGTYOSPLIAYVADGRVVAL 2932
 QY 660 GAGGKGLRLSRKSKRYDGKNTVFPGLNGKALVVDGARAQSGSLPGNSTISPREOYL 719
 DB GAGGKGLRLSRKSKRYDGKNTVFPGLNGKALVVDGARAQSGSLPGNSTISPREOYL 3052
 QY 2993 GTDGKGLRLSRKSKRYDGKNTVFPGLNGKALVVDGARAQSGSLPGNSTISPREOYL 3052
 DB GTDGKGLRLSRKSKRYDGKNTVFPGLNGKALVVDGARAQSGSLPGNSTISPREOYL 3052
 QY 720 GLPLSRKPKSLPOHSFVGCILRDPLQNSKPLDPSAPRGVSPCLGSLKGIYFSOGGSHV 779
 DB GLPLSRKPKSLPOHSFVGCILRDPLQNSKPLDPSAPRGVSPCLGSLKGIYFSOGGSHV 3112
 QY 3053 GSPSPGKPKSLPTNSFVGCILRDPLQNSKPLDPSAPRGVSPCLGSLKGIYFSOGGSHV 3112
 DB GSPSPGKPKSLPTNSFVGCILRDPLQNSKPLDPSAPRGVSPCLGSLKGIYFSOGGSHV 3112
 QY 780 ILANSVSLGPELKLTPSIRPRSLTGVLIVHVSQSGQRLSYMEAGKTYTSVSDAGGSVT 839
 DB ILANSVSLGPELKLTPSIRPRSLTGVLIVHVSQSGQRLSYMEAGKTYTSVSDAGGSVT 3172
 QY 3113 VLAHSVSLGPEFLVFSIRPRSLTGVLIVHVSQSGQRLCYLLEAGKTYTASMDSGAGGTST 3172
 DB VLAHSVSLGPEFLVFSIRPRSLTGVLIVHVSQSGQRLCYLLEAGKTYTASMDSGAGGTST 3172
 QY 840 SITPKOSLCDQWHSAVSIKORILH 866
 DB SITPKOSLCDQWHSAVSIKORILH 866

DB 3173 SVTPKQSLCDGQWHSVAVTIKOHILHL 3199

RESULT 5

Q6VU68 PRELIMINARY; PRT; 3333 AA.

ID Q6VU68

AC Q6VU68;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

GN Lamtin alpha 3 splice variant b1.

GN Name=LAMA3;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;

RA McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V., Coleman-Campbell C.M., Mellerio J.E., Ashton G.S., Dopping-Hepner P.J., Rader R.A., Jamil T., Phillips R.J., Shabir S.G., Haroon T.S., Khurshid K., Moore J.B., Page B., Darling J., Atcherson D.J., Van Steensel M.A., Munro C.S., Smith F.J., McGrath J.A.;

RA "An unusual N-terminal deletion of the lamtin (alpha)3 isoform leads to the chronic granulation tissue disorder laryngo-onycho-cutaneous syndrome.";

RT Hum. Mol. Genet. 12:2395-2409 (2003).

RL [2]

RN SEQUENCE FROM N.A.

RA McLean W.H.1.;

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

EMBL: AY327115; AAC72570.1; -.

DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.

DR GO: GO:0005606; C:lamtin-1; IEA.

DR GO: GO:0005102; F:receptor binding; IEA.

DR GO: GO:0005198; F:structural molecule activity; IEA.

DR GO: GO:0030155; P:regulation of cell adhesion; IEA.

DR GO: GO:0030334; P:regulation of cell migration; IEA.

DR GO: GO:0045995; P:regulation of embryonic development; IEA.

DR InterPro: IPR001844; Chaprin_Cp60.

DR InterPro: IPR008985; Cona_like_1ec_g1.

DR InterPro: IPR006209; EGF like.

DR InterPro: IPR006210; Gal_bind_like.

DR InterPro: IPR006210; IEGF.

DR InterPro: IPR000034; Laminin_B.

DR InterPro: IPR002049; Laminin_EGF.

DR InterPro: IPR001791; Laminin_G.

DR InterPro: IPR009254; Laminin_I.

DR InterPro: IPR010307; Laminin_II.

DR InterPro: IPR008211; Laminin_N.

DR InterPro: IPR003129; TSP_N.

DR Pfam: PF00052; Laminin_B; 1.

DR Pfam: PF00053; Laminin_EGF; 8.

DR Pfam: PF02210; Laminin_G_2; 4.

DR Pfam: PF06008; Laminin_I; 1.

DR Pfam: PF06009; Laminin_II; 1.

DR Pfam: PF00055; Laminin_N; 1.

DR PRINTS: PR00011; EGF_LAMININ.

DR PRODOM: PD003031; Laminin_B; 1.

DR SMART: SM00181; EGF; 8.

DR SMART: SM00180; EGF_Lam; 14.

DR SMART: SM00281; LamE; 1.

DR SMART: SM00282; LamG; 1.

DR SMART: SM00136; LamNT; 1.

DR PROSITE: PS00296; CHAPERONINS_CPN60; UNKNOWN_1.

DR PROSITE: PS00022; EGF_1; 12.

DR PROSITE: PS01186; EGF_2; 1.

DR PROSITE: PS01248; LAMTIN_TYPE_EGF; 13.

DR PROSITE: PS50025; LAM_G_DOMAIN; 5.

KW Laminin EGF-like domain.

SQ SEQUENCE 3333 AA; 36646 MW; 9P99AF49B8EF27DD CRC64;

Query Match 79.3%; Score 3562.5; DB 2; Length 3333;
Best Local Similarity 78.4%; Pred. No. 4.7e-230;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRFNGSGVEYRLPNDELKGYTSLSLFLOPPDLRENGGTEDMFMTLGNKDSKDYIG 60

DB 2391 MRFNGSGVEYRLPNDELKGYTSLSLFLOPPDLRENGGTEDMFMTLGNKDSKDYIG 2450

QY 61 MAVVDGOLTCVYNGDRABVQIDOVLFESSQBAVMVRKORLYOPAKLNTYEATSN 120

DB 2451 MAVVDGOLTCVYNGDRABVQIDOVLFESSQBAVMVRKORLYOPAKLNTYEATSN 2510

QY 121 KKKAAVYDLEGGSSNTLLNLDPEDAVFYVGGYPDPFLPSLRREPPYKGCIEIDLLEN 180

DB 2511 KPEYGVYDMDORNSNTLLNLDPEDAVFYVGGYPDPFLPSLRREPPYKGCIEIDLLEN 2570

QY 181 VLSLYNFKTENTLNTTEVEPCRRKRESDKNYFEGTGYARLPTOPNADPPNFIOITTV 240

DB 2571 VLSLYNFKTENTLNTTEVEPCRRKRESDKNYFEGTGYARLPTOPNADPPNFIOITTV 2630

QY 241 DRGLFPANONDFSLNIEDGNLMVRKYKNSPEKKGIDTINDGKHSLITIGLQ 300

DB 2631 DRGLFPANNGDRFSLNIEDGKLMVRKYKNSPEKKGIDTINDGKHSLITIGLQ 2690

QY 301 KKMWINNERSVRIEGEIPDEFSTYVYLGIPAIRRRFNISIPAFQGMKNLKTSGVVRL 360

DB 2691 KKMWINNVDQNTIIDGVFDFSTYVYLGIPAIRRRFNISIPAFQGMKNLKTSGVVRL 2750

QY 361 NDTVGYTKCSBDMKLVRTASFRGGQMSFTNLDVPSIDRQLSGFOTFQPSGLTLMHQ 420

DB 2751 NDTVGYTKCSBDMKLVRTASFRGGQMSFTNLDVPSIDRQLSGFOTFQPSGLTLMHQ 2810

QY 421 TPTSSLVLTIEDGHIELSTRNSNTEIPKSPGYMDGLHHVSVSDTSGRLRLIDDOYLR 480

DB 2811 TPTSSLVLTIEDGHIELSTRNSNTEIPKSPGYMDGLHHVSVSDTSGRLRLIDDOYLR 2870

QY 481 RNQRLPSEFNAQOSRLGCGHEGCI SNVLVQRFQSPSEVLDLASKSTKQASLGCSLN 540

DB 2871 NKRLLKHISSQSLRLGSGNBEICISNVFVQRLSLSEVLDLTSNLSKRDVSLGCSLN 2930

QY 541 KPPFLMLFKSPFRNKGRIFNVNQLMODAPQAT-RSTAMQDGRSLCPPLNTKASHRLQ 599

DB 2931 KPPFLMLFKGSTFRNKGTFRINQLDTPVAPSPSVKWMQD--ACSPLPKQAHNGLQ 2988

QY 600 PGDSPTSHLLKLPOLKPRSQFSLDIQTSPKLVYAGTKDSFLALYVADGVVPL 659

DB 2989 PGDIPSHLLKLPOLKPRSQFSLDIQTSPKLVYAGTKDSFLALYVADGVVPL 3048

QY 660 GAGGKKLRLSKERYHDGKMTVVFVGLNGKARLVVDGLRAQEGSLPGNSTISPREOYVL 719

DB 3049 GIDGKKLRLSKERYHDGKMTVVFVGHGKRLVVDGLRAREGSLPGNSTISIPAPYVL 3108

QY 720 GLPLSRKPKSLPQHSFVGLRDFOINSKPLSDSPARFVSPCLGSLGKGIYFGQGGHV 779

DB 3109 GSPPGKPKSLPQHSFVGLRDFOINSKPLSDSPARFVSPCLGSLGKGIYFGQGGHV 3168

QY 780 ILANSVSLGPELKLFTSIRPSLTGLVLHVGSQSQRLSYVWEAKKTTVSSDAGSVT 839

DB 3169 VLAHSVSLGPELKLFTSIRPSLTGLVLHVGSQSQRLSYVWEAKKTTVSSDAGSVT 3228

QY 840 SITPKQSLCDGQWHSVAVTIKOHILHL 866

DB 3229 SVTPKQSLCDGQWHSVAVTIKOHILHL 3255

RESULT 6

LMA3 HUMAN STANDARD; PRT; 1713 AA.

ID LMA3 HUMAN

AC Q16787; Q13679; Q13680;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Laminin alpha-3 chain precursor (Epiligrin 170 kDa subunit) (E170)
 DE (Nlcein alpha subunit).
 GN Name=LAMA3;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SSOURCE FROM N.A.
 RC TISSUE=Keratinocytes;
 RX MEDLINE=94357926; PubMed=8077230;
 RA Ryan M.C., Tizard R., Vandevanter D.R., Carter W.G.;
 RT "Cloning of the lamna3 gene encoding the alpha 3 chain of the adhesive
 RT ligand epiligrin. Expression in wound repair.";
 RL J Biol. Chem. 269:22779-22787 (1994).
 RN [2]
 RP SSOURCE OF 1-1331 FROM N.A. (ISOFORMS A AND B).
 RX MEDLINE=96163880; PubMed=8586427;
 RA Vidal F., Baudoin C., Miquel C., Galliano M.-F., Christiano A.M.,
 RA Uitto J., Ortome J.-P., Meneguzzi G.,
 RT "Cloning of the laminin alpha 3 chain gene (LAMA3) and identification
 RT of a homozygous deletion in a patient with Herlitz junctional
 RT epidermolysis bullosa.";
 RL Genomics 30:273-280 (1995).
 RN [3]
 RP DISEASE.
 RX PubMed=12915477; DOI=10.1093/hmg/ddg234;
 RA Irwin McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
 RA Dopping-Hepenstall P.J.H., Bady R.A.J., Jamil T., Phillips R.J.,
 RA Shabir S.G., Haroon T.S., Khurehd K., Moore J.R., Page B.,
 RA Darling J., Atherton D.J., Van Steensel M.A.M., Munro C.S.,
 RA Smith F.J.D., McGrath J.A.;
 RT "An unusual N-terminal deletion of the laminin alpha3 isoform leads
 RT to the chronic granulation tissue disorder laryngo-oncho-cutaneous
 RT syndrome.";
 RL Hum. Mol. Genet. 12:2395-2409 (2003).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
 CC via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-
 CC 6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
 CC phosphorylation of p125-FAK and p80, (3) differentiation of
 CC keratinocytes.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end. The alpha-3 chain is a subunit of laminin-5
 CC (epiligrin/kalinin/nicein), and possibly also a component of
 CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=A;
 CC IsoId=Q16787-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=Q16787-2; Sequence=VSP_003037;
 CC Note=Incomplete sequence;
 CC -1- TISSUE SPECIFICITY: Skin; respiratory, urinary, and digestive
 CC epithelia and in other specialized tissues with prominent
 CC secretory or protective functions. Epithelial basement membrane,
 CC and epithelial cell tongue that migrates into a wound bed. A
 CC differential and focal expression of the alpha-3 chain is observed
 CC in the CNS.
 CC -1- INDUCTION: Laminin-5 is up-regulated in wound sites of human skin.
 CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact
 CC with other laminin chains to form a coiled coil structure.
 CC -1- DISEASE: Defects in LAMA3 are a cause of junctional epidermolysis

CC bullosa gravis (JEB) [MIM:226700]; also known as junctional
 CC epidermolysis bullosa Herlitz-Pearson type. JEB is a blistering
 CC disorder in skin that is characterized by a separation of basal
 CC cells from the basement membrane due to a decreased number of
 CC hemidesmosomes. Laminin-5 is missing from the basement membrane of
 CC patients with the gravis form of epidermolysis bullosa.
 CC -1- DISEASE: Defects in LAMA3 are the cause of laryngochochocutaneous
 CC syndrome (LOCS) [MIM:245601]. LOCS is an autosomal recessive
 CC epithelial disorder confined to the Punjabi Muslim population. The
 CC condition is characterized by cutaneous erosions, nail dystrophy
 CC and exuberant vascular granulation tissue in certain epithelia,
 CC especially conjunctiva and larynx.
 CC -1- SIMILARITY: Contains 3 laminin EGF-like domains.
 CC -1- SIMILARITY: Contains 5 laminin G-like domains.
 CC -----
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 CC -----
 CC DR EMBL; L34155; AAA59483.1; -;
 CC DR EMBL; X85107; CAAS9428.1; -;
 CC DR EMBL; X85108; CAAS9429.1; -;
 CC DR PIR; A55347; A55347.
 CC DR HSSP; P02468; INPB.
 CC DR Genew; HGNC:6483; LAMA3.
 CC DR MIM; 600805; -;
 CC DR MIM; 226700; -;
 CC DR MIM; 245601; -;
 CC DR GO; GO:0005604; C:basement membrane; TAS.
 CC DR GO; GO:0008544; P:epidermal differentiation; TAS.
 CC DR InterPro; IPR008985; Conn_1ike_1ec_g1.
 CC DR InterPro; IPR006209; EGF_1ike.
 CC DR InterPro; IPR009030; Grov_fac_recept.
 CC DR InterPro; IPR002049; Laminin_EGF.
 CC DR InterPro; IPR001791; Laminin_G.
 CC DR InterPro; IPR009254; Laminin_I.
 CC DR InterPro; IPR010307; Laminin_II.
 CC DR InterPro; IPR003129; TSP_N_1.
 CC DR Pfam; PF00053; Laminin_EGF; 2.
 CC DR Pfam; PF00054; Laminin_G; 2.
 CC DR Pfam; PF06008; Laminin_I; 1.
 CC DR Pfam; PF06009; Laminin_II; 1.
 CC DR PROSITE; PS00022; EGF_1; 1.
 CC DR PROSITE; PS01186; EGF_2; 1.
 CC DR PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
 CC DR PROSITE; PSS0025; LAM_G_DOMAIN; 5.
 CC KW Alternative splicing; Basement membrane; Cell adhesion; Coiled coil;
 CC KW Epidermolysis bullosa; Extracellular matrix; Glycoprotein;
 CC Laminin EGF-like domain; Repeat; Signal.
 CC FT SIGNAL 1 20 Potential.
 CC FT CHAIN 21 1713 Laminin alpha-3 chain.
 CC FT DOMAIN 46 201 Domain III A.
 CC FT DOMAIN 67 113 Laminin EGF-like 1.
 CC FT DOMAIN 114 166 Laminin EGF-like 2.
 CC FT DOMAIN 157 185 Laminin EGF-like 3 (incomplete).
 CC FT DOMAIN 164 185 Laminin G-1like 1.
 CC FT DOMAIN 186 769 Domain II and I.
 CC FT DOMAIN 186 769 Domain II and I.
 CC FT DOMAIN 770 971 Laminin G-1like 1.
 CC FT DOMAIN 978 1140 Laminin G-1like 2.
 CC FT DOMAIN 1147 1307 Laminin G-1like 3.
 CC FT DOMAIN 1366 1530 Laminin G-1like 4.
 CC FT DOMAIN 1537 1710 Laminin G-1like 5.
 CC FT DOMAIN 231 327 Coiled coil (Potential).
 CC FT DOMAIN 396 548 Coiled coil (Potential).
 CC FT DOMAIN 594 621 Coiled coil (Potential).
 CC FT DOMAIN 702 765 Coiled coil (Potential).
 CC FT DOMAIN 1686 1713 Coiled coil (Potential).
 CC FT DISULFID 67 76 By similarity.
 CC FT DISULFID 69 83 By similarity.
 CC FT DISULFID 86 95 By similarity.

FT DISULFID 98 111 By similarity.
FT DISULFID 114 126 By similarity.
FT DISULFID 116 135 By similarity.
FT DISULFID 137 146 By similarity.
FT DISULFID 149 164 By similarity.
FT DISULFID 202 202 Interchain (Probable).
FT DISULFID 205 205 Interchain (Probable).
FT SITTE 658 660 Cell attachment site (Potential).
FT CARBOHYD 542 542 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 645 645 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 745 745 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 882 882 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 964 964 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1108 1108 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1131 1131 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1325 1325 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1477 1477 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1667 1667 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 1 45 MCHLMTFGALGCGCLGYSQQQVPPFLQPPGSGQLQASYVE
FRPS -> KVSSTGGYLYTQAKSFALPGDMVLEKKPVOL
TQGMKSIYEETTPRDLHGRVAVNEGNFHASRAV
SREELMTVLSRLADVRILQGLYFTETRLTSEGLEEADT
GSGRIALAVRICACPPAYAGDSC (in isoform B).
/FtId=VSP_003037.
W -> R (in Ref. 2).
ATG -> GWC (in Ref. 2).
M -> K (in Ref. 2).
R -> L (in Ref. 2).
E -> Q (in Ref. 2).
D -> A (in Ref. 2).
G -> A (in Ref. 2).
SQ SEQUENCE 1713 AA; 189304 MW; 45EAB9E1017860B3 CRC64;
Query Match 79.3%; Score 3560.5; DB 1; length 1713;
Best Local Similarity 78.4%; Pred. No. 2,3e-230;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;
QY 1 MRNNGSGVYVRLPNLEDKGTTSLFLQRPDLBENGTEPMFYMTLGNKQASQDYIG 60
DB 771 MRNNGSGVYVRLPNLEDKGTTSLFLQRPDNRNGTEPMFYMTLGNKQASRDYIG 830
QY 61 MAVVDQQLCVVNLGPREAEVQIDVLTSESEQAVMDRKPQRIQPAKLNTKRAATN 120
DB 831 MAVVDQQLCVVNLGPREAEVQIDVLTSESEQAVMDRKPQRIQPAKLNTKRAATN 890
QY 121 KPRKAPVYDLEGGSSNTLNTLDEEDAVFYVGYPPFELPSRLRFPYKGCIELDLINEN 180
DB 891 KPRKAPVYDLEGGSSNTLNTLDEEDAVFYVGYPPFELPSRLRFPYKGCIELDLINEN 950
QY 181 VLSLVNFKTTFNLTTEVEPCRRRKESDNKYEFGTYARIPTQPNAPFPNFIQTITTV 240
DB 951 VLSLVNFKTTFNLTTEVEPCRRRKESDNKYEFGTYARIPTQPNAPFPNFIQTITTV 1010
QY 241 DRGLLFFAENQDFISLNTIEDGLMRYKLNSEPKKGRDITNGKSHLITIGKIQ 300
DB 1011 DRGLLFFAENQDFISLNTIEDGLMRYKLNSEPKKGRDITNGKSHLITIGKIQ 1070
QY 301 KRWMINNERSVRIEESIPDFSTYYLGGIPAIAREFNISTPAFQCGMKLTKTSGVNL 360
DB 1071 KRWMINNERSVRIEESIPDFSTYYLGGIPAIAREFNISTPAFQCGMKLTKTSGVNL 1130
QY 361 NDTVGVYTKKCSBDMKLVRTASFRGGQMSFTNLVDVSTDRFQSLFSGFQTFQPSGTLINQ 420
DB 1131 NDTVGVYTKKCSBDMKLVRTASFRGGQMSFTNLVDVSTDRFQSLFSGFQTFQPSGTLINQ 1190
QY 421 TRTSLLVLTDEGHIELSTRDSNIPFKSPQYTMQGLHHVSYISPTSGRLIIDQVLR 480
DB 1191 TRTSLLVLTDEGHIELSTRDSNIPFKSPQYTMQGLHHVSYISPTSGRLIIDQVLR 1250
QY 481 RNQRLPFSNAQOQLRIGGHEFGCISNVLVQRFQSPSEVLTDLASTKQKASIGGCSLN 540
DB 1251 RNQRLPFSNAQOQLRIGGHEFGCISNVLVQRFQSPSEVLTDLASTKQKASIGGCSLN 1310

QY 541 KPPFLMTKSPKREKKEKRIENVNQLMODAPQAT-RSTEAQDGRSCPLPLNTKASHRALQ 599
DB 1311 KPPFLMTKSPKREKKEKRIENVNQLMODAPQATPVASPRSVWQD--ACSLPPTQANHGALQ 1368
QY 600 PCDSPSHLLKLPQELLKPRSPQSLDIQTSFKLVYVYAGKQSLFLVYADGRVVAL 659
DB 1369 PCDSPSHLLKLPQELLKPRSPQSLDIQTSFKLVYVYAGKQSLFLVYADGRVVAL 1428
QY 660 GAGGKKRLRSKERYHDKMHTVVGALNGKRAVLVVDGIRAOEGSLPQNSTISPREQVYL 719
DB 1429 GTDGGKKRLRSKEREKNDGKMHVVGHDGKRLVVDGIRAREGSLPQNSTISIRAPVYL 1488
QY 720 GLPLRKPKSLPQHSFVGLADPQLNSKPLDPSAPRFGVSPCLGSLKGIYFSQGGHV 779
DB 1489 GSPPGKPKSLPQHSFVGLADPQLNSKPLDPSAPRFGVSPCLGSLKGIYFSQGGHV 1548
QY 780 IIANVSIGPELKLFPFSIRPSRLTGVLLIHVSQSGQRLSYVMEAKVYTSVSSDGGSVT 839
DB 1549 IIANVSIGPELKLFPFSIRPSRLTGVLLIHVSQSGQRLSYVMEAKVYTSVSSDGGSVT 1608
QY 840 SITPKQSLCDGQMSVAVSIXQRIHL 866
DB 1609 SITPKQSLCDGQMSVAVSIXQRIHL 1635
RESULT 7
Q96TGO PRELIMINARY; PRT; 1806 AA.
AC Q96TGO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha 3B chain of laminin-5 (fragment).
GN Name=LAMA3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Aberdam D., Vidal, Baudoin, Miguel, Ortonne, Meneguzzi;
RL Submitted (FEB-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL; X84960; CAA59325.1; -.
DR HSSP; P02468; INPE.
DR GO; GO:0005606; C:laminin-1; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR GO; GO:0030334; P:regulation of cell migration; IEA.
DR GO; GO:0045995; P:regulation of embryonic development; IEA.
DR InterPro; IPR001844; Chaprinin Cpn60.
DR InterPro; IPR008985; Cona like lec_g1.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000034; laminin B.
DR InterPro; IPR002049; laminin_BGF.
DR InterPro; IPR001791; laminin_G.
DR InterPro; IPR009254; laminin_I.
DR InterPro; IPR010307; laminin_II.
DR InterPro; IPR003129; TSP N.
DR Pfam; PF00052; laminin_B_1.
DR Pfam; PF00053; laminin_BGF_2.
DR Pfam; PF02210; laminin_G_2; 4.
DR Pfam; PF06008; laminin_I_1.
DR Pfam; PF06009; laminin_II_1.
DR ProDom; PD003031; laminin_B_1.
DR SMART; SM00180; EGF_lam; 2.
DR SMART; SM00281; lamB; 1.
DR SMART; SM00282; lamB; 5.
DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKOWN_1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.

KM Laminin EGF-like domain.
 FT NON TER 1 1
 SQ SEQUENCE 1806 AA; 199411 MW; EF94CBE2A5A52B93 CRC64;
 Query Match 79.3%; Score 3560.5; DB 2; Length 1806;
 Best Local Similarity 78.4%; Pred. No. 2.5e-230;
 Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRNNGSGVAVRLPNDLEDKGTTSLSLFLQRPDLRENGGTEDMFWYLGAKDASXDYIG 60
 DB 864 MRNNGSGVAVRLPNDLEDKGTTSLSLFLQRPDLRENGGTEDMFWYLGAKDASXDYIG 923
 QY 61 MAVVDGQLTCVYMLGDEAEVQIDQVLTSESGOAVMDRYKFORIYQPAKANTTKAATSN 120
 DB 924 MAVVDGQLTCVYMLGDEAEVQIDQVLTSESGOAVMDRYKFORIYQPAKANTTKAATSN 983
 QY 121 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYGPPDFELPSRLRPPPYKGCIELDLNEN 180
 DB 984 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYGPPDFELPSRLRPPPYKGCIELDLNEN 1043
 QY 181 VLSLNFKTTNNTTEVEPCRRKESDKNYREGGYANIPQOPNAPFPNFIQTITTY 240
 DB 1044 VLSLNFKTTNNTTEVEPCRRKESDKNYREGGYANIPQOPNAPFPNFIQTITTY 1103
 QY 241 DRGLLFAENQDNPISINIDGNLWRYKLNSEBPXKGRDPTINDGKHSIIITGKIQ 300
 DB 1104 DRGLLFAENQDNPISINIDGNLWRYKLNSEBPXKGRDPTINDGKHSIIITGKIQ 1163
 QY 301 KRWMINVNSVRIEIEIPDFSTYLLGDIPIAIRERFNISTPAFQCGMKLKTTSGVVRL 360
 DB 1164 KRWMINVNSVRIEIEIPDFSTYLLGDIPIAIRERFNISTPAFQCGMKLKTTSGVVRL 1223
 QY 361 NDTVGVTKKCESEDMKLVIRASFSRGGQMSFTNLDVPESTRFQSLFSGFTQPSGTLINQ 420
 DB 1224 NDTVGVTKKCESEDMKLVIRASFSRGGQMSFTNLDVPESTRFQSLFSGFTQPSGTLINQ 1283
 QY 421 TRTSLLVLTLEDHIELSTDSNIPFKSGPTMDGLHIVSVISDSGRLIIDQVLR 480
 DB 1284 TRTSLLVLTLEDHIELSTDSNIPFKSGPTMDGLHIVSVISDSGRLIIDQVLR 1343
 QY 481 RNORLPSFNAOOLSLRGAGHFGAGCISNVVYORFOSPEVYDLASKSTKDAALGCGSLN 540
 DB 1344 RNORLPSFNAOOLSLRGAGHFGAGCISNVVYORFOSPEVYDLASKSTKDAALGCGSLN 1403
 QY 541 KPPFLMLFKSPKPKNGRIINVOQADAPQAT-RSTEANODGSCILPINTAKSHRALQ 599
 DB 1404 KPPFLMLFKSPKPKNGRIINVOQADAPQAT-RSTEANODGSCILPINTAKSHRALQ 1461
 QY 600 RGDSPSHLLKLPQELIKRSPQSLDIQTTSFKGIVFYAGTDSPLATVVAAGRVVRL 659
 DB 1462 RGDSPSHLLKLPQELIKRSPQSLDIQTTSFKGIVFYAGTDSPLATVVAAGRVVRL 1521
 QY 660 GAGGKQLRLSKERHYDGHKMTVVFGLNGKARLVVDGLRAOEGSLPGNSTISPREOVL 719
 DB 1522 GAGGKQLRLSKERHYDGHKMTVVFGLNGKARLVVDGLRAOEGSLPGNSTISPREOVL 1581
 QY 720 GLPLSRXPKSLPOHSFVGLCLADPQLNSKPLDSPARFVSPCLGSLKGIYRSGGSHV 779
 DB 1582 GLPLSRXPKSLPOHSFVGLCLADPQLNSKPLDSPARFVSPCLGSLKGIYRSGGSHV 1641
 QY 780 ILANSVSLGPELKLTPSIRPSRLTGVLINHGSGOGLSYVMKAGKTTSVSDAGASVT 839
 DB 1642 ILANSVSLGPELKLTPSIRPSRLTGVLINHGSGOGLSYVMKAGKTTSVSDAGASVT 1701
 QY 840 SITPKOSLCDGOWHSAVASIKORILHL 866
 DB 1702 SITPKOSLCDGOWHSAVASIKORILHL 1728

RESULT 8
 Q76E14 PRELIMINARY; PRT; 3333 AA.
 AC Q76E14;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Laminin alpha 3b chain.
 GN Name=LAMA3;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SOURCE: FROM N.A.
 RA Kariya Y., Yasuda C., Nakashima Y., Iehida K., Teubota Y.,
 RA Miyazaki K.;
 RT "Characterization of laminin 5B and NH2-terminal proteolytic fragment
 of its alpha3b chain: promotion of cellular adhesion, migration, and
 proliferation.";
 RL J. Biol. Chem. 279:24774-24784 (2004).
 DR EMBL; AB107369; BAD13428.1; -;
 DR GO; GO:0005578; Extracellular matrix (sensu Metazoa); IEA.
 DR GO; GO:0005606; C.laminin-1; IEA.
 DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0030155; P:regulation of cell adhesion; IEA.
 DR GO; GO:0030334; P:regulation of cell migration; IEA.
 DR GO; GO:0045995; P:regulation of embryonic development; IEA.
 DR InterPro; IPR001844; Chapterin_Cpno.
 DR InterPro; IPR008985; Cona_like_1ec_g1.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000034; Laminin_B.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR009254; Laminin_I.
 DR InterPro; IPR010307; Laminin_II.
 DR InterPro; IPR008211; Laminin_N.
 DR InterPro; IPR003129; TSP_N.
 DR Pfam; PF00052; Laminin_B_1.
 DR Pfam; PF00053; Laminin_EGF; 8.
 DR Pfam; PF02210; Laminin_G_2; 4.
 DR Pfam; PF06008; Laminin_I; 1.
 DR Pfam; PF06009; Laminin_II; 1.
 DR Pfam; PF00055; Laminin_N; 1.
 DR PRINTS; PRO0011; EGF/LAMININ.
 DR ProDom; PD003031; Laminin_B; 1.
 DR SMART; SM00181; EGF; 8.
 DR SMART; SM00180; EGF_Lam; 14.
 DR SMART; SM00281; LamB; 1.
 DR SMART; SM00282; LamG; 5.
 DR SMART; SM00136; LamNT; 1.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; 12.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 13.
 DR PROSITE; PS00025; LAM_G_DOMAIN; 5.
 KM Laminin EGF-like domain.
 SQ SEQUENCE 3333 AA; 366616 MW; 6F99A4D4B99FCB0 CRC64;
 Query Match. 79.3%; Score 3560.5; DB 2; Length 3333;
 Best Local Similarity 78.4%; Pred. No. 6.4e-230;
 Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRNNGSGVAVRLPNDLEDKGTTSLSLFLQRPDLRENGGTEDMFWYLGAKDASXDYIG 60
 DB 2391 MRNNGSGVAVRLPNDLEDKGTTSLSLFLQRPDLRENGGTEDMFWYLGAKDASXDYIG 2450
 QY 61 MAVVDGQLTCVYMLGDEAEVQIDQVLTSESGOAVMDRYKFORIYQPAKANTTKAATSN 120
 DB 2451 MAVVDGQLTCVYMLGDEAEVQIDQVLTSESGOAVMDRYKFORIYQPAKANTTKAATSN 2510
 QY 121 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYGPPDFELPSRLRPPPYKGCIELDLNEN 180
 DB 2511 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYGPPDFELPSRLRPPPYKGCIELDLNEN 2570


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FT DISULFID 269 269 Interchain (Probable).
FT CARBOHYD 104 104 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 215 215 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 308 308 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 458 458 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 524 524 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 550 550 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 571 571 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 574 574 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 631 631 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 639 639 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 735 735 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 751 751 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 754 754 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 780 780 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 803 803 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 1086 1086 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 1281 1281 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 1359 1359 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 1411 1411 N-linked (GlcNAc...) (Potential)
FT CONFLICT 143 143 A -> P (in Ref. 1).
FT CONFLICT 178 178 L -> F (in Ref. 1).
FT CONFLICT 265 265 G -> GMDCTPIS (in Ref. 4).
FT CONFLICT 276 276 D -> A (in Ref. 4).
FT CONFLICT 491 491 Y -> H (in Ref. 2 and 3).
FT CONFLICT 1057 1057 T -> P (in Ref. 1).
FT CONFLICT 1110 1112 SGR -> GGP (in Ref. 4).
SQ SEQUENCE 1816 AA; 201908 MW; 04B9AF379A0FAAD CRC64;

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Query Match 26.5%; Score 1190; DB 1; Length 1816;
Best Local Similarity 33.2%; Pred. No. 1.le-10;
Matches 310; Conservative 161; Mismatches 372; Indels 90; Gaps 27;

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QY 1 MRFNKSGVRLPNDLEDIKGYTSLFL-----QRPDLKNGSTEMFMVYAGNDASK 56
DB 829 MHPDGGAVVSHRTSMDDIKAFISLTYMKPKYKRELTE---TADQFLTYLGSNAKK 885
QY 57 DYIGMAVVDQQLTCVYVNLGDEARVQIDQVLTSESQGEAVMDKRFQRIQPAKLTATYKE 116
DB 886 EWMGLAIKNDNLVYVNLGDKVDIPLDS--KPVSSMPAFSVIKLERVGKHKRFLVTP 943
QY 117 ATSNKPKAPAVYDLEGGSSNTLLNLDPEDAVFYGVGYPDPPELPSRLRPYKICIELDD 176
DB 944 SLSTSEKEKFKKGEFSGDSDLDLDPEDVTFVYGVGYPSPKFKPTSLNTEGFGCLELAT 1003
QY 177 LNSNVSLVYKTTNTNTEVEPCRRK-----EESDKYFPGTGA--RIYQNR--A 227
DB 1004 LNDVSLVYKHTIYNDPSTVPCARDKLAFTQSRASYFPDGSQYAVVRDITRRGKFG 1063
QY 228 PFPNFIQTITQTVDRGLLFFAENQDNFISLNIEDGNLMVY-----KLNSEPKKGI 280
DB 1064 QVTRFDEIVRTPADNGILLMNVGSMFRLKEMNGYLAHYVDGFGSSGRHLEDYTKKA- 1122
QY 281 RDTINDGKDSIIITIGKLOKRMVINVESVRI--EGEIFPSTYIAGIP-----I 331
DB 1123 --OINAKYHIBISI-IYHNDKKMILVDRHVKVSMDEKKKIFPTDIYIGAPPEILOSR 1179
QY 332 AIRERFNISTPAFOGCKMKNL---KTISSGVRLNDTVGVTKKSGEDMVLVTASFSRGGM 388
DB 1180 ALPAHPLDI-NRRCCKGKGFQPKDKRNLLIEQETTLGVGVCPEDSLISRRAFFN--GQS 1236
QY 389 SFTNLD--VPSTDRFOLSFQTFQFQPSGTLNHOQRTSLAVLTLEDGHIIEISTDNSNPIF 447
DB 1237 FMSIQKISFPDGEFGFNFRITQPNGLLFYVAGSVFPISLDNGVIMDK--GIKVQ 1294
QY 448 KSPFTYMDGLLHVSVISDTSGLR--LLID-DQVLRNRQLPFSFNAQSLR--LGG-- 499
DB 1295 SVDKQYVDGISHF--VISSVSPRYEYLIVDKSRGSKNPKGKILBQQAEEKKFFFGGSP 1352
QY 500 -----GHFECCISNVLVQRFSGSEPVLDLASKYKQDASIGCGSINKPPLMKPKSKRF 554
DB 1353 ISAQVAFNFTGCSISNAVYTRVDRDVEVDFORYTEKVTSLYECPIESSPLFLHKKGKNL 1412

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QY 555 NKGRIFNVNQ--IMODAPQATSTRAMODGSCLEPLNT-----KASHRALQF 600
DB 1413 SKPKASQNKKGKSKSDAP-----SWDPVALKPKPERVTPRNHCHLSNPRAIETHAYQ 1465
QY 601 GDSPLSHLLKLPQELTRPSQPSLDIOTTPSKGLVFAFGTKD--SFLALYADRRVPA 658
DB 1466 GGTANSRQEFHILKIDFGAKSQFSIRLTRSSHGMI FVYSQDEENDFMTLFLAHRLLVYM 1525
QY 659 LDAGGKCLRISKERYHDKHTTVFGLNGCARLVNDQAEQSL--PGNSTISPRQV 717
DB 1526 FVVGHKTKIRSGEKTNDGLMHDVIFIRBSRGRVLDGLRYLESLEPTETATMKIKGPI 1585
QY 718 YLGLPSRKPESLPQ-----HSFVGLRDPOLNSKELDSPARFVSPCLGSGLEKGIYFS 773
DB 1586 YLGGVAPGAVANVQDINSIYSPSGLSNLQNLGASITSQTFVSTPCBEGMETGYFS 1645
QY 774 QCGGVYILANSVLSPELKLTRSIIPRSLITGLVHVGSQSGQRLSVYMEAGVYTTVSDD 833
DB 1646 TEGGVYVLDSESNIGIKKEIAFEVRPRSSGTLVHGHSVNGEYILNVHMKGVIVKVNNG 1705
QY 834 AGGSVTSITPKQSLCDGGQHSVAVSIXQRIIHL 866
DB 1706 IHPSTSVTPKQSLCDGRNHRITVIRDSNVOL 1738

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RESULT 11
Q91V00 PRELIMINARY; PRT; 1254 AA.
AC Q91V00;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lame4 protein (Fragment).
GN Name=Lame4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mx FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,
RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smalins D.E., Scherch A., Schein J.B.,
RA Jones S.U., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mx FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008533; AA008533.1; -.
DR HSSP; 060675; 10U0.
DR MGD; MGI:109321; Lama4.
DR GO; GO:0005605; C:basal lamina; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0001568; P:blood vessel development; IMP.

```


QY 392 NLD-VPSTDRFOLSPFGOTFOPSGTLLNHTQRTSLVLEEDGHIELSTDSNIPKSP 450
 DB 1242 SIOKISFPDGEFEGFNRTIQPNLFLYTSGSVSEISLDNGVVDVK--GIKWSTD 1299
 QY 451 GTYMDGLLHH-VSVISPTSGRLRLIDQVLRNORLPSPFSAOQS-----LRLG--- 499
 DB 1300 KOYHDGLPHVTVMSISDTR-YELVVDKSRLRGKN--PTKGABEQTOTTEKKFVGGSPIS 1356
 QY 500 ---GHEPGCISNVLVORFOSPEVLDLASKSTYKDAISLGGCSLANKPPLMLFSPKPK 556
 DB 1357 POYANFGICISNMYFTLDRDVEVEDFORYSSEKHTSLYRCPIESSPLFLHKKGNKSK 1416
 QY 557 GRIFNVQALQADAP-----OATRSTEAMQGRGSLPPLNFKASHRALOPGDP 604
 DB 1417 PKTKKQKSKDAPSMPTGLKFLKQKAPRDSH-----CHUSSFRAIEHAVOYQCTA 1469
 QY 605 TSHLLKLPOELLKPRSPFSLDIQTTSFKGLVFPYAGTKD--SFPLVYADGRVVFALGAG 662
 DB 1470 NSHOEFHEHGGDGEKSGQFALRLKTRNSHGMIFVSDQENDEFWTLFLANGRLVFMNVG 1529
 QY 663 GKTLRLSKRYNDGKMTTVFGLNGSKALVVDGLFAQGSGL-PGNSSTISPREQVTL-G 720
 DB 1530 HKTLKTRSQEKYNDGLMHDVIFIREKSGRLVIDGLVLEBRLPFGSAWKIKGPIYLCG 1589
 QY 721 LPLSRKPKSL---PQHSFVGLCLDPOLSKPLDPSPARFGVSPCLGSLKGIYFGQGG 777
 DB 1590 VAPGRVKNVQITSVYSFSGCLGNLQNGASITSAOSTFVTPTCEBPMETGTFSTEGG 1649
 QY 778 HVLIANSVSLPELKLFTSIRPSRLNGLVHVSQSGQRLSVVMEAGKVTTSVSDAGGS 837
 DB 1650 YVVLDBSFNIGLKEFLAEFRPRSSGTLVHGHSVNGEYLVNHRNQVYVKNNGVGRDF 1709
 QY 838 VTSITPKQSLCDGQWHSVAVSIKORILH 866
 DB 1710 STSVTPKQNLCDGWRHRTYTRDSNVQL 1738

RESULT 13
 LMA5_HUMAN STANDARD; PRT; 3695 AA.
 AC 015230; Q8WZ47; Q9H1P1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Laminin alpha-5 chain precursor.
 GN Name=LMA5; Synonyms=K1AA0533, KIAA1907;
 OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
 RA DeLorkas P., Matthews L.H., Ashurst J.L., Burton J.G., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagunley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard D.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grahame D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leveson-Hall M.H., Leverhwa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McManus L.J., McIlroy K., McMurtry A.A.,
 RA Milne S.A., Mistry D., Moore M.U.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Stuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,

RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whiteaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RP SEQUENCE OF 197-1934 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=21456161; PubMed=11572484;
 RA Nagase T., Kikuno R., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XXI.
 RT The complete sequences of 60 new cDNA clones from brain which code for
 RT large proteins.";
 RL DNA Res. 8:179-187(2001).
 RP SEQUENCE OF 2051-3695 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96280545; PubMed=9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:31-39(1998).
 RP SEQUENCE OF 2743-3695 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97415425; PubMed=9271224; DOI=10.1016/S0014-5793(97)00686-8;
 RA Durkin M.E., Leochel F., Mattei M.-G., Gilpin B.J., Albrechtsen R.,
 RA Newer U.M.;
 RT "Tissue-specific expression of the human laminin alpha5-chain, and
 RT mapping of the gene to human chromosome 20q13.2-13.3 and to distal
 RT mouse chromosome 2 near the locus for the ragged (Ra) mutation.";
 RL FEBS Lett. 411:296-300(1997).
 RP EXPRESSION IN RETINA.
 RX MEDLINE=20422761; PubMed=10964957;
 RA Libby R.T., Champiand M.-F., Claudepierre T., Xu Y., Gibbons E.P.,
 RA Koch M., Burgess R.E., Hunter D.D., Brunken W.U.;
 RT "Laminin expression in adult and developing retinae: evidence of two
 RT novel CNS laminins.";
 RL J. Neurosci. 20:6517-6528(2000).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin-15 complex is an heterotrimer composed of three
 CC chains (alpha-5/beta-2/gamma-3) which are bound to each other by
 CC disulfide bonds into a cross-shaped molecule comprising one long
 CC and three short arms with globules at each end.
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -1- TISSUE SPECIFICITY: Expressed in heart, lung, kidney, skeletal
 CC muscle, pancreas, retina and placenta. Little or no expression in
 CC brain and liver.
 CC -1- DOMAIN: Domain G is globular and is part of the major cell-binding
 CC site located in the long arm of the laminin heterotrimer.
 CC -1- SIMILARITY: Contains 22 laminin EGF-like domains.
 CC -1- SIMILARITY: Contains 5 laminin G-like domains.
 CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 DR EMBL; AL354836; CAC22309.1; ALT_SEQ.

Db 3471 GIPASSHSKLPYTVFSGCVKRLRHGRPLGAPITMAGVTPCIIIGPLRAGLFFPGSGGV 3530
 QY 779 VILANSVSLGPELKTFFSIRPSRLTGVLIVHG-SOSGQRLSYMEAGKTTTSVSDAGGS 837
 Db 3531 ITLDLPGALTLFVGLSEYRPLAVLTGILHGOAKRPPIYLOLVTEKQVILRADGAGF 3590
 QY 838 VTSITPKQSLCDGQMSVAVSIRKORILHT 866
 Db 3591 STSVTRPSVLCDGQMRHLAVMKSGNVRL 3619

RESULT 15

Q6ZQAI PRELIMINARY; PRT; 1524 AA.
 ID 06ZQAI
 AC 06ZQAI
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE MKIA0533 protein (Fragment).
 GN Name=MKIA0533;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryonic tail;
 RX PubMed=14621295;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
 RA Saga Y., Nagase T., Ohara O., Koga H.,
 RT Prediction of the coding sequences of mouse homologues of KIA gene:
 RT I1. the complete nucleotide sequences of 500 mouse KIA-homologous
 RT cDNAs identified by screening of terminal sequences of cDNA clones
 RT randomly sampled from size-fractionated libraries.";
 RL DNA Res. 10:167-180(2003).
 DR EMBL AK129157; BAC97967.2; -;
 DR GO; GO:0005604; C:basement membrane; IDA.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005178; P:integrin binding; IDA.
 DR GO; GO:0005515; P:protein binding; IPT.
 DR GO; GO:0030324; P:limb development; IMP.
 DR GO; GO:0007517; P:muscle development; IMP.
 DR InterPro; IPR008985; Cona like_1ec_g1.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR009030; Grow fac. recept.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR009254; Laminin_I.
 DR InterPro; IPR010307; Laminin_II.
 DR InterPro; IPR001368; TNFR c6.
 DR InterPro; IPR003129; TSP_N.
 DR Pfam; PF00053; Laminin_EGF; 2.
 DR Pfam; PF02210; Laminin_G_2; 4.
 DR Pfam; PF02008; Laminin_I; 1.
 DR Pfam; PF06009; Laminin_II; 1.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR SMART; SM00282; EGF_Lam; 2.
 DR SMART; SM00282; LamG; 5.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_3.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 KW Laminin EGF-like domain.
 FT NON_TER 1
 FT NON_TER 1524
 SQ SEQUENCE 1524 AA; 166516 MW; F43411828F8B691 CRC64;

Query Match 21.2%; Score 950; DB 2; Length 1524;
 Best local Similarity 30.6%; Pred. No.1.3e-54;
 Matches 285; Conservative 167; Mismatches 360; Indels 120; Gaps 37;

QY 1 MRFNKGSEVAVLPNDLEDLKGYSLSLFLQRPDLRENG--TEDMFVYMLGNKADSKDY 58
 Db 572 MKEFNRSQVRLRTPRLDLADLAAYTALKFHIQSPVAPAPRPKNKGTHFVLVNGSSQATDY 631
 QY 59 IGMVAVDQQLTCVYVNLGR-EAEVQIDQVLTESESGEAVMDRYKQRTYQAKNTYEA 117
 Db 632 MGVSLRNQKVMHVVYVLGAGPTTSLIDENIBQ-----FAVSLDRTLQGFHMSVYE- 684
 QY 118 TSNKPKADAVYDLBGS-----SNTLLNLPEDAVFYVGGYPPDFELPRLPPPKGIC 173
 Db 685 -----KQWHEIKQDITYAPGSEGLNHPDDFVYVGGYSNTPPRLPFPGLGIC 738
 QY 174 LDDLNENYLSLYNFKTFTNLTTEVEPCRRKE-----SDKNYEGTGVARIPTQNPAP 228
 Db 739 METLEBVVSLYNFQTPMLDTAVDKPCARSKATGDPMLTDSYLDGSGFARISPEXQ-- 796
 QY 229 PPN--PQTQITVYDRGLPFAENQDNFISLNTEDGMLMRYKLS-----EPK- 276
 Db 797 FSNTRRFOEHLVSYNGIIFFLKQSQFLCIVQEGTLVFPYFGSLKPADPLQPPQA 856
 QY 277 -----EKGRDITNDKDSILITIGKLQKRMWINNERSVRLEGIFPFSYVYLGCI-- 329
 Db 857 LTAASKALQVFLAAGNRKRVLV--RVRATVPSVDQDML--EMAD--AYLGAVPE 908
 QY 330 --PIAIRERFNISTPAFGQCMKNLK--KTSGVRLNDTVGVYKXCSMDKLVPTASFSR 384
 Db 909 QLPFLSLRLFP-SGGSVRCIGIKIKALKKYVDLKRLL-TTGISFCGTADLLVGRMTFHG 966
 QY 365 GQGMFPMLDV-RSDRQQLSRGQTPQPSGLTNHQRTSSLVTLTDGHIELSTRSN 443
 Db 967 HGFLLALPDVAITLVVYSGFGFGTQDNMLLYRTSPDGPYQVLSBGHVTLEFMQOE 1026
 QY 444 IIFKSPGYMDGLHHYVSDTSGRLLLID--QVLRBQRQLPSFNAQ-----QSRL 497
 Db 1027 V---ETQVVPADGAHHVAFNSVTGWLVYDDQQLVKSHERTTPMLQLQPEESRLL 1083
 QY 498 GQ-----GHEGCSIVLVQRFQSPPEVLDAKSKTKKQASLGCSLKNRPFLMFKS 550
 Db 1084 GGLPVSGTFHNSGCSISNVFQRLRGQRFVDLHQMGSVNVSV-GCT-----PAQLIETS 1138
 QY 551 PRRFRKGLFNNQMODAPQATRSTEAW-----ODGSCLPRLNTKASHALQF-GSP 604
 Db 1139 RATAQK-----VSRSRQPSQDLACTPMLPQTIDAVQFGGRLPS-----YLQVGLSP 1188
 QY 605 TSHLLKLPOELKPKRSQFSLDIOTSPKGLVFYAGTQSFALVYADGRVVFALGAGAK 664
 Db 1189 SHRNRLHLM-LVRPHASQGLLSTAP-----MSGRSPS-LVFLNIGHFVAQTEGCP 1241
 QY 665 KILRSKERYHDGKWHVTVFGLNGKARLVVDGLRA-QEGSLPGNSTISPREQVYL---- 719
 Db 1242 RLQVQSRQHSRAGQNHVSVRWGMQQLQVVDGSGQWQKALHHRVPAERPPQYTLVG 1301
 QY 720 GIPLRKPKSLP-QHSFPGCLRDPLNPKRPDPSARKGVSPCLGSLSEKGIYFSGGGH 778
 Db 1302 GIPASSYSKLPVSVGFGCLKQLQDKQPLRTPQWGVVPCVSPLEDGILFFPGSGGV 1361
 QY 779 VILANSVSLGPELKTFFSIRPSRLTGVLIVHGSQSGQRLSY-MEAGKTTTSV--SSDA 834
 Db 1362 VTLLEPKAMRYVSLLEMRPLAAGLIFHL-----GQALATPYMLQKVLTEVYLQANDG 1417
 QY 835 GGSVTSITPKQSLCDGQMSVAVSIRKORILHT 866
 Db 1418 AGSFSTWYTPCLCDGMRHRAVAVINGRDTLRL 1449

Search completed: February 22, 2005, 08:24:20
 Job time : 151.522 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:04:10 ; Search time 159.651 Seconds
(without alignments)
2097.921 Million cell updates/sec

Title: US-10-817-423-2

Perfect score: 4491

Sequence: 1 MRFNGKSGYVRLPNDL.....LDCGMHSAVAIKRIHL 866

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq.16Dec04:*
1: geneseq1390s:*
2: geneseq1390s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4491	100.0	1694	3 AAB48461	Aab48461 Rat lamin
2	4491	100.0	1725	3 AAB48460	Aab48460 Rat lamin
3	3560.5	79.3	1693	3 AAB48459	Aab48459 Human lam
4	3560.5	79.3	1693	3 AAB48457	Aab48457 Human lam
5	3560.5	79.3	1713	3 AAB48458	Aab48458 Human lam
6	3560.5	79.3	1713	6 ABR92102	Ab92102 Human cer
7	3560.5	79.3	1713	7 ADD29904	Add29904 Human lam
8	3560.5	79.3	1713	7 ADG37225	Adg37225 Human lam
9	3560.5	79.3	1713	8 ABM61957	Abm61957 Tumour-as
10	3560.5	79.3	1713	8 ADR87606	Adr87606 Human lam
11	3560.5	79.3	1724	3 AAB48456	Aab48456 Human lam
12	3560.5	79.3	3332	7 ADB08094	Adb08094 Novel pro
13	3552.5	79.1	1713	2 AAR70148	Aar70148 Deduced s
14	1599	35.6	469	4 AAG75103	Ag75103 Human col
15	1310	29.2	770	2 AAW26584	Aaw26584 Rat hemid
16	1198	26.7	1792	3 AAB48443	Aab48443 Human lam
17	1198	26.7	1800	3 AAB48445	Aab48445 Human lam
18	1198	26.7	1816	3 AAB48442	Aab48442 Human lam
19	1198	26.7	1816	8 ADR87600	Adr87600 Human lam
20	1198	26.7	1824	3 AAB48444	Aab48444 Human lam
21	1192	26.5	1823	5 ABP63020	Abp63020 Human pol
22	1190	26.5	1561	7 ADJ68348	Adj68348 Human hea
23	1190	26.4	1816	8 ADP08401	Adp08401 Human lam
24	1187	26.4	984	5 ABB80819	Abb80819 Heparin b
25	1187	26.4	1816	7 ADC01877	Adc01877 Human lam

26	1185	26.4	1816	7 ADC01879	Adc01879 Human lam
27	1183	26.3	1792	3 AAB48447	Aab48447 Mouse lam
28	1183	26.3	1816	3 AAB48446	Aab48446 Mouse lam
29	1181.5	26.3	1815	5 ABB80853	Abb80853 Heparin b
30	1170.5	26.1	983	5 ABB80818	Abb80818 Heparin b
31	1045.5	23.3	1677	8 ADM87708	Adm87708 Human EST
32	1045.5	23.3	3695	8 ADI28030	Adi28030 ECMCAD pr
33	1045.5	23.3	3695	8 ADN04478	Adn04478 Antipeori
34	1045.5	23.3	3696	5 AAE17310	Aae17310 Human lam
35	1045.5	23.3	3705	5 AAE17309	Aae17309 Human lam
36	1042.5	23.2	1601	4 AAM39009	Aam39009 Human pol
37	1042.5	23.2	1645	7 ADL15098	Adl15098 Human mal
38	1042.5	23.2	1645	7 ADN95658	Adn95658 Human BEC
39	1042.5	23.2	3695	5 ABB81588	Abb81588 Human lam
40	1042	23.2	1640	8 ABO9504	Ab09504 Human lam
41	1042	23.2	1640	8 ADO10049	Ado10049 Novel hum
42	1041	23.2	3690	8 ADM87254	Adm87254 Human pro
43	1015.5	22.6	953	5 AAM50358	Aam50358 Human lam
44	948	21.1	3635	5 ABB81589	Abb81589 Mouse lam
45	948	21.1	3635	5 AAM50357	Aam50357 Mouse lam

ALIGNMENTS

RESULT 1
ID AAB48461 standard; protein, 1694 AA.
XX
AC AAB48461;
XX
DT 02-MAR-2001 (first entry)
XX
DE Rat laminin 5 polypeptide, SEQ ID NO: 12.
XX
XX Rat; laminin 5; vulnery; antitumor; antiinflammatory; antidiabetic;
KM cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS Rattus norvegicus.
XX
PN W0200066731-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000NO-US011459.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (BIOS-) BIOSTATUM INC.
PI Boutaud A;
DR WPI, 2000-687538/67.
DR N-PSDB; AAC83722.
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burn, acute wounds and skin grafts.
XX
XX Claim 3; Page 117-122; 232pp; English.
XX
XX The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotrimeric laminin, whereas

CC prior art cell lines have been created that produce but do not secrete
 CC only one or two chain laminins
 XX
 XX
 SQ Sequence 1694 AA;

Query Match 100.0%; Score 4491; DB 3; Length 1694;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRFNKSGVRLPNDLEDKGYTSLFLQRPDLRENGTDMFVMTLGNDAKSDYIG 60
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 DB 751 MRNKGSGVRLPNDLEDKGYTSLFLQRPDLRENGTDMFVMTLGNDAKSDYIG 810
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 QY MAVVDQQLTCVYNLGDREAEVQIDQVLTBESQEAVMDRVKFORIYOPANLNTKEATSN 120
 |||||
 DB 811 MAVVDQQLTCVYNLGDREAEVQIDQVLTBESQEAVMDRVKFORIYOPANLNTKEATSN 870
 |||||
 QY 121 KKPAPAVYDLEGGSSNTLNLDPEDAVFYGGYPPDFELPSRLRPPYKGCIELDLNEN 180
 |||||
 DB 871 KKPAPAVYDLEGGSSNTLNLDPEDAVFYGGYPPDFELPSRLRPPYKGCIELDLNEN 930
 |||||
 QY VLSVNFKTTFNLTTEVEPCRRKESDKNFEFGYARIPTQNPAPFPNFIOIQTIV 240
 |||||
 DB 931 VLSVNFKTTFNLTTEVEPCRRKESDKNFEFGYARIPTQNPAPFPNFIOIQTIV 990
 |||||
 QY 241 DRGLLFFAENQDNFISLINEDGNLWRYKLNSEPPKEKIRDTINDKSHLITIGKIQ 300
 |||||
 DB 991 DRGLLFFAENQDNFISLINEDGNLWRYKLNSEPPKEKIRDTINDKSHLITIGKIQ 1050
 |||||
 QY 301 KRWIVNERSVRIEGRIPEFSTYTGILAIAREPNISTPAPOGCKMLKKTSGVNL 360
 |||||
 DB 1051 KRWIVNERSVRIEGRIPEFSTYTGILAIAREPNISTPAPOGCKMLKKTSGVNL 1110
 |||||
 QY 361 NDTVGYTKKCESEPMKLVRTASFSRGQMSFTNLDPVSTDFOLSPFGOTQPSGTLNHO 420
 |||||
 DB 1111 NDTVGYTKKCESEPMKLVRTASFSRGQMSFTNLDPVSTDFOLSPFGOTQPSGTLNHO 1170
 |||||
 QY 421 TRTSSLVLTLEDGHIESTDSNIPFSPGTMDGLHHVYSIDTSGRLIIDQVLR 480
 |||||
 DB 1171 TRTSSLVLTLEDGHIESTDSNIPFSPGTMDGLHHVYSIDTSGRLIIDQVLR 1230
 |||||
 QY 481 RNORLPSFSNAQOSLRLGGHFGCCISNVLPORSGPEVLDLASKSTKDAKSGCSLN 540
 |||||
 DB 1231 RNORLPSFSNAQOSLRLGGHFGCCISNVLPORSGPEVLDLASKSTKDAKSGCSLN 1290
 |||||
 QY 541 KPPFLMLFKSPKRPNGRIFNVMQMODAPQATSTAMODGRSCPLNTKASHRALOR 600
 |||||
 DB 1291 KPPFLMLFKSPKRPNGRIFNVMQMODAPQATSTAMODGRSCPLNTKASHRALOR 1350
 |||||
 QY 601 GDSPTSHLLKLPQELLKPRSQPSLDIQTTPSKGLVFACTKOSPLALVYADGRVVFALQ 660
 |||||
 DB 1351 GDSPTSHLLKLPQELLKPRSQPSLDIQTTPSKGLVFACTKOSPLALVYADGRVVFALQ 1410
 |||||
 QY 661 AGGKCLRLRKEKERYHOGKMTTVFGLNGKARLVVDGLAQBSGLPENSTISPREQVYIG 720
 |||||
 DB 1411 AGGKCLRLRKEKERYHOGKMTTVFGLNGKARLVVDGLAQBSGLPENSTISPREQVYIG 1470
 |||||
 QY 721 LPLSRKPSLPPQSPVGCCLDPOLNSKPLDPSARREGVSPCLGSLSEKGYFSGGGGHV 780
 |||||
 DB 1471 LPLSRKPSLPPQSPVGCCLDPOLNSKPLDPSARREGVSPCLGSLSEKGYFSGGGGHV 1530
 |||||
 QY 781 LANSVSLGPELKLTFISIRPSLTVGLIHVSGSGQRLSVYMEAGKVTTSVSSAGGSVTS 840
 |||||
 DB 1531 LANSVSLGPELKLTFISIRPSLTVGLIHVSGSGQRLSVYMEAGKVTTSVSSAGGSVTS 1590
 |||||
 QY 841 ITPKOSLCDGQMSVAVSIKORILHL 866
 |||||
 DB 1591 ITPKOSLCDGQMSVAVSIKORILHL 1616
 |||||

RESULT 2
 AAB48460
 ID AAB48460 standard; protein; 1725 AA.

XX AAB48460;
 AC
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Rat laminin 5 polypeptide, SEQ ID NO: 10.
 XX
 KW Rat; laminin 5; vulnary; antilecer; antiinflammatory; antidiabetic;
 cell adhesion promoter; wound healing; ulcers; burn; skin graft;
 periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
 XX
 OS Rattus norvegicus.
 XX
 PN WO20066731-A2.
 XX
 PD 09-NOV-2000.
 XX
 PF 28-APR-2000; 2000MO-US011459.
 XX
 PR 30-APR-1999; 99US-0131720P.
 PR 21-AUG-1999; 99US-0149738P.
 PR 24-SEP-1999; 99US-0155945P.
 XX
 PA (BIO5-) BIOSYSTEMS INC.
 XX
 PI Boutaud A;
 XX
 DR WPI; 2000-687538/67.
 DR N-PSDB; AAC83721.
 XX
 PT Laminin 5-expressing cells, used to accelerate wound healing associated
 with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
 burns, acute wounds and skin grafts.
 XX
 PS Claim 3; Page 104-109; 232pp; English.
 XX
 CC The present sequence is a laminin 5 chain polypeptide. Recombinant
 CC laminin 5-expressing cells are used to accelerate wound healing,
 CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
 CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
 CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
 CC improve the biocompatibility of medical devices, and to promote cell
 CC adhesion to a surface. They can be used for the ex vivo treatment of Type
 CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
 CC line produces and secretes recombinant heterotrimeric laminin, whereas
 CC prior art cell lines have been created that produce but do not secrete
 CC only one or two chain laminins
 CC
 XX
 SQ Sequence 1725 AA;
 Query Match 100.0%; Score 4491; DB 3; Length 1725;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRFNKSGVRLPNDLEDKGYTSLFLQRPDLRENGTDMFVMTLGNDAKSDYIG 60
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 DB 782 MRNKGSGVRLPNDLEDKGYTSLFLQRPDLRENGTDMFVMTLGNDAKSDYIG 841
 |||||
 QY 61 MAVVDQQLTCVYNLGDREAEVQIDQVLTBESQEAVMDRVKFORIYOPAKLNTYKEATSN 120
 |||||
 DB 842 MAVVDQQLTCVYNLGDREAEVQIDQVLTBESQEAVMDRVKFORIYOPAKLNTYKEATSN 901
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 QY 121 KKPAPAVYDLEGGSSNTLNLDPEDAVFYGGYPPDFELPSRLRPPYKGCIELDLNEN 180
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 DB 902 KKPAPAVYDLEGGSSNTLNLDPEDAVFYGGYPPDFELPSRLRPPYKGCIELDLNEN 961
 |||||
 QY 181 VLSVNFKTTFNLTTEVEPCRRKESDKNFEFGYARIPTQNPAPFPNFIOIQTIV 240
 |||||
 DB 962 VLSVNFKTTFNLTTEVEPCRRKESDKNFEFGYARIPTQNPAPFPNFIOIQTIV 1021
 |||||
 QY 241 DRGLLFFAENQDNFISLINEDGNLWRYKLNSEPPKEKIRDTINDKSHLITIGKIQ 300
 |||||
 DB 1022 DRGLLFFAENQDNFISLINEDGNLWRYKLNSEPPKEKIRDTINDKSHLITIGKIQ 1081
 |||||

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QY 301 KRWIVNERSVRIEGRIPDRSTYYLGIPAIAREFNISTPAFOGCMKUKKTSQVRL 360
DB 1082 KRWIVNERSVRIEGRIPDRSTYYLGIPAIAREFNISTPAFOGCMKUKKTSQVRL 1141
QY 361 NDTVGVTKKCESEDMKLVRTASFSRGGOMSFNLDVSTDRFOLSPFGFTQPSGTLINHQ 420
DB 1142 NDTVGVTKKCESEDMKLVRTASFSRGGOMSFNLDVSTDRFOLSPFGFTQPSGTLINHQ 1201
QY 421 TRRSSLLVTLDEGHIELSTDSNIPFKSPGTMDGLHHVSVISDTSGRLIIDQVLR 480
DB 1202 TRRSSLLVTLDEGHIELSTDSNIPFKSPGTMDGLHHVSVISDTSGRLIIDQVLR 1261
QY 481 RNORLPSFSNAOOSLRIGGHPFGCISNVAVORPSQSPYLDLASKTKDASIGGCSLN 540
DB 1262 RNORLPSFSNAOOSLRIGGHPFGCISNVAVORPSQSPYLDLASKTKDASIGGCSLN 1321
QY 541 KPPELMLFKSPKPKFNKGRIFNVNQMODAPQATSTETAMODGRSCLPPLNTKASHRALQ 600
DB 1322 KPPELMLFKSPKPKFNKGRIFNVNQMODAPQATSTETAMODGRSCLPPLNTKASHRALQ 1381
QY 601 GDSPTSHLLKLPQELKPKRSQPSLDIQTTSFKGLVFACTKOSFLALVYADGRVPAAG 660
DB 1382 GDSPTSHLLKLPQELKPKRSQPSLDIQTTSFKGLVFACTKOSFLALVYADGRVPAAG 1441
QY 661 AGGKCLRLSKERYHDKMTTVFGLNGGAKRLVVDGLRAOEGSLPKNSTIISPREQVYL 720
DB 1442 AGGKCLRLSKERYHDKMTTVFGLNGGAKRLVVDGLRAOEGSLPKNSTIISPREQVYL 1501
QY 721 LPLSRKPKSLPOHSFVGCALDPOLNSKPLDPSARFVSPCLGGSLKGIYFSGGGHVI 780
DB 1502 LPLSRKPKSLPOHSFVGCALDPOLNSKPLDPSARFVSPCLGGSLKGIYFSGGGHVI 1561
QY 781 IANSVSLGPELKLTFISIRPSRLTGVLIHVSGSQSQRSLVYMEAGKVTTSVSDAGSVTS 840
DB 1562 IANSVSLGPELKLTFISIRPSRLTGVLIHVSGSQSQRSLVYMEAGKVTTSVSDAGSVTS 1621
QY 841 ITPKQSLCDGQMSVAVSIRKRIHL 866
DB 1622 ITPKQSLCDGQMSVAVSIRKRIHL 1647

RESULT 3
AAB48459
ID AAB48459 standard; protein; 1693 AA.
XX
AC AAB48459;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human laminin 5 polypeptide, SEQ ID NO: 8.
XX
KW Human; laminin 5; vulnerability; antiulcer; antiinflammatory; antidiabetic;
KW cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW periodontitis; gingivitis; type 1 diabetes; angiogenesis regulation.
XX
OS Homo sapiens.
XX
PN WO200066731-A2.
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011459.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (BIOS-) BIOSTATUM INC.
XX
PI Boutaud A;
XX
DR WPI; 2000-687538/67.

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DR N-PSDB; AAC83720.
XX
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts.
XX
PS Claim 3; Page 91-97; 232pp; English.
XX
CC The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing, skin
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotimeric laminin, whereas
CC prior art cell lines have been created that produce but do not secrete
CC only one or two chain laminins
XX
SQ Sequence 1693 AA;
XX
Query Match 79.3%; Score 3560.5; DB 3; Length 1693;
Best Local Similarity 78.4%; Pred. No. 2.9e-307;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;
QY 1 MRFNGSGVVRVLPNDLEDKGTTSLPQRPDLAENGTEDMFWYLGKMKASHDYIG 60
DB 751 MRFNGSGVVRVLPNDLEDKGTTSLPQRPDLAENGTEDMFWYLGKMKASHDYIG 810
QY 61 MAVVDGQLTCVYNLGDREAVOIDOYLTESESOEAVMDRYKFORIYOPALNTYKATSN 120
DB 811 MAVVDGQLTCVYNLGDREAVOIDOYLTESESOEAVMDRYKFORIYOPALNTYKATSN 870
QY 121 KPRAPAVYDLEGSSNTLNLDEDAVFYVGGYPPPELPSRLRFPYKGCIBLDLNN 180
DB 871 KPRAPAVYDLEGSSNTLNLDEDAVFYVGGYPPPELPSRLRFPYKGCIBLDLNN 930
QY 181 VLSLVNFKTTNTNTTEVEPCRRRKESSDNRYBEGGYARIIPQNPAPFPNFIOTITV 240
DB 931 VLSLVNFKTTNTNTTEVEPCRRRKESSDNRYBEGGYARIIPQNPAPFPNFIOTITV 990
QY 241 DRGLPFAENQDNFISINIEDGNLWRYKLNSEPEKKGIRDTINDOKHSILITIKLO 300
DB 991 DRGLPFAENQDNFISINIEDGNLWRYKLNSEPEKKGIRDTINDOKHSILITIKLO 1050
QY 991 DRGLPFAENQDNFISINIEDGNLWRYKLNSEPEKKGIRDTINDOKHSILITIKLO 1050
DB 1051 KRWIVNERSVRIEGRIPDRSTYYLGIPAIAREFNISTPAFOGCMKUKKTSQVRL 1110
QY 301 KRWIVNERSVRIEGRIPDRSTYYLGIPAIAREFNISTPAFOGCMKUKKTSQVRL 360
DB 1051 KRWIVNERSVRIEGRIPDRSTYYLGIPAIAREFNISTPAFOGCMKUKKTSQVRL 1110
QY 361 NDTVGVTKKCESEDMKLVRTASFSRGGOMSFNLDVSTDRFOLSPFGFTQPSGTLINHQ 420
DB 1111 NDTVGVTKKCESEDMKLVRTASFSRGGOMSFNLDVSTDRFOLSPFGFTQPSGTLINHQ 1170
QY 421 TRRSSLLVTLDEGHIELSTDSNIPFKSPGTMDGLHHVSVISDTSGRLIIDQVLR 480
DB 1171 TRRSSLLVTLDEGHIELSTDSNIPFKSPGTMDGLHHVSVISDTSGRLIIDQVLR 1230
QY 481 RNORLPSFSNAOOSLRIGGHPFGCISNVAVORPSQSPYLDLASKTKDASIGGCSLN 540
DB 1231 RNORLPSFSNAOOSLRIGGHPFGCISNVAVORPSQSPYLDLASKTKDASIGGCSLN 1290
QY 541 KPPELMLFKSPKPKFNKGRIFNVNQMODAPQAT-RSTETAMODGRSCLPPLNTKASHRALQ 599
DB 1291 KPPELMLFKSPKPKFNKGRIFNVNQMODAPQAT-RSTETAMODGRSCLPPLNTKASHRALQ 1348
QY 599 RGSPTSHLLKLPQELKPKRSQPSLDIQTTSFKGLVFACTKOSFLALVYADGRVPAAG 659
DB 1349 RGSPTSHLLKLPQELKPKRSQPSLDIQTTSFKGLVFACTKOSFLALVYADGRVPAAG 1408
QY 659 GAGGKCLRLSKERYHDKMTTVFGLNGGAKRLVVDGLRAOEGSLPKNSTIISPREQVYL 719
DB 1409 GAGGKCLRLSKERYHDKMTTVFGLNGGAKRLVVDGLRAOEGSLPKNSTIISPREQVYL 1468

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OS Homo sapiens.
 PN MO200066731-A2.
 PD 09-NOV-2000.
 XX 28-APR-2000; 2000MO-US011459.
 PF 30-APR-1999; 99US-0131720P.
 PR 21-NOV-1999; 99US-0149738P.
 PR 24-SEP-1999; 99US-0155945P.
 PA (BIOS-) BIOSTATUM INC.
 XX Boutaud A;
 XX WPI; 2000-687538/67.
 DR N-PSDB; AAC83719.
 XX Laminin 5-expressing cells, used to accelerate wound healing associated
 PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
 PT burns, acute wounds and skin grafts.
 PS Claim 3; Page 79-84; 232pp; English.
 XX The present sequence is a laminin 5 chain polypeptide. Recombinant
 CC laminin 5-expressing cells are used to accelerate wound healing, skin
 CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
 CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
 CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
 CC improve the biocompatibility of medical devices, and to promote cell
 CC adhesion to a surface. They can be used for the ex vivo treatment of Type
 CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
 CC line produces and secretes recombinant heterotrimeric laminin, whereas
 CC prior art cell lines have been created that produce but do not secrete
 CC only one or two chain laminins
 XX
 XX Sequence 1713 AA;
 Query Match 79.3%; Score 3560.5; DB 3; Length 1713;
 Best Local Similarity 78.4%; Pred. No. 2.9e-307;
 Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;
 QY 1 MRNNGSGVGVRLPNLEDDIKGTTSLSPQRPDLAENGTEPMFWYLGNCASRDYTG 60
 DB 771 MRNNGSGVGVRLPNLEDDIKGTTSLSPQRPDLAENGTEPMFWYLGNCASRDYTG 830
 QY 61 MAYVDDQLTCVYMLGDRBAEVOIDVLTESBQEAAMDRAVKFORIYQFAKLNTTKATSN 120
 DB 831 MAYVDDQLTCVYMLGDRBAEVOIDVLTESBQEAAMDRAVKFORIYQFAKLNTTKATSN 890
 QY 121 KPRAPAVYDLEGGSSNTLNLDEDAVFYVGGYPPPELPSRLRFPYKGCIELDLNEN 180
 DB 891 KPRAPAVYDLEGGSSNTLNLDEDAVFYVGGYPPPELPSRLRFPYKGCIELDLNEN 950
 QY 181 VLSLVNFKTTFNLTTEVEPCRRKESDKNYBEGTAYARIPTQPNAPFPNPTQTIOTTV 240
 DB 951 VLSLVNFKTTFNLTTEVEPCRRKESDKNYBEGTAYARIPTQPNAPFPNPTQTIOTTV 1010
 QY 241 DRGLTFAENQDPFISINIDGNLMDVRYKLNSEBPKEKGRDPTINOKHSHIITIGKQ 300
 DB 1011 DRGLTFAENQDPFISINIDGNLMDVRYKLNSEBPKEKGRDPTINOKHSHIITIGKQ 1070
 QY 301 KRWMINVNSVRIEGERIPDFSTYLLGDIPIAIRERFNISTPAFQGMKNLKTSGVRL 360
 DB 1071 KRWMINVNSVRIEGERIPDFSTYLLGDIPIAIRERFNISTPAFQGMKNLKTSGVRL 1130
 QY 361 NDVYGVTKKSGEMKLVRTASFSRGGMSNTNLDVETDFOLSRFGQTQPSGTILNHQ 420
 DB 1131 NDVYGVTKKSGEMKLVRTASFSRGGMSNTNLDVETDFOLSRFGQTQPSGTILNHQ 1190
 QY 421 TRTSLLVLTLEDGIELSTSDSNPIKSPGTWMDGLHHVSVSDTSGRLIIDPOVLR 480

1b 1191 TWTBRLQVLTBEGYTELSTSDSGPIFKSPQTYMDGLHHVSVSDNIGRLIIDPOVLR 1250
 QY 481 RNQRLPSFSAQAQSLRIGGHEGCI SNLYORFSSPBYDLASKSTKASIGGCSIN 540
 Db 1251 NSKRLKHSSRSQSLRIGGHEGCI SNLYORFSSPBYDLASKSTKASIGGCSIN 1310
 QY 541 KPPFLMLFKSPKRFNFKRIFNVNQLMDAPQAT-RSTAMODGRSCLPPLNTKASHRALQ 599
 Db 1311 KPPFLMLKSGTRFNKTKFRINQLLDTPVASPREVKWQD--ACSPLEKQANHALQ 1368
 QY 600 FSDSPSHLLKLPQELKPRSQFSLDIOTTSPPKGLVFACTGDSFLALVADGRVFL 659
 Db 1369 FGDIPSHLLFKLPQELKPRSQFSLDIOTTSPPKGLVFACTGDSFLALVADGRVFL 1428
 QY 660 GAGGKTLRKRKHNDGKMTVVRGNGXRLVNDGLRABGSLPGNSTISPREQVYL 719
 Db 1429 GTDGKTLRKRKHNDGKMTVVRGNGXRLVNDGLRABGSLPGNSTISPREQVYL 1488
 QY 720 GLPLSRKPSLPOHSGVGLRDFQNLKPELSPSARFVSPCLGSLKGIYPSQGGHY 779
 Db 1489 GSPSGKPSLPLNSVGLKRFQDLKPLTPSSFGVSSCLGSLKGIYPSQGGHY 1548
 QY 780 IIAVSYSLGPELKLTPESIRPSLTVGLIHVGSQSGRLSVYMEAGVTTSSSDAGSVY 839
 Db 1549 VLAHSLGPBFLVPSIRPSLTVGLIHVGSQSGRLSVYMEAGVTTSSSDAGSVY 1608
 QY 840 SITPKOSLDCGQWHSVAVSIKQRIHL 866
 Db 1609 SITPKOSLDCGQWHSVAVSIKQRIHL 1635
 RESULT 6
 ABR92102
 ID ABR92102 standard; protein; 1713 AA.
 XX ABR92102;
 AC 10-SEP-2003 (first entry)
 XX
 DT Human cervical cancer cell marker encoding cDNA SEQ ID NO:113.
 DE Human; cervical cancer; cervical cancer marker; cancer therapy;
 XX Human; cervical cancer; cervical cancer marker; cancer therapy;
 KM detection; gene therapy; vaccine.
 XX Homo sapiens.
 OS
 PN MO2002101075-A2.
 XX
 PD 19-DEC-2002.
 XX
 PF 12-JUN-2002; 2002MO-US018638.
 PR 13-JUN-2001; 2001US-0298155P.
 PR 13-JUN-2001; 2001US-0298155P.
 PR 14-NOV-2001; 2001US-0335936P.
 XX (MILL-) MILLENNID PHARM INC.
 PA
 XX Schlegel R, Chen Y, Zhao X, Monahan JB, Kamatkar S;
 PI Gamavazapu M, Glatt K, Hoersch S;
 PI WPI; 2003-156967/15.
 DR N-PSDB; ACF12884.
 DR
 XX New isolated nucleic acid molecule useful for detecting, characterizing,
 PT preventing and treating human cervical cancers, in various prognostic and
 PT diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
 PS Claim 4; Page 269-273; 386pp; English.
 XX ACF12828 to ACF12947 encode the human cervical cancer marker proteins (1)
 CC given in ABR92047 to ABR92164. A higher level of expression of (1) than
 CC normal indicates the presence of cervical cancer. Also described: (1) a

CC vector (II) containing (1); (2) a host cell (III) containing (1); and (3)
CC assessing (M1) whether a patient is afflicted with cervical cancer,
CC comprising comparing the level of expression of a marker in a patient's
CC sample, and the normal level of expression of the marker in a control non
CC -cervical cancer sample, where a significant increase in the level of
CC expression of the marker in the patient's sample relative to that in the
CC control sample is an indication that the patient is afflicted with
CC cervical cancer. (1) has cytostatic activity, and can be used in gene
CC therapy and in vaccines. (1) is useful in detecting, characterizing,
CC preventing and treating human cervical cancers. (1) may also be used in
CC various prognostic and diagnostic assays, pharmacogenomics and in
CC monitoring clinical trials

XX Sequence 1713 AA;

Query Match 79.3%; Score 3560.5; DB 6; Length 1713;
Best Local Similarity 78.4%; Pred. No. 2.9e-307;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTDMFVMTLGNKDSKDYIG 60
DB MRFNGSGVEVRLPNDLEDKGYTSLFLQRPNSRNGTDMFVMTLGNKDSRDYIG 830
QY 61 MAVVDGQLTCVNLGDRBAVQIDVLTBSRSGEAVMDRVRKQRIYQFALNTTKATSN 120
DB MAVVDGQLTCVNLGDRBAELQVDQILTKSEKBAVMDRVRKQRIYQFALNTTKATSS 890
QY 121 KKPAPAVYDLGGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLINEN 180
DB KKPAPAVYDMDGNSTLNLDPENAVFYVGGYPPDFKPLPSRLSPFYKGCIELDLINEN 950
QY 181 VLSLYNFKTTFNLTTEVEPCRRRKEESDKNYFEQGYARIPTQNPAPFNF1QTIQTTV 240
DB VLSLYNFKTFFNLTTEVEPCRRRKEESDKNYFEQGYARVPTQNPAPFNF1QTIQTTV 1010
QY 241 DRELTPFAENQDMFISLNTEDGNLMRYKLNSEPRKEKGRDITNGKHSILITIGKQ 300
DB DRELTPFAENGDRFISLNTEDGFLMRYKLNSELPEREGADLNNGRDHSIDIKIGKQ 1070
QY 301 KRWMINNERSVRIEGRIFPSTYVGGIPIAIRERFNISTPAFOGCMKYLKKTSGVNL 360
DB KRWMINVDVONTIIDGVRPFSTYVGGIPIAIRERFNISTPAFOGCMKYLKKTSGVNL 1130
QY 361 NDTVGYTKKCSBDMKLVRTASFSRGGQMSPTNLDVSTDRFQSLFGFQTPQSPGTLINQ 420
DB NDTVGYTKKCSBDMKLVRSASFRRGQLSFTDGLPTDMLQSLFGFQTPQSGTLLDQ 1130
QY 421 TRSSSLVLTEDGHIELSTDSNIPFKSPGTMDGLHNVSYISDTSGLRLIDQVLR 480
DB TRSSSLVLTEDGYIELSTDSGSPFKSPGTMDGLHNVSVISDTSGLRLIDQVLR 1250
QY 481 RNORLPSFNAQSLRLGGHFGGCI SNVLFQSFQSPVYLDLASKSTKQDASIGGCSLN 540
DB RNORLKHISRSRSLRGGSNFEGCISNVFQSLSPVYLDLNSLKRQVSLIGGCSLN 1310
QY 541 KPPFLMLFKSPKPFNKGRIFNVNQLMDAPQAT-RSTEAWQDGRSCLPPLNTKASHRALQ 599
DB KPPFLMLTKGSTRFNKTKTRINQILDTPVAPRSVYKWD--ACSPLPKTOQANGALQ 1368
QY 600 FGGSPSHLLKLPQELIKRSPSLDIQTSFKGLVFAIGTQDFALAYVADGRVFL 659
DB FGGSPSHLLKLPQELIKRSPSOASDIQTSFKGLVFAIGTQDFALAYVADGRVFL 1428
QY 1369 FGGIPIPSHLLFKLPQELIKRSPSOAVDMQTTSSRGVLFHGTGNSFPVALSLSGRLVFL 1428
DB GAGGKLRSLRKRERDGHKMTVVFGLNGGKARLVVDGLAORGSLPGNNTISPRQVYL 719
DB GTTGKLRIRKSKKCKNDGKMTVVFHGDGKGRVLVDGLPAKRGSLPGNNTISIRAPVL 1488
QY 720 GLPLSRKPKSLPQHSFVGLRLDPLQNSKPLDSPARGVSPCLGSLKXGIYSQGGGHV 779
DB GSPPSGKPKSLPNTNSFVGLKQDLQSLYLTSSSRFSVSSCLGGLPKXGIYSSBGGHV 1548
QY 780 ILANSVSLGRELKLTBSIRPSRLTGVLIHVSQSGRLSYMEAGKTYTSSVSDAGGSVT 839
DB VLSLYNFKTTFNLTTEVEPCRRRKEESDKNYFEQGYARIPTQNPAPFNF1QTIQTTV 240

DB 1549 VLAHSVLLGPEPKLVFSIRPSRLTGILIHISQPEKHLCTYLEAGKTASMDSGAGTST 1608
QY 840 SITPKQSLCDGQMSHVAVSIRKORILHL 866
DB SITPKQSLCDGQMSHVAVTIKQIHILHL 1635

RESULT 7
ADD29904
ID ADD29904 standard; protein; 1713 AA.
XX
AC ADD29904;

XX 15-JAN-2004 (first entry)

XX Human laminin alpha 3 seq id 2.

KW ophthalmological; dermatological; laminin alpha 3; G3 domain;
KW cell adhesion function; cell movement effect; epithelial tissue function;
KW retinal detachment; cosmetic surgery; skin graft; human.

OS Homo sapiens.

PN JP2003093064-A.

XX 02-APR-2003.

PF 20-SBP-2001; 2001JP-00287519.

PR 20-SEP-2001; 2001JP-00287519.

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

PA (KIHA-) ZH KIHARA KINEN YOKOHAMA SEIMEI KAGAKU.

XX WPI: 2003-817304/77.

DR N-PSDB; ADD29903.

PT Novel adhesion G3 domain of laminin alpha 3 chain useful for controlling
cell adhesion and cell movement.

PS Claim 1; SEQ ID NO 2; 49pp; Japanese.

CC The invention describes a modified laminin alpha3 chain comprising one or
CC more amino acid deletions, substitutions or additions at region
CC corresponding to a region of G3 domain having amino acids 1214-1324 of
CC laminin alpha3 chain having a fully defined sequence of 1713 amino acids
CC as given in the specification. (1) can control cell adhesion function and
CC cell movement effect. A composition comprising laminin is useful for
CC maintaining or treating the function of epithelial tissue and for
CC treatment or prevention of retinal detachment and in cosmetic surgery and
CC skin graft. The modified region of laminin alpha3 chain can control cell
CC adhesion function and cell movement effect. This is the amino acid
CC sequence of human laminin alpha 3.

XX Sequence 1713 AA;

Query Match 79.3%; Score 3560.5; DB 7; Length 1713;
Best Local Similarity 78.4%; Pred. No. 2.9e-307;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTDMFVMTLGNKDSKDYIG 60
DB MRFNGSGVEVRLPNDLEDKGYTSLFLQRPNSRNGTDMFVMTLGNKDSRDYIG 830
QY 771 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPNSRNGTDMFVMTLGNKDSRDYIG 830
DB MAVVDGQLTCVNLGDRBAELQVDQILTKSEKBAVMDRVRKQRIYQFARLNTTKATSS 890
QY 61 MAVVDGQLTCVNLGDRBAVQIDVLTBSRSGEAVMDRVRKQRIYQFALNTTKATSN 120
DB MAVVDGQLTCVNLGDRBAELQVDQILTKSEKBAVMDRVRKQRIYQFARLNTTKATSS 890
QY 121 KKPAPAVYDLGGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLINEN 180
DB KKPAPAVYDMDGNSTLNLDPENAVFYVGGYPPDFKPLPSRLSPFYKGCIELDLINEN 950
QY 891 KEPTGVDYDMDGNSTLNLDPENAVFYVGGYPPDFKPLPSRLSPFYKGCIELDLINEN 950
DB VLSLYNFKTTFNLTTEVEPCRRRKEESDKNYFEQGYARIPTQNPAPFNF1QTIQTTV 240

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Db 951 VSLVYFKTPTNNTTEVEPCRRKESDKNYEGGYAVLPQPHAPITPFGQITQTV 1010
QY 241 DRGLLFAENQDNFISLNTEDGNLAVRYKLNSEPPYKGIKIDTINDGKHSIIITGKQ 300
Db 1011 DRLLFFAENGDFRISLNTEDGKLMVRYKLNSELPKRGVGDADINNGRDHSIQIKIGKQ 1070
QY 301 KRMWIVNERSVABEGRIPDSFTYYLGGPIAIRERPNISTPAFGCMKMLKXTSGVRL 360
Db 1071 KRMWIVNVDVNTIIDGVDFSTYYLGGPIAIRERPNISTPAFGCMKMLKXTSGVRL 1130
QY 361 NDVGVYKCCSEDMKLVRTASFRGGQMSFTNLDVSTDRFOLSPFGQTFQPSGTLINHQ 420
Db 1131 NDVGVYKCCSEDMKLVRSASFRCGLSTFDGLPPTDHLQASFGQTFQPSGTLINHQ 1190
QY 421 TRTSLSLVLTEDGHIESTRDSNIPFKSPGYMDGLLHVSVISDTSGLRLIIDQVLR 480
Db 1191 TWTRNLQVLTLEDGYIELSTDSGGPIFKSPGYMDGLLHVSVISDTSGLRLIIDQVLR 1250
QY 481 RNRGLPSFNAQOSLRLGGHPEGCISNVLVORFSGSPETLDLASKTKDASLGCGSLN 540
Db 1251 NSRRLKHISRSQSLRGGSNFEGCISNVFQRLSISPEVLDLTSNLRKDVSLGGCGLN 1310
QY 541 KPFFMLFKSPKPFNKGRIFNVNQLMODAPQAT-RSTEAMODGRSCLPPLNTKASHRALQ 599
Db 1311 KPFFMLFKSGTFFNKTRINQLQDTVPASPRSVKQWD--ACSPLEKTOANGALQ 1368
QY 600 FGDSPSHLLKLPOELIKERSQPSLDIQTSPKGLVFAVAGTOSFLATLVADGRVVAL 659
Db 1369 FGDIPSHLLFKLPOLILKERSQPAVDMQTTSSRGVLFHTGTGNSFWALYLSKRLVFL 1428
QY 660 GAGGKTLRLSKRYDKKNTTVFGLNGKARLVYDGLRAQSGSLPGNSTISPREVYL 719
Db 1429 GTDGKTLRLSKRYDKKNTTVFGLNGKARLVYDGLRAQSGSLPGNSTISIRAVYL 1488
QY 720 GLPLSRPKSLPQHSFVGLRDPLQNSKPLDPSARFVGPCLGSLKGIYPSGGGSHV 779
Db 1489 GSPSPGKPSLPTNSFVGLKNSFQDPSKPLYPSSSGVSSCLGSLKGIYPSGGGSHV 1548
QY 780 ILANSVSLGPELKLTSIRPSRLTGLVLIHVSGSGGRLSYMEAGKVTTSVSSDAGSVT 839
Db 1549 VLHSLVSLGPEFLVPSIRPSRLTGLIHLHGSQPKMLCYLLBAGKVTATAMDSGAGSTST 1608
QY 840 STTPKQSLCDGQMSVAVSIKORILHL 866
Db 1609 SVTPKQSLCDGQMSVAVSIKORILHL 1635

RESULT 8
ADG37225
ID ADG37225 standard; protein; 1713 AA.
XX
AC ADG37225;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human laminin-6 alpha 3 subunit.
XX
KW human; laminin-6; alpha 3; B1 subunit; B2 subunit; cell-movement;
KW cell-adhesion; dermatological; neuroprotective; muscular;
KW epithelial tissue; nervous tissue; varicella disease.
XX
OS Homo sapiens.
XX
PN JP2003212791-A.
PD 30-JUL-2003.
PF 17-JAN-2002; 2002JP-00009227.
PR 17-JAN-2002; 2002JP-00009227.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

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XX WPI; 2003-819867/77.
JR N-FSDB; ADG37224.
PT Composition comprising laminin-6 for regulation of cell-movement activity
PT and/or cell-adhesion activity, useful for treating or maintaining
PT function of epithelial tissue, nervous tissue and muscles.
XX
PS Claim 2; SEQ ID NO 2; 55pp; Japanese.
XX
CC This invention describes a novel composition comprising the human laminin
CC -6 alpha 3, B1 or B2 subunits for regulation of cell-movement activity
CC and/or cell-adhesion activity. The products of the invention have
CC dermatological, neuroprotective and muscular activity. The composition of
CC the invention is useful for treating or maintaining the function of the
CC epithelial tissue, the nervous tissue and muscles and is also useful for
CC treatment or prevention of varicella disease.
XX
SQ Sequence 1713 AA;
Query Match 79.3%; Score 3560.5; DB 7; Length 1713;
Best Local Similarity 78.4%; Pred. No. 2.9e-307;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;
QY 1 MRFNGSGVEVRLPNDLBDLKGYSLSLFLQREDLRENGGTEDMFVYLGAKNDASRDYIG 60
Db 771 MRFNGSGVEVRLPNDLBDLKGYSLSLFLQRENSHNGTETMFVYLGAKNDASRDYIG 830
QY 61 MAVVDQGLTCVYNLGDREAEVQIDQVLTSEBSQEAAMDVRKFORIYQPAKANTYKATSN 120
Db 831 MAVVDQGLTCVYNLGDREAEVQIDQVLTSEBSQEAAMDVRKFORIYQPAKANTYKATSN 890
QY 121 KPAAPAVYDLEGGSSNTLNLDPEDAVFYVGYGPPPELPSRLRPPYKCCIFLDLNLN 180
Db 891 KPETPGYMDGNSNTLNLDPENVFYVGYGPPPELPSRLRPPYKCCIFLDLNLN 950
QY 181 VSLVYFKTPTNNTTEVEPCRRKESDKNYEGGYAVLPQPHAPITPFGQITQTV 240
Db 951 VSLVYFKTPTNNTTEVEPCRRKESDKNYEGGYAVLPQPHAPITPFGQITQTV 1010
QY 241 DRGLLFAENQDNFISLNTEDGNLAVRYKLNSEPPYKGIKIDTINDGKHSIIITGKQ 300
Db 1011 DRLLFFAENGDFRISLNTEDGKLMVRYKLNSELPKRGVGDADINNGRDHSIQIKIGKQ 1070
QY 301 KRMWIVNERSVABEGRIPDSFTYYLGGPIAIRERPNISTPAFGCMKMLKXTSGVRL 360
Db 1071 KRMWIVNVDVNTIIDGVDFSTYYLGGPIAIRERPNISTPAFGCMKMLKXTSGVRL 1130
QY 361 NDVGVYKCCSEDMKLVRTASFRGGQMSFTNLDVSTDRFOLSPFGQTFQPSGTLINHQ 420
Db 1131 NDVGVYKCCSEDMKLVRSASFRCGLSTFDGLPPTDHLQASFGQTFQPSGTLINHQ 1190
QY 421 TRTSLSLVLTEDGHIESTRDSNIPFKSPGYMDGLLHVSVISDTSGLRLIIDQVLR 480
Db 1191 TWTRNLQVLTLEDGYIELSTDSGGPIFKSPGYMDGLLHVSVISDTSGLRLIIDQVLR 1250
QY 481 RNRGLPSFNAQOSLRLGGHPEGCISNVLVORFSGSPETLDLASKTKDASLGCGSLN 540
Db 1251 NSRRLKHISRSQSLRGGSNFEGCISNVFQRLSISPEVLDLTSNLRKDVSLGGCGLN 1310
QY 541 KPFFMLFKSPKPFNKGRIFNVNQLMODAPQAT-RSTEAMODGRSCLPPLNTKASHRALQ 599
Db 1311 KPFFMLFKSGTFFNKTRINQLQDTVPASPRSVKQWD--ACSPLEKTOANGALQ 1368
QY 600 FGDSPSHLLKLPOELIKERSQPSLDIQTSPKGLVFAVAGTOSFLATLVADGRVVAL 659
Db 1369 FGDIPSHLLFKLPOLILKERSQPAVDMQTTSSRGVLFHTGTGNSFWALYLSKRLVFL 1428
QY 660 GAGGKTLRLSKRYDKKNTTVFGLNGKARLVYDGLRAQSGSLPGNSTISPREVYL 719
Db 1429 GTDGKTLRLSKRYDKKNTTVFGLNGKARLVYDGLRAQSGSLPGNSTISIRAVYL 1488
QY 720 GLPLSRPKSLPQHSFVGLRDPLQNSKPLDPSARFVGPCLGSLKGIYPSGGGSHV 779

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DB 1489 GSPSPGKPSLPTNSFVGLCKNFOLDKPLPTSSSFVSSCLGGGLKGIYSEEGHY 1548
QY 780 ILANSVSLGPELTLTFPSIRPSLTGVLIVHGSQSGORLSTYMBAGVTVSSDAGSVT 839
DB 1549 VLAHSLVLPBEFLVFSIRPSLTGLIHGSPQKHLCVYLEAKVTASMDSGAGTST 1608
QY 840 SITPKQSLCDGQWHSVAVSIRKRIHL 866
DB 1609 SVTPKQSLCDGQWHSVAVTIKRIHL 1635

RESULT 9
ABM81957 standard; protein; 1713 AA.
XX
XX ABM81957;
AC
XX 18-NOV-2004 (first entry)
DT
XX
XX Tumour-associated antigenic target (TAT) polypeptide PRO2799, SEQ:5041.
DE
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KM tumour; diagnosis; cell proliferative disorder; breast cancer;
KM colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KM central nervous system cancer; bladder cancer; pancreatic cancer;
KM cervical cancer; melanoma; leukaemia; hybridisation probe;
KM chromosome identification; chromosome mapping; gene mapping;
KM gene therapy; cytostatic.
XX
XX Homo sapiens.
OS
XX MO2004030615-A2.
PN
XX 15-APR-2004.
PD
XX 29-SEP-2003; 2003MO-US028547.
PF
XX 02-OCT-2002; 2002US-0414971P.
PR
XX (GETH) GENENTECH INC.
PA Wu TD, Zhang Z, Zhou Y,
PI
XX WPI; 2004-347921/32.
DR N-PSDB; ACN40327.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
XX Claim 12; SEQ ID NO 5041; 7273pp; English.

XX The invention relates to human tumour-associated antigenic target (TAT)
XX polypeptides, and their related nucleic acids. The TAT polypeptides are
XX overexpressed in cancer tissues compared to normal tissues, and may thus
XX serve as effective targets for the diagnosis and treatment of cancer in
XX mammals. The invention also relates to nucleic acid and polypeptide
XX sequences at least 80% identical to the TAT nucleic acids and
XX polypeptides; expression vectors and host cells comprising a TAT nucleic
XX acid; an antibody specific for a TAT polypeptide; a peptide or organic
XX molecule which binds to a TAT polypeptide; fusion proteins comprising a
XX TAT polypeptide; and methods and compositions for the treatment or
XX diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
XX antibodies, antagonists, binding molecules and compositions are useful
XX for diagnosing or treating a cell proliferative disorder associated with
XX increased TAT expression, particularly cancers such as breast cancer,
XX colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
XX cancer, pancreatic cancer, cervical cancer, cancers of the central
XX nervous system, melanoma and leukaemia. TAT nucleic acids may further be
XX used as hybridisation probes, in chromosome and gene mapping, in
XX chromosome identification and in gene therapy. The present sequence

CC represents a TAT polypeptide of the invention
XX
XX Sequence 1713 AA;
SQ
Query Match 79.3%; Score 3560.5; DB 8; Length 1713;
Best Local Similarity 78.4%; Pred. No. 2.9e-307;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MFNFGSGVEVRLPNDLEDLKGYSLSPLORPDLRENGGTEDEMTYAGNKDASKDYIG 60
DB 771 MFNFGSGVEVRLPNDLEDLKGYSLSPLORPDLRENGGTEDEMTYAGNKDASKDYIG 830
QY 61 MAVVDGQLTCVYNIADREAEVQIDVLTESBSQEAAMDVYKFORIYQPAKNTYTEATSN 120
DB 831 MAVVDGQLTCVYNIADREAEVQIDVLTESBSQEAAMDVYKFORIYQPAKNTYTEATSN 890
QY 121 KPAKAVYDLEGGSSNTLLNDPEBAVYVYGGYPPDPFLBRLRPPKGCIEHLDLEN 180
DB 891 KPEYGVYDMDGRNSNTLLNDPENAVYVYGGYPPDPFLBRLRPPKGCIEHLDLEN 950
QY 181 VLSLNFKTTPLNTTEVEPCRRRKEBSDKNYFEGTYARLPTQPAEPNFIQTITTV 240
DB 951 VLSLNFKTTPLNTTEVEPCRRRKEBSDKNYFEGTYARLPTQPAEPNFIQTITTV 1010
QY 241 DEGLLPFAENQDNFISLNIEDGNLVRYKLNSEPPKEKGIQDITNDGHSILITIGKIQ 300
DB 1011 DEGLLPFAENQDRFISLNIEDGKLMVRYKLNSELPKEKGVGDALINNGDHSIQIKGIKIQ 1070
QY 301 KRMWLNVAERSVRIIGEIPDPSTYLLGSIPLAIRRFENISPPAPGCKMNLKKTSGVRL 360
DB 1071 KRMWLNVDQNTIIDGEVDFSTYLLGSIPLAIRRFENISPPAPGCKMNLKKTSGVRL 1130
QY 361 NDTVGATKCSBDMFLVRTASFSRGGQMSFTLVDPSTDRFOLSGFQTFQPSGTLINHQ 420
DB 1131 NDTVGATKCSBDMFLVRTASFSRGGQMSFTLVDPSTDRFOLSGFQTFQPSGTLINHQ 1190
QY 421 TRTSSILVTLBEDGHIELSTRDSNIPFKSPGTVMGDLHHVSVISDTSGLRLLIDDQVLR 480
DB 1191 TWTRNLQVTLBEDGYIELSTDSGGEIPFKSPQTYMGDLHHVSVISDTSGLRLLIDDQVLR 1250
QY 481 RNQRLPSPSNMOQSIRLGGHREGCISNVLVORFQSPRYVLDLAKSTKQASLGCGSLN 540
DB 1251 NSKRLKH1SSRSQSLRLGSGNBEGCI SNVFPVGRSLSPBEVLDLTNSLKRQVSLGCSLN 1310
QY 541 KPPFLMLFKSPRRFNKGRIFNVNQMODAPQAT-RSTEAQMDGRGCLPILNTKASHRALQ 599
DB 1311 KPPFLMLKSTRFNKKTFRINQLODTPVASPSSVAVMQD-ACSPILKTAQNHGALQ 1368
QY 600 FQDSPTSHLLKLPOELLKPRSQFSLDIQTTSPKGLVFACTKDSPLALVYADGVEVRL 659
DB 1369 FQDIPFTHLLFLPOELLKPRSQFAVDMQTTSSRGLVFTHTKNSFMALYSKRLVFL 1428
QY 660 GAGGKKLRLRSKERHNDGKMTVTVVGLNGKRLVYVDGLRAQEGSLPKNSTISPREQVTL 719
DB 1429 GTDGGKRLRKSRKKNCDGMHTVVFHGDEKRLVVDGLRAQEGSLPKNSTISIRAPVTL 1488
QY 720 GLPLRKRPKSLRQHSFVGLCLRDFOILNSKPLDSRFVSPCLAGSLKGIYFSGGGHY 779
DB 1489 GSPSPGKPSLPTNSFVGLCKNFOLDKPLPTSSSFVSSCLGGGLKGIYFSEEGHY 1548
QY 780 ILANSVSLGPELTLTFPSIRPSLTGVLIVHGSQSGORLSTYMBAGVTVSSDAGSVT 839
DB 1549 VLAHSLVLPBEFLVFSIRPSLTGLIHGSPQKHLCVYLEAKVTASMDSGAGTST 1608
QY 840 SITPKQSLCDGQWHSVAVSIRKRIHL 866
DB 1609 SVTPKQSLCDGQWHSVAVTIKRIHL 1635

RESULT 10
ADR87606 standard; protein; 1713 AA.
ID ADR87606
XX

AC ADR87606;
 XX 02-DEC-2004 (first entry)
 XX XX
 DE Human Laminin alpha 3 (nicein), SEQ ID NO. 10.
 XX XX
 KM Cytostatic; Gene Therapy; renal cell carcinoma; Wilms tumour; human;
 KM Laminin alpha 3, nicein.
 XX
 OS Homo sapiens.
 XX
 PN WO2004075835-A2.
 XX
 PD 10-SEP-2004.
 XX
 PF 20-FEB-2004; 2004WO-US005042.
 XX
 PR 21-FEB-2003; 2003US-00372683.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Gerltzen ME, Peale FV, Wu TD;
 XX
 DR WPI; 2004-676901/66.
 XX
 DR N-PSDB; ADR87605.
 XX
 XX
 PT New anti-EDNRA antibody, useful in preparing a composition for diagnosing
 PT or inhibiting the growth of renal cell carcinoma or Wilms tumor.
 XX
 PS Example 1; SEQ ID NO 10; 257pp; English.
 XX
 CC The present invention relates to novel antibodies which bind to proteins
 CC which are overexpressed in renal cell carcinomas or Wilms tumor. The
 CC antibody can bind to a protein comprising CXCR4 (ADR87598), Laminin alpha
 CC 4 (ADR87600), TIMP1 (ADR87602), Type IV collagen alpha 1 (ADR87604),
 CC Laminin alpha 3 (nicein) (ADR87606), Adrenomedullin (ADR87608), Type IV
 CC collagen alpha 2 (ADR87610), Thrombospondin 2 (ADR87612), Type I collagen
 CC alpha 2 (ADR87614), Type VI collagen alpha 3 (ADR87616), Latent TGFbeta
 CC binding protein 2 (LTBP2) (ADR87618), Serine or cysteine protease
 CC inhibiting heat shock protein 47 (HSP47) (ADR87620), Procollagen-lysine, 2
 CC -oxoglutarate 5-dioxygenase (ADR87622), connexin 43 (ADR87624), Type IV
 CC collagen alpha 2 (ADR87626), Connexin 37 (ADR87628), Ephrin A1
 CC (ADR87630), Laminin beta 2 (ADR87632), Integrin alpha 1, hevin
 CC (ADR87633), Stanniocalcin 1 (ADR87637), Thrombospondin 4 (ADR87639), CD36
 CC polypeptide (ADR87641), Endothelin receptor A (EDNRA, ADR87643) or
 CC Endothelin receptor B (EDNRB, ADR87645). The proteins of ADR87598-ADR87641
 CC and ADR87645 are all overexpressed in renal cell carcinoma, and ADR87643
 CC (EDNRA) is overexpressed in Wilms tumour. The antibodies are useful in
 CC preparing a composition for diagnosing or inhibiting the growth of renal
 CC cell carcinoma or Wilms tumour. The present sequence is one such protein
 CC of the invention.
 CC
 XX
 SQ Sequence 1713 AA;
 Query Match 79.3%; Score 3560.5; DB 8; Length 1713;
 Best Local Similarity 78.4%; Pred. No. 2.9e-307;
 Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;
 QY 1 MRFNGKSGVEVRLPNLEDELDKGYTSLPFLORPDLRNGGTEDMFVWYLGKNDKASKYIG 60
 DB 771 MRFNGKSGVEVRLPNLEDELDKGYTSLPFLORPDLRNGGTEDMFVWYLGKNDKASKYIG 830
 QY 61 MAVVDGQLTVCVYVNGDREAEVQIDVLTSEBSQBAVNDRYVFORIYQFARKLNTYKATSN 120
 DB 831 MAVVDGQLTVCVYVNGDREAEVQIDVLTSEBSQBAVNDRYVFORIYQFARKLNTYKATSN 890
 QY 121 KPRAPAYDLEGGSSNTLLNLPEDAVFYVGGVPDPDELRSRLAPFPYKGTIBLDDINEN 180
 DB 891 KPRAPAYDLEGGSSNTLLNLPEDAVFYVGGVPDPDELRSRLAPFPYKGTIBLDDINEN 950
 QY 181 VLSTLYNFKTFTNLTTEVEPCRRKESDKNYFEGTGYARIPTOPNAPFPNFITOTYV 240
 DB 951 VLSTLYNFKTFTNLTTEVEPCRRKESDKNYFEGTGYARIPTOPNAPFPNFITOTYV 1010

QY 241 DRGLFPAENQDNFISLNTEDGNLAVRYKLNSEPPKEKGIKDTINDKSHLITIGKLQ 300
 DB 1011 DRGLFPAENQDNFISLNTEDGNLAVRYKLNSEPPKEKGIKDTINDKSHLITIGKLQ 1070
 QY 301 KRMWVNERSVRIEGERIPDSTYYLGGIPAIARERNISTPAPOGCMKUKTKTSGVRL 360
 DB 1071 KRMWVNERSVRIEGERIPDSTYYLGGIPAIARERNISTPAPOGCMKUKTKTSGVRL 1130
 QY 361 NDTVGVTKKCSSEWKLVRKTSFRRGOMSTNIDVSTDFQSLFSGQTQPSGTLNMQ 420
 DB 1131 NDTVGVTKKCSSEWKLVRKTSFRRGOMSTNIDVSTDFQSLFSGQTQPSGTLNMQ 1190
 QY 421 TRTSLLVLTEDGHIEISTDSNIPFKSGQTMGLLHVYSISDPSGLRLIIDQVLR 480
 DB 1191 TRTSLLVLTEDGHIEISTDSNIPFKSGQTMGLLHVYSISDPSGLRLIIDQVLR 1250
 QY 481 RNORLPSFNAQSLRIGGHPGCTSNVLYVQRFSSPEVLDLASKSTKDAISLGGCSLN 540
 DB 1251 RNORLPSFNAQSLRIGGHPGCTSNVLYVQRFSSPEVLDLASKSTKDAISLGGCSLN 1310
 QY 541 KPPFLMLFKSPKPKFNKGRIFNVNQLMODAPQAT-RSTEWQDGRSCLPINTKASHRALQ 599
 DB 1311 KPPFLMLFKSPKPKFNKGRIFNVNQLMODAPQAT-RSTEWQDGRSCLPINTKASHRALQ 1368
 QY 600 FGDSPTSHLLKLPQELIKRSGPSLDIOTTSRKLGVFYGTDSFLALVADGRVYAL 659
 DB 1369 FGDSPTSHLLKLPQELIKRSGPSLDIOTTSRKLGVFYGTDSFLALVADGRVYAL 1428
 QY 660 GAGGKTLRLSKRYHDGKMTVVFGLNGSKALVVDGLRQBSLPGNSTISPREQVYL 719
 DB 1429 GAGGKTLRLSKRYHDGKMTVVFGLNGSKALVVDGLRQBSLPGNSTISPREQVYL 1488
 QY 720 GLPLSRPKSLPQHSFVGCIRDPLQNSKPLDSPARFVSPCLGGSLKGIYRSGGSHV 779
 DB 1489 GLPLSRPKSLPQHSFVGCIRDPLQNSKPLDSPARFVSPCLGGSLKGIYRSGGSHV 1548
 QY 780 ILANSVSLGRELKLTISRSLITGVLIHVGSGSGRLSYMMARKYTSVSSDAGGSVY 839
 DB 1549 ILANSVSLGRELKLTISRSLITGVLIHVGSGSGRLSYMMARKYTSVSSDAGGSVY 1608
 QY 840 SITPKOSLCDQGMHSAVSIKORILMH 866
 DB 1609 SITPKOSLCDQGMHSAVSIKORILMH 1635
 RESULT 11
 AAB48456
 ID AAB48456 standard; protein; 1724 AA.
 XX
 AC AAB48456;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Human laminin 5 polypeptide, SEQ ID NO: 2.
 XX
 KM Human, laminin 5; vulnery; antiulcer; antiinflammatory; antidiabetic;
 KM cell adhesion promoter; wound healing; ulcers; burn; skin graft;
 KM periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
 OS Homo sapiens.
 XX
 PN WO200066731-A2.
 XX
 PD 09-NOV-2000.
 XX
 PF 28-APR-2000; 2000WO-US011459.
 XX
 PR 30-APR-1999; 99US-0131720P.
 PR 21-AUG-1999; 99US-0149738P.
 PR 24-SEP-1999; 99US-0155945P.
 XX
 PA (BIOS-) BIOTATUM INC.

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XX  Boutaud A;
PI  WPI: 2000-687538/67.
XX  DR  N-PSDB; AAC83717.
XX  PT  Laminin 5-expressing cells, used to accelerate wound healing associated
XX  with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
XX  burns, acute wounds and skin grafts.
XX  PS  Claim 3; Page 53-59; 232pp; English.
CC  The present sequence is a laminin 5 chain polypeptide. Recombinant
CC  laminin 5-expressing cells are used to accelerate wound healing, skin
CC  especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC  surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC  intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC  improve the biocompatibility of medical devices, and to promote cell
CC  adhesion to a surface. They can be used for the ex vivo treatment of Type
CC  I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC  line produces and secretes recombinant heterotrimeric laminin, whereas
CC  prior art cell lines have been created that produce but do not secrete
CC  only one or two chain laminins
XX  SQ  Sequence 1724 AA;
XX
XX  Query Match      79.3%; Score 3560.5; DB 3; Length 1724;
XX  Best Local Similarity 78.4%; Pred. No. 3e-307;
XX  Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;
XX
XX  1 MRNGSGGVRLPNDLEDIKGTSLSLFLQRPDLRENGTDMFVYLGKNDASDYIG 60
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX  782 MRNGSGGVRLPNDLEDIKGTSLSLFLQRPDSRENGTDMFVYLGKNDASDYIG 841
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  61 MAVVDQQLTCVNLGDEAEVQIDVLTSESEQAVMDRPRQRIQAPALNTKATSN 120
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  842 MAVVDQQLTCVNLGDEAEVQIDVLTSESEQAVMDRPRQRIQAPALNTKATSN 901
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  121 KRPAPAVYDLGSSNTLNLDPEDAVFYVGYPPFELPSRARPPYKCIELDLNEN 180
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  902 KPBTPEVYDMGNSNTLNLDPENVFYVGYPPFELPSRARPPYKCIELDLNEN 961
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  181 VLSLVNFKTTPNLTTEVEPCRRKESDKNYEGTGAVRIPIQPNAPFPNFQITQTV 240
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  962 VLSLVNFKTTPNLTTEVEPCRRKESDKNYEGTGAVRIPIQPNAPFPNFQITQTV 1021
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  241 DRGLTFPANEQDFISLNTEDGMLWRYKLNSEPRKEGRDITNGKHSILITGKQ 300
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  1022 DRGLTFPANEQDFISLNTEDGMLWRYKLNSEPRKEGRDITNGKHSILITGKQ 1081
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  301 KRWMINVRSVRIEGLPDPSTYVYLGIPAIAREPFIPTPAFGCMKYLKTSGVNRL 360
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  1082 KRWMINVQNTIIDDEVFPSTYVYLGIPAIAREPFIPTPAFGCMKYLKTSGVNRL 1141
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  361 NDTVGVTKKCESEDMKLVRTASFSRGGQMSFTNLDPBETDRFQLSFGFOTFQPSGTLINQ 420
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  1142 NDTVGVTKKCESEDMKLVRTASFSRGGQMSFTNLDPBETDRFQLSFGFOTFQPSGTLINQ 1201
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  421 TRTSSLLVLTEDHILSTDSNIPFKSRGTMDGLHNVYSITDTSGLRLIIDQVLR 480
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  1202 TWRNLTQVLTEDYIELSTSDSGPIFKSPQTYMDGLHNVYSITDTSGLRLIIDQVLR 1261
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  481 RNQRLSPSNAQSLRLGGHFGECISNVLVQRFOSPEVLDAASKSTKDAISGGCSLN 540
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  1262 NSRRLHIISSRSLSLGGSNFEGCISNVLVQRLSPVLDTLSLKRVDVLSGGCSLN 1321
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  541 KPPFLMLFKSPKRFNKGRIFNVLQMODAPQAT-RSTEAQDGRSCPLPLNTKASHRALQ 599
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  1322 KPPFLMLKSTFTFNKTKFRINQLQDTPVASPRSVKWD--ACSPLEKTOANHALQ 1379
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  600 FGDSPTSHLLKLPOLKLRSPQSLDIOTSPKGLVFGVGTDSPLALVADGRVFL 659
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  1380 FGDIPTSHLLKLPOLKLRSPQFAVDMQTTSSRGLVPHGTGNSFMALYLSKRLVFL 1439
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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XX  660 GAGGKKLRSLRSKERYHDKMTVVFGLNGKARLVVDGLRAQSGSLPGNSTISPREQVYL 719
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  1440 GTDGGKLRSLRSKERYHDKMTVVFGLNGKARLVVDGLRAQSGSLPGNSTISAPVYL 1499
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  720 GLPLSRKPKSLPQHSFVVGCLRDPLNLSKPLDPSAPRFGVSPCLGSLKGIYFSGQGHV 779
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  1500 GSPPGSKPKSLPQHSFVVGCLRDPLNLSKPLDPSAPRFGVSPCLGSLKGIYFSGQGHV 1559
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  780 ILANSVSLGPELKLFPSTRPRLTGVLTHVSGSGQRLSYVWEAKVTTVSDDGGSVT 839
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  1560 VLAHSVLAGPBEKLVPSIRPSLTSLTHISQPKHLGVNLEAKVTTASMDSGAGYST 1619
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  840 SITPKQSLCDGQMSVAVSIRKRIHL 866
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX  1620 SITPKQSLCDGQMSVAVSIRKRIHL 1646
XX  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX
XX  RESULT 12
XX  ADE08094
XX  ID  ADE08094 standard; protein; 3332 AA.
XX  AC  ADE08094;
XX  DT  29-JAN-2004 (first entry)
XX  DE  Novel protein (useful for identifying genetic disorders) #249.
XX  KW  novel gene; novel protein; tissue marker; molecular weight marker;
XX  chromosome marker; genetic disorder.
XX  OS  unidentified.
XX  PN  MO2003054152-A2.
XX  PD  03-JUL-2003.
XX  PF  10-DEC-2002; 2002WO-US039555.
XX  PR  10-DEC-2001; 2001US-0339739P.
XX  PR  11-DEC-2001; 2001US-0339453P.
XX  PR  14-MAR-2002; 2002US-0365091P.
XX  PR  12-APR-2002; 2002US-0372381P.
XX  PR  12-APR-2002; 2002US-0372615P.
XX  PR  22-APR-2002; 2002US-00128558.
XX  PR  24-APR-2002; 2002US-0376045P.
XX  PA  (HYSE-) HYSEQ INC.
XX  PI  Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
XX  Ghosh M, Xue AJ, Wehrman T, Wang G, Zhou P, Dmanac RT, Wang Z,
XX  Ma Y, Wang D, Chen R, Xu C, Boyle B;
XX  DR  WPI: 2003-569235/53.
XX  DR  N-PSDB; ADB07183.
XX  PT  New polynucleotides, useful for expressing recombinant proteins for
XX  analysis, characterization or therapeutic use, or as markers for tissues
XX  in which the corresponding protein is preferentially expressed.
XX  PS  Claim 20; SEQ ID NO 1160; 1177pp; English.
XX  CC  The invention comprises the amino acid and coding sequences of novel
XX  proteins. The DNA and protein sequences of the invention are useful as:
XX  markers for tissues in which the corresponding protein is preferentially
XX  expressed; as molecular weight markers on gels; as chromosome markers or
XX  tags; to identify chromosomes or to map related gene positions; and to
XX  compare with endogenous DNA sequences in patients to identify potential
XX  genetic disorders. The present amino acid sequence represents a protein
XX  of the invention.
XX  SQ  Sequence 3332 AA;

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Query Match 79.3%; Score 3560.5; DB 7; Length 3332;
 Best Local Similarity 78.4%; Pred. No. 8.8e-307; Indels 3; Gaps 2;
 Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRPNKSGVEVRLPNLEDEKGYTSLPLQRPDLRENGTEMDPMFVYLVGNKASKDYIG 60
 DB 2390 MRPNKSGVEVRLPNLEDEKGYTSLPLQRPDLRENGTEMDPMFVYLVGNKASKDYIG 2449

QY 61 MAVVDQQLTCVNLGDRBAEVOIDVLTSEESQBAWMDRYKFORIYQFALNTTKATSN 120
 DB 2450 MAVVDQQLTCVNLGDRBAEVOIDVLTSEESQBAWMDRYKFORIYQFALNTTKATSN 2509

QY 121 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDFELSRIRFPYKCIELDLNEN 180
 DB 2510 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDFELSRIRFPYKCIELDLNEN 2569

QY 181 VLSLVNFKTNTNTTEVEPCRRRKESDKNYEGTGVARIPQPNAPFPNFQITQTV 240
 DB 2570 VLSLVNFKTNTNTTEVEPCRRRKESDKNYEGTGVARIPQPNAPFPNFQITQTV 2629

QY 241 DRGLFFAENQDNFISLINEDGNLMVYKLNSEPKKGIKDTINDGKHSILITGKIQ 300
 DB 2630 DRGLFFAENQDNFISLINEDGNLMVYKLNSEPKKGIKDTINDGKHSILITGKIQ 2689

QY 301 KRWMINNERSVAREGIFDPSTYYLGIPAIARERNISTPAFGCKMLKTKTSGVRL 360
 DB 2690 KRWMINNERSVAREGIFDPSTYYLGIPAIARERNISTPAFGCKMLKTKTSGVRL 2749

QY 361 NDVGVYTKCESEDMKLVRTASFSRGGOMSFNLDPVSTDFPQSPFGQTPQSGTLLNHQ 420
 DB 2750 NDVGVYTKCESEDMKLVRTASFSRGGOMSFNLDPVSTDFPQSPFGQTPQSGTLLNHQ 2809

QY 421 TRTSSLVLTLEDGHIELSTDSNIPFKSBGTMDGLHNVSVISDTSGRLIIDQVLR 480
 DB 2810 TRTSSLVLTLEDGHIELSTDSNIPFKSBGTMDGLHNVSVISDTSGRLIIDQVLR 2869

QY 481 RNRRLSFSNAQSLRGLGSHFEGCISNVLYORSPSPVTLDAKSTKQDASLGGSIN 540
 DB 2870 RNRRLSFSNAQSLRGLGSHFEGCISNVLYORSPSPVTLDAKSTKQDASLGGSIN 2929

QY 541 KPPFLMLFKSPKPKGRIRFNVMQMODAPQAT-RSTBAWODGRCCLPINTKASHRALQ 599
 DB 2930 KPPFLMLFKSPKPKGRIRFNVMQMODAPQAT-RSTBAWODGRCCLPINTKASHRALQ 2987

QY 600 FGDSPSTSHLLKLPOELIKPERSQFSLDIQTSFKGLVFAGTQDSFLATLVADGRVVAL 659
 DB 2988 FGDSPSTSHLLKLPOELIKPERSQFSLDIQTSFKGLVFAGTQDSFLATLVADGRVVAL 3047

QY 660 GAGGKTLRLSKERYHDGKMTTVFGLNGKAKALVYDGLRAQSGSLFGNSTISPREOYL 719
 DB 3048 GAGGKTLRLSKERYHDGKMTTVFGLNGKAKALVYDGLRAQSGSLFGNSTISPREOYL 3107

QY 720 GLPLSRPKSLPOHSFYGLRDFOLNSKPLDSPARFVSPCLGSLSEKGIYSSQGGHY 779
 DB 3108 GLPLSRPKSLPOHSFYGLRDFOLNSKPLDSPARFVSPCLGSLSEKGIYSSQGGHY 3167

QY 780 ILANSVSLGPELKLTSIRPSRLTGVLIHVGSQSGRLSYVMEAGKTVTSVSSDAGSVT 839
 DB 3168 ILANSVSLGPELKLTSIRPSRLTGVLIHVGSQSGRLSYVMEAGKTVTSVSSDAGSVT 3227

QY 840 SITPKQSLCDGQWHSVAVSTIKORILHL 866
 DB 3228 SITPKQSLCDGQWHSVAVSTIKORILHL 3254

RESULT 13
 AAR70148 standard; protein; 1713 AA.

AC AAR70148;
 XX
 DT 25-MAR-2003 (revised)

QY 05-OCT-1995 (first entry)
 XX Deduced sequence of cDNA corresp. to the alpha-3Bpa transcript.
 DB E170; epithelial ligand glycoprotein; epiligrin complex;
 KW epithelial cell binding.
 OS Homo sapiens.
 XX
 XX W09506660-A1.
 PN
 PD 09-MAR-1995.
 XX
 PE 02-SEP-1994; 94MO-US010261.
 XX
 PR 02-SEP-1993; 93US-00115918.
 XX
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 PI Carter WG, Gil SG, Ryan MC;
 XX
 DR WPI, 1995-115398/15.
 DR N-PSDB; AA083236.
 XX
 PT New nucleic acid encoding epiligrin, an epithelial ligand complex - also
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT therapeutically and diagnostically, e.g., in cases of inflammation and to
 PT induce cancer cell differentiation.
 XX
 PS Claim 12; Fig 15A-F; 187pp; English.
 XX
 CC AA083235 depicts the nt. sequence compiled from sequencing cDNA clones
 CC corresp. to the alpha-3 Bpa transcript. The invention includes nt
 CC sequences in the gp. comprising the nt sequence shown in AA083235, the
 CC cDNA clone Bp-1 (ATCC No. 75540) shown in AA083234, the cDNA clone 1-1
 CC (ATCC No. 75539), and the cDNA clone 8-6 (ATCC No. 75538), or the nt.
 CC sequences shown in AA083236. The entire nt region encoding E170 is
 CC depicted in AA083236, and corresp. to the SQ of alpha-3. AA083236
 CC consists of a composite sequence derived from several overlapping clones.
 CC A synthetic polypeptide of at least 5 AAs that corresp. to part or all of
 CC the nt. sequence shown in AA083236 is claimed. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 1713 AA;

Query Match 79.1%; Score 3552.5; DB 2; Length 1713;
 Best Local Similarity 78.3%; Pred. No. 1.5e-306;
 Matches 679; Conservative 86; Mismatches 99; Indels 3; Gaps 2;

QY 1 MRPNKSGVEVRLPNLEDEKGYTSLPLQRPDLRENGTEMDPMFVYLVGNKASKDYIG 60
 DB 771 MRPNKSGVEVRLPNLEDEKGYTSLPLQRPDLRENGTEMDPMFVYLVGNKASKDYIG 830

QY 61 MAVVDQQLTCVNLGDRBAEVOIDVLTSEESQBAWMDRYKFORIYQFALNTTKATSN 120
 DB 831 MAVVDQQLTCVNLGDRBAEVOIDVLTSEESQBAWMDRYKFORIYQFALNTTKATSN 890

QY 121 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDFELSRIRFPYKCIELDLNEN 180
 DB 891 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDFELSRIRFPYKCIELDLNEN 950

QY 181 VLSLVNFKTNTNTTEVEPCRRRKESDKNYEGTGVARIPQPNAPFPNFQITQTV 240
 DB 951 VLSLVNFKTNTNTTEVEPCRRRKESDKNYEGTGVARIPQPNAPFPNFQITQTV 1010

QY 241 DRGLFFAENQDNFISLINEDGNLMVYKLNSEPKKGIKDTINDGKHSILITGKIQ 300
 DB 1011 DRGLFFAENQDNFISLINEDGNLMVYKLNSEPKKGIKDTINDGKHSILITGKIQ 1070

QY 301 KRWMINNERSVAREGIFDPSTYYLGIPAIARERNISTPAFGCKMLKTKTSGVRL 360
 DB 1071 KRWMINNERSVAREGIFDPSTYYLGIPAIARERNISTPAFGCKMLKTKTSGVRL 1130

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QY 361 NDTVGVTKKCSDEWVKLTASAFSRGGQMSFTNLDVSTDRFQLSFGQTFQPSGTLINHQ 420
DB 1131 NDTVGVTKKCSDEWVKLTASAFSRGGQMSFTNLDVSTDRFQLSFGQTFQPSGTLINHQ 1190
QY 421 TRRSLLVLTEDHILSTRDSNIPFKSPGTYMDGLHHVYSITSGRLIIDQVLR 480
DB 1191 TWFRNLQVLTEDHILSTRDSNIPFKSPGTYMDGLHHVYSITSGRLIIDQVLR 1250
QY 481 RNORLSPFNAQOGLRGLGGHFEQCSNVLVQRFQSPSEVLDLASKSTKDAISLGGCSIN 540
DB 1251 NSGRLLHISSSRSQSLDGGNFBGCSINPVQRLSLSPVLDLITNSLKRQVSLGGCSIN 1310
QY 541 KPEFLMLFKSPKPKFNKRIENVNQLMODAPQAT-RSTEAMQDGRSCLPLANTKASHRALQ 599
DB 1311 KPEFLMLFKSTFENKTKTFRIQLQDPFVAPRPAVKWQD--ACSPLEPKTOANNGALQ 1368
QY 600 FQGSFPTSHLLKLPQBLKLRPSQPSIDQTSFKGLVPAAGTQSLALVADGRVPL 659
DB 1369 FQDIPFTHLLFKLPQBLKLRPSQPAVDMQTSRGLVFHTGTNSFMALYLSKGRLVPL 1428
QY 660 GAGGKTLRLSKRYHDGKWHYVFGNLGAKRLVVDGLRAQSGSLPGNSTISPRQVYL 719
DB 1429 GTDQKTLRKSKKCKNDGKMHYVFGHDEKGLVVDGLRAKRGSLPGNSTISIRAPVYL 1488
QY 720 GLPLSRKPKSLPQHSFVGLRDFQLNSKPLDSPAARFVSPCLGSLKGIYPSQGGGHV 779
DB 1489 GSPSPGKPSLPTNSFVGLCKNFQDLSKPLYTSSSFVSSCLGPLEKGIYPSSEGGHY 1548
QY 780 ILANSYSLPELKLTVTSIRPSRLTVYLHHVSGSGQRLSYMMAGKYTVSSVDAGGSYT 839
DB 1549 VLASHVLLGPEFLVLSIRPSRLTGLIHGSPQGRHLCVYLBAKVTAASMDGAGTST 1608
QY 840 SITPKOSLDCQWHSAVASIKQRIHL 866
DB 1609 SVTPKOSLDCQWHSAVAVTIKQHILHL 1635

RESULT 14
AAG75103
ID AAG75103 standard; protein; 469 AA.
XX
AC AAG75103;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:5867.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
  colorectal carcinoma; chromosome 18.
XX
OS Homo sapiens.
XX
PN MO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000MO-US026524.
XX
PR 29-SEP-1999; 99US-0157137P.
  PR 03-NOV-1999; 99US-0163280P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
  WPI, 2001-235357/24.
  DR N-PSDB; AAB34508.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
  useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS Claim 11; Page 7385-7387; 9803P; English.
XX
```

```
CC AAH32943 to AAH31195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patient's own production of P. Additionally, N may be used
CC to produce the colon cancer-associated P8, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB7789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
  CC to 1052, 7921 and 7922
XX
SQ Sequence 469 AA;
XX
Query Match 35.6%; Score 1599; DB 4; Length 469;
Best Local Similarity 65.9%; Pred. No. 3.6e-133; Indels 30; Gaps 5;
Matches 323; Conservative 55; Mismatches 82;
XX
QY 379 TASAFSRGGQMSFTNLDVSTDRFQLSFGQTFQPSGTLINHQTRTSLLVLTEDHILS 438
DB 1 SASAFSRGQMSFTDGLPPTDHLQASFGQTFQPSGTLINHQTRRXQLVLTEDHYIELS 60
QY 439 TRDSNIPFKSPGTYMDGLHHVYSITSGRLIIDQVLRNRORLSPFNAQOGLRGL 498
DB 61 TDSXGPIFKSPQTYMDGLHHVYSITSGRLIIDQVLRNRSRLKHISSSRSQSLRLG 120
QY 499 GGHFEQCSNVLVQRFQSPSEVLDLASKSTKDAISLGGCSINPKPEFLMLFKSPKPKNGR 558
DB 121 GSNFEQCSINPVQRLSLSPVLDLITNSLKRQVSLGGCSINPKPEFLMLKSTFENKTK 180
QY 559 IFNVNQLMODAPQAT-RSTEAMQDGRSCLPLANTKASHRALQFGDPSPTSHLLKLPQBL 617
DB 181 TFRINQLQDPFVAPRPAVKWQD--ACSPLEPKTOANNGALQFGDIPTSHLLFKLPQBL 238
QY 618 KPSQPSLDIQTSPKGLVPAAGTQSLALVADGRVPLVAGGKTLRLSKRYHDG 677
DB 239 KPSQPAVDMQTSRGLVFHTGTNSFMALYLSKGRLVPLALGTQDKLRLSKKCKNDG 298
QY 678 KHTVVFGLNGAKRLVVDGLRAQSGSLPGNSTISPRQVYLGLPLSRKPKSLPQHSFV 737
DB 299 KHTVVFGLNGAKRLVVDGLRAKRGSLPGNSTISIRAPVYLGSPSPGKPSLPTNSFV 358
QY 738 CLRDQLNSKPLDSPAARFVSPCLGSLKGIYPSQGGGHVILANSYSLPELKLTVTSI 797
DB 359 CLKQFQDLSKPLYTSSSFVGLSSCLGPLEKGIYPSSEGGHYVLASHVLLGPEFLVSI 418
QY 798 RPRSLTGLIHHVSGSGQRLSYMMAGKYTVSSVDAGGSYTSITPKOSLDCQWH-- 852
DB 419 RPRSLTGLIHHGSPQGRHLCVYLBAKVTAASMDGAGTST-----KSHGLYGMQGRWDL 459
QY 853 ---HSAVASI 859
DB 460 NVGHTKAVSV 469

RESULT 15
AAW26584
ID AAW26584 standard; protein; 770 AA.
XX
AC AAW26584;
XX
DT 25-MAR-2003 (revised)
  DT 21-JAN-1998 (first entry)
XX
DE Rat hemidesmosome formation inducing protein 154 kDa subunit.
XX
```

KW Hemidesmosome; laminin; epithelial cell; cell attachment; adhesion;
KM bladder carcinoma; 804G; NBT-II; rat; dental implant.

XX
XX
OS Rattus sp.

PN US5658789-A.

PD 19-AUG-1997.

PF 19-MAY-1995; 95US-00445135.

PR 12-NOV-1993; 93US-00151134.

PA (DESM-) DESMOS INC.

PI Hormia M, Quaranta V;

DR WPI; 1997-424242/39.

PT Soluble protein that induces hemidesmosome formation in epithelial cells
- useful for stimulating epithelial cell attachment, e.g. to dental
implants or teeth.

PS Claim 2; Col 21-26; 20pp; English.

CC This polypeptide comprises the 154 kDa alpha chain of an isolated soluble
protein that induces hemidesmosome formation in epithelial cells normally
unable to form hemidesmosomes. The 146 kD gamma chain (see AAW26584) and
the N-terminal portion (see AAW26585) of the 139 kDa beta chain sequence
were also determined. The protein has properties including: (a)
solubility in aqueous media; (b) binding by antibodies present in the
serum of rabbits inoculated with an extracellular matrix deposited by
804G rat bladder carcinoma cells or NBT-II rat bladder carcinoma cells;
(c) being bound by monoclonal antibodies generated against extracellular
matrix; (d) promoting rapid epithelial cell adhesion to substrates coated
with at least one of the three protein chains; and (e) being obtainable
from 804G rat bladder carcinoma cells or NBT-II rat bladder carcinoma
cells. The protein (secreted laminin) is used to induce hemidesmosome
formation in epithelial cells and to facilitate their growth (claimed).
It may be used to promote cell attachment to solid surfaces, e.g. to
dental implants, and may also be of use in studies concerning
hemidesmosome morphogenesis and alpha 6 beta 4 integrin interactions with
the epithelial extracellular matrix. (Updated on 25-MAR-2003 to correct
pp field.)

CC
XX
SQ Sequence 770 AA;

Query Match 29.2%; Score 1310; DB 2; Length 770;

Best Local Similarity 90.9%; Pred. No. 4,9e-107; Mismatches 13; Indels 10; Gaps 4;

Matches 259; Conservative 3; Mismatches 13; Indels 10; Gaps 4;

QY 1 MRFNKSGVVRLEPNDELDKGYTSLFLQRPDLRENGTDMFVYLGAKDKASKDYIG 60

DB 491 MRFNKSGVVRLEPNDELDKGYTSLFLQRPDLRENGTDMFVYLGAKDKASKDYIG 550

QY 61 MA---VVDGQLTCVNLGPREAEVQIDV-LTSESQBAVMRVRKQRIYQFAKLNYYTK 115

DB 551 IGGCRWPAAD--VCLQPGGR--SVSSDRSLTESESQBAVMRVRKQRIYQFAKLNYYTK 605

QY 116 EATSNKRAVAVVDLEGGSSNTLTLNLPEDAVFVVGYPDPFELPSRLRPPYKCTELD 175

DB 606 EATSNKRAVAVVDLEGGSSNTLTLNLPEDAVFVVGYPDPFELPSRLRPPYKCTELD 665

QY 176 DLNENVLSTLYNFKTTFNLTTEVPCRRRKEESDKNYFEGTGYARIPTOPNAPPNFIQT 235

DB 666 DLNENVLSTLYNFKTTFNLTTEVPCRRRKEESDKNYFEGTGYARIPTOPNAPPNFIQT 725

QY 236 IQTTVDGLLFPANQONFISINTEGDLNWRYYKLANSPPKCKGI 280

DB 726 IQTTVARGLLFPANQONFISINTEGDLNWRYYKLANSPPKCKGI 770

Search completed: February 22, 2005, 08:18:44

Job time : 164.651 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 22, 2005, 08:19:00 ; Search time 116.062 Seconds
(without alignments)
2441.722 Million cell updates/sec

Title: US-10-817-423-2

Perfect score: 4491

Sequence: 1 MRFNGKSGVGRVRLPNLEDL.....LDCGMHSAVATKRIHL 866

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/prodata/2/pubppa/US07_PUBCOMB.pep:*

2: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4491	100.0	1694	US-10-603-725-12	Sequence 12, App1
2	4491	100.0	1725	US-10-603-725-10	Sequence 10, App1
3	3560.5	79.3	1693	US-10-603-725-4	Sequence 4, App1
4	3560.5	79.3	1693	US-10-603-725-8	Sequence 8, App1
5	3560.5	79.3	1713	US-10-171-311-113	Sequence 113, App
6	3560.5	79.3	1713	US-10-372-683-10	Sequence 10, App1
7	3560.5	79.3	1713	US-10-603-725-6	Sequence 6, App1
8	3560.5	79.3	1724	US-10-603-725-2	Sequence 2, App1
9	1599	35.6	469	US-10-106-698-5877	Sequence 5877, Ap
10	1198	26.7	1816	US-10-372-683-4	Sequence 4, App1
11	1192	26.5	1823	US-10-363-616-457	Sequence 457, App
12	1190	26.5	1581	US-10-408-765A-154	Sequence 154, App
13	1187	26.4	1816	US-10-299-058-2	Sequence 2, App1

14	1185	26.4	1816	US-10-299-058-4	Sequence 4, App1
15	1045.5	23.3	1634	US-10-037-417-49	Sequence 49, App1
16	1045.5	23.3	1677	US-10-112-944-801	Sequence 801, App
17	1045.5	23.3	1695	US-10-312-352-22	Sequence 22, App1
18	1045.5	23.3	1696	US-10-312-088-31	Sequence 31, App1
19	1045.5	23.3	1695	US-10-312-088-30	Sequence 30, App1
20	1042.5	23.2	1695	US-10-037-182-2	Sequence 2, App1
21	1042	23.2	1640	US-10-037-417-8	Sequence 8, App1
22	1041	23.2	1640	US-10-112-944-347	Sequence 347, App
23	1015.5	22.6	953	US-09-845-583-4	Sequence 4, App1
24	1015.5	22.6	953	US-10-037-417-50	Sequence 50, App1
25	948	21.1	1635	US-09-845-583-2	Sequence 2, App1
26	948	21.1	1635	US-10-037-182-4	Sequence 4, App1
27	948	21.1	1635	US-10-037-417-47	Sequence 47, App1
28	943	21.0	1635	US-10-037-417-6	Sequence 6, App1
29	943	21.0	1635	US-10-037-417-2	Sequence 2, App1
30	908	20.2	908	US-10-037-417-4	Sequence 4, App1
31	636.5	14.2	3712	US-10-108-605-103	Sequence 103, App
32	636.5	14.2	3712	US-10-037-417-48	Sequence 48, App1
33	636.5	14.2	3712	US-10-037-417-51	Sequence 51, App1
34	600.5	13.4	3672	US-10-369-493-6146	Sequence 6146, Ap
35	545	12.1	3084	US-09-938-275-4	Sequence 4, App1
36	545	12.1	3084	US-10-262-670-2	Sequence 2, App1
37	529.5	11.8	3075	US-09-938-275-5	Sequence 5, App1
38	484.5	10.8	3070	US-09-961-403-7	Sequence 7, App1
39	323.5	7.2	1514	US-10-336-603A-36	Sequence 36, App1
40	322.5	7.2	226	US-10-299-058-5	Sequence 5, App1
41	322.5	7.2	226	US-10-299-058-6	Sequence 6, App1
42	321	7.1	289	US-10-299-058-13	Sequence 13, App1
43	316	7.0	463	US-10-264-049-3039	Sequence 3039, Ap
44	314.5	7.0	342	US-10-264-049-3068	Sequence 3068, Ap
45	313.5	7.0	1399	US-10-187-975-26	Sequence 26, App1

ALIGNMENTS

RESULT 1

US-10-603-725-12

Sequence 12, Application US/10603725

Publication No. US20040014665A1

GENERAL INFORMATION:

APPLICANT: Bontand, Arnel

TITLE OF INVENTION: Recombinant Laminin 5

FILE REFERENCE: 99-274-C

CURRENT APPLICATION NUMBER: US/10/603,725

CURRENT FILING DATE: 2003-06-25

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 12

LENGTH: 1694

TYPE: PRT

ORGANISM: Rattus norvegicus

US-10-603-725-12

Query Match 100.0%; Score 4491; DB 15; Length 1694;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFNGKSGVGRVRLPNLEDLKGYTSLFLFQRLDRNGTBMFVYILGNKASKOYIG 60

DB 751 MRFNGKSGVGRVRLPNLEDLKGYTSLFLFQRLDRNGTBMFVYILGNKASKOYIG 810

QY 61 MAVVDQQLTCVYNIAGREAEVQIDQVLTSESGEAVMDRVKFORIYQFALNTYKATSN 120

DB 811 MAVVDQQLTCVYNIAGREAEVQIDQVLTSESGEAVMDRVKFORIYQFALNTYKATSN 870

QY 121 KPRAPAVYDLGGSSNTLNLDPEDAVFYVGGVPPPELPSRLRPYKCCIELDLNN 180

DB 871 KPRAPAVYDLGGSSNTLNLDPEDAVFYVGGVPPPELPSRLRPYKCCIELDLNN 930

QY 181 VLSLYPKTFNNNTVEVEPCRRKESDKNYEGTGAYRIPTQNPAPFNNFIQTIQTV 240

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Db 931 VLSYNFKTTFNLTTEVEPCRRRKEESDKNYEGTGVAIPIPTONAPFPNF1QTIQTTV 990
QY 241 DRGLLFAENODNFIISLNIEDGNLAVRYKLNSEPPKRGIRDTINDGKHSLITIGKQ 300
Db 991 DRGLLFAENODNFIISLNIEDGNLAVRYKLNSEPPKRGIRDTINDGKHSLITIGKQ 1050
QY 301 KKMWINNERSVRIEGBIFDSTYYLGGIPAIIRERFNIISTPAFOGCMKMLKKTSGVRL 360
Db 1051 KKMWINNERSVRIEGBIFDSTYYLGGIPAIIRERFNIISTPAFOGCMKMLKKTSGVRL 1110
QY 361 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSRFGQTFQPSGTLNMQ 420
Db 1111 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSRFGQTFQPSGTLNMQ 1170
QY 421 TRTSSLVLTLEBDEHIELSTDSNIPIFKSPGTMDGLAHVSVISDTSGLRLIIDQVLR 480
Db 1171 TRTSSLVLTLEBDEHIELSTDSNIPIFKSPGTMDGLAHVSVISDTSGLRLIIDQVLR 1230
QY 481 RNQRLPSFSNAQOSLRIGGHEGCI SNVLVORFQSPEVLDLASKSTKQDASLGCSLN 540
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QY 541 KPPFLMLFSPKPKFKGRI FNVNQLMODAPQATRSTEMODGRSCPLPNTKASHRALQF 600
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QY 601 GDSPTSHLLKLPOELKPRSQPSLDIQTSPKGLVFYAGTDSFLALVYADGRVVPALG 660
Db 1351 GDSPTSHLLKLPOELKPRSQPSLDIQTSPKGLVFYAGTDSFLALVYADGRVVPALG 1410
QY 661 AGGKRLRLSKERYHDGKHTVVFGLNGKARLVVDGLRAQBSLPGNSTISPREQVYLG 720
Db 1411 AGGKRLRLSKERYHDGKHTVVFGLNGKARLVVDGLRAQBSLPGNSTISPREQVYLG 1470
QY 721 LPLSRKPKSLPOHSFVGCCLRDPLNSKPLDSPSARFGVSPCLGSLBKGIYFSGGGHYI 780
Db 1471 LPLSRKPKSLPOHSFVGCCLRDPLNSKPLDSPSARFGVSPCLGSLBKGIYFSGGGHYI 1530
QY 781 LANSVSLGPELKLTFESIRPSRLTGVLIVHGSQSGQRLSYMEAGKVTTSVSSDAGSVTS 840
Db 1531 LANSVSLGPELKLTFESIRPSRLTGVLIVHGSQSGQRLSYMEAGKVTTSVSSDAGSVTS 1590
QY 841 ITPKQSLCDGQWHSVAVS1KQRIIHL 866
Db 1591 ITPKQSLCDGQWHSVAVS1KQRIIHL 1616

RESULT 2
US-10-603-725-10
; Sequence 10, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boudand, Arlet
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-603-725-10

Query Match 100.0%; Score 4491; DB 15; Length 1725;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRFNKSGVAVRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFWVYLGKNDASDYIG 60
Db 782 MRFNKSGVAVRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFWVYLGKNDASDYIG 841

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QY 61 MAVVDGQLTCVYNIAGDEAREVQIDQVLTSSBSQBAVMDRVKORIYQAKNTYKATSN 120
Db 842 MAVVDGQLTCVYNIAGDEAREVQIDQVLTSSBSQBAVMDRVKORIYQAKNTYKATSN 901
QY 121 KKPAAVYDLBEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPPKGCIELDDLNN 180
Db 902 KKPAAVYDLBEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPPKGCIELDDLNN 961
QY 181 VLSYNFKTTFNLTTEVEPCRRRKEESDKNYEGTGVAIPIPTONAPFPNF1QTIQTTV 240
Db 962 VLSYNFKTTFNLTTEVEPCRRRKEESDKNYEGTGVAIPIPTONAPFPNF1QTIQTTV 1021
QY 241 DRGLLFAENODNFIISLNIEDGNLAVRYKLNSEPPKRGIRDTINDGKHSLITIGKQ 300
Db 1022 DRGLLFAENODNFIISLNIEDGNLAVRYKLNSEPPKRGIRDTINDGKHSLITIGKQ 1081
QY 301 KKMWINNERSVRIEGBIFDSTYYLGGIPAIIRERFNIISTPAFOGCMKMLKKTSGVRL 360
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Db 1202 TRTSSLVLTLEBDEHIELSTDSNIPIFKSPGTMDGLAHVSVISDTSGLRLIIDQVLR 1261
QY 481 RNQRLPSFSNAQOSLRIGGHEGCI SNVLVORFQSPEVLDLASKSTKQDASLGCSLN 540
Db 1262 RNQRLPSFSNAQOSLRIGGHEGCI SNVLVORFQSPEVLDLASKSTKQDASLGCSLN 1321
QY 541 KPPFLMLFSPKPKFKGRI FNVNQLMODAPQATRSTEMODGRSCPLPNTKASHRALQF 600
Db 1322 KPPFLMLFSPKPKFKGRI FNVNQLMODAPQATRSTEMODGRSCPLPNTKASHRALQF 1381
QY 601 GDSPTSHLLKLPOELKPRSQPSLDIQTSPKGLVFYAGTDSFLALVYADGRVVPALG 660
Db 1382 GDSPTSHLLKLPOELKPRSQPSLDIQTSPKGLVFYAGTDSFLALVYADGRVVPALG 1441
QY 661 AGGKRLRLSKERYHDGKHTVVFGLNGKARLVVDGLRAQBSLPGNSTISPREQVYLG 720
Db 1442 AGGKRLRLSKERYHDGKHTVVFGLNGKARLVVDGLRAQBSLPGNSTISPREQVYLG 1501
QY 721 LPLSRKPKSLPOHSFVGCCLRDPLNSKPLDSPSARFGVSPCLGSLBKGIYFSGGGHYI 780
Db 1502 LPLSRKPKSLPOHSFVGCCLRDPLNSKPLDSPSARFGVSPCLGSLBKGIYFSGGGHYI 1561
QY 781 LANSVSLGPELKLTFESIRPSRLTGVLIVHGSQSGQRLSYMEAGKVTTSVSSDAGSVTS 840
Db 1562 LANSVSLGPELKLTFESIRPSRLTGVLIVHGSQSGQRLSYMEAGKVTTSVSSDAGSVTS 1621
QY 841 ITPKQSLCDGQWHSVAVS1KQRIIHL 866
Db 1622 ITPKQSLCDGQWHSVAVS1KQRIIHL 1647

RESULT 3
US-10-603-725-4
; Sequence 4, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boudand, Arlet
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1693
; TYPE: PRT
; ORGANISM: Homo sapiens

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QY 1 MRFNKSGVAVRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFWVYLGKNDASDYIG 60
Db 782 MRFNKSGVAVRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFWVYLGKNDASDYIG 841

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US-10-603-725-4

Query Match 79.3%; Score 3560.5; DB 15; Length 1693;
Best Local Similarity 78.4%; Pred. No. 5.1e-283;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

1 MRENGSGVEVRLPNDLEDKGYTSLFLQREPDLENGGTEGDMFVYLGNDKASXDYIG 60
DB 751 MRENGSGVEVRLPNDLEDKGYTSLFLQRENSENGTEGDMFVYLGNDKASXDYIG 810
QY 61 MAVVDQGLTCVYMLGDRBAELQVDQILTKSETKEAVMDRVKFORIYQFARLANTKATSN 120
DB 811 MAVVDQGLTCVYMLGDRBAELQVDQILTKSETKEAVMDRVKFORIYQFARLANTKATSN 870
QY 121 KKPAPAVYDLBEGSSNTLNLDPEDAVFYVGYPPDFBLPSRLRPPYKGCIELDLNEN 180
DB 871 KKPAPAVYDLBEGSSNTLNLDPEDAVFYVGYPPDFBLPSRLRPPYKGCIELDLNEN 930
QY 181 VLSLVNPKTFFNLTTEVEPCRRRKEESDKNYEGGYARIPQPNAPPNFIQTIQTV 240
DB 931 VLSLVNPKTFFNLTTEVEPCRRRKEESDKNYEGGYARIPQPNAPPNFIQTIQTV 990
QY 241 DRGLTFFAENQDNFISLNIEDGNLAVRYKLNSEPPKEKIRDTYINDKHSILITIGKQ 300
DB 991 DRGLTFFAENQDNFISLNIEDGNLAVRYKLNSEPPKEKIRDTYINDKHSILITIGKQ 1050
QY 301 KRWMINVNSRVARIEGIFDFSTYYLGGPIAIRERFNISTPAFPGCMKMLKKTSGVRL 360
DB 1051 KRWMINVNSRVARIEGIFDFSTYYLGGPIAIRERFNISTPAFPGCMKMLKKTSGVRL 1110
QY 361 NDVGVYTKKCSBEMKLVRTASFSRGOMSFYTNLDVSTDRFOLSPFGOTFQPSGTLINQ 420
DB 1111 NDVGVYTKKCSBEMKLVRTASFSRGOMSFYTNLDVSTDRFOLSPFGOTFQPSGTLINQ 1170
QY 421 TRTSLSLVLEBDGHEILSTRDSNIPFKSPGYMDGLHNVSYISDPSGRLIIDQVLR 480
DB 1171 TWTRNLQVTLBDEYIELSTSDSGPIFKSPGYMDGLHNVSYISDPSGRLIIDQVLR 1230
QY 481 RNQRLPSFNAQOSLRLGGHPEGCISNVLVORFSSPEVLDLASKSTKDAISLGGCSLN 540
DB 1231 NSRRLKHISRSQSLRLGGHPEGCISNVLVORFSSPEVLDLASKSTKDAISLGGCSLN 1290
QY 541 KRPFLMLFKSPKPKFNKGRIFNNVQMLQDAPQAT-RSTEAMODGRSCPLPNTASRHALQ 599
DB 1291 KRPFLMLFKSPKPKFNKGRIFNNVQMLQDAPQAT-RSTEAMODGRSCPLPNTASRHALQ 1348
QY 600 FGDSPFTHLLKLPQELILKPSQFSLDIQTSPEKLVFVAGTQSFALTYVADGRVFL 659
DB 1349 FGDSPFTHLLKLPQELILKPSQFSLDIQTSPEKLVFVAGTQSFALTYVADGRVFL 1408
QY 720 GLPLSRKPKSLPQHSFVGCILRDQOLNSKPLDPSARFVSPCCGSLKGIYSSQGGGHV 779
DB 1469 GLPLSRKPKSLPQHSFVGCILRDQOLNSKPLDPSARFVSPCCGSLKGIYSSQGGGHV 1528
QY 780 ILANSVSLGPELKLTSIRPRSLTGVLIVHSGSGQRLSYVMEAGKYTTSVSDAGGSVT 839
DB 1529 ILANSVSLGPELKLTSIRPRSLTGVLIVHSGSGQRLSYVMEAGKYTTSVSDAGGSVT 1588
QY 840 SITPKQSLCDGQWHSVAVSIKQRIHL 866
DB 1589 SITPKQSLCDGQWHSVAVSIKQRIHL 1615

RESULT 4
US-10-603-725-8
; Sequence 8, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boudand, Ariel

TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/10/603,725
CURRENT FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 1693
TYPE: PR1
ORGANISM: Homo sapiens
US-10-603-725-8

Query Match 79.3%; Score 3560.5; DB 15; Length 1693;
Best Local Similarity 78.4%; Pred. No. 5.1e-283;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

1 MRENGSGVEVRLPNDLEDKGYTSLFLQREPDLENGGTEGDMFVYLGNDKASXDYIG 60
DB 751 MRENGSGVEVRLPNDLEDKGYTSLFLQRENSENGTEGDMFVYLGNDKASXDYIG 810
QY 61 MAVVDQGLTCVYMLGDRBAELQVDQILTKSETKEAVMDRVKFORIYQFARLANTKATSN 120
DB 811 MAVVDQGLTCVYMLGDRBAELQVDQILTKSETKEAVMDRVKFORIYQFARLANTKATSN 870
QY 121 KKPAPAVYDLBEGSSNTLNLDPEDAVFYVGYPPDFBLPSRLRPPYKGCIELDLNEN 180
DB 871 KKPAPAVYDLBEGSSNTLNLDPEDAVFYVGYPPDFBLPSRLRPPYKGCIELDLNEN 930
QY 181 VLSLVNPKTFFNLTTEVEPCRRRKEESDKNYEGGYARIPQPNAPPNFIQTIQTV 240
DB 931 VLSLVNPKTFFNLTTEVEPCRRRKEESDKNYEGGYARIPQPNAPPNFIQTIQTV 990
QY 241 DRGLTFFAENQDNFISLNIEDGNLAVRYKLNSEPPKEKIRDTYINDKHSILITIGKQ 300
DB 991 DRGLTFFAENQDNFISLNIEDGNLAVRYKLNSEPPKEKIRDTYINDKHSILITIGKQ 1050
QY 301 KRWMINVNSRVARIEGIFDFSTYYLGGPIAIRERFNISTPAFPGCMKMLKKTSGVRL 360
DB 1051 KRWMINVNSRVARIEGIFDFSTYYLGGPIAIRERFNISTPAFPGCMKMLKKTSGVRL 1110
QY 361 NDVGVYTKKCSBEMKLVRTASFSRGOMSFYTNLDVSTDRFOLSPFGOTFQPSGTLINQ 420
DB 1111 NDVGVYTKKCSBEMKLVRTASFSRGOMSFYTNLDVSTDRFOLSPFGOTFQPSGTLINQ 1170
QY 421 TRTSLSLVLEBDGHEILSTRDSNIPFKSPGYMDGLHNVSYISDPSGRLIIDQVLR 480
DB 1171 TWTRNLQVTLBDEYIELSTSDSGPIFKSPGYMDGLHNVSYISDPSGRLIIDQVLR 1230
QY 481 RNQRLPSFNAQOSLRLGGHPEGCISNVLVORFSSPEVLDLASKSTKDAISLGGCSLN 540
DB 1231 NSRRLKHISRSQSLRLGGHPEGCISNVLVORFSSPEVLDLASKSTKDAISLGGCSLN 1290
QY 541 KRPFLMLFKSPKPKFNKGRIFNNVQMLQDAPQAT-RSTEAMODGRSCPLPNTASRHALQ 599
DB 1291 KRPFLMLFKSPKPKFNKGRIFNNVQMLQDAPQAT-RSTEAMODGRSCPLPNTASRHALQ 1348
QY 600 FGDSPFTHLLKLPQELILKPSQFSLDIQTSPEKLVFVAGTQSFALTYVADGRVFL 659
DB 1349 FGDSPFTHLLKLPQELILKPSQFSLDIQTSPEKLVFVAGTQSFALTYVADGRVFL 1408
QY 720 GLPLSRKPKSLPQHSFVGCILRDQOLNSKPLDPSARFVSPCCGSLKGIYSSQGGGHV 779
DB 1469 GLPLSRKPKSLPQHSFVGCILRDQOLNSKPLDPSARFVSPCCGSLKGIYSSQGGGHV 1528
QY 780 ILANSVSLGPELKLTSIRPRSLTGVLIVHSGSGQRLSYVMEAGKYTTSVSDAGGSVT 839
DB 1529 ILANSVSLGPELKLTSIRPRSLTGVLIVHSGSGQRLSYVMEAGKYTTSVSDAGGSVT 1588
QY 840 SITPKQSLCDGQWHSVAVSIKQRIHL 866

Db 1589 SVTPKQSLCDGQWHSVAVTIKQHILHL 1615

RESULT 5

US-10-171-311-113
Sequence 113, Application US/10171311
Publication No. US20030087270A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
APPLICANT: Monahan, John
APPLICANT: Kamackar, Shubhangi
APPLICANT: Ghatt, Karen
APPLICANT: Ganavaram, Manjula
APPLICANT: Hoersch, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
PRIOR FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 113
LENGTH: 1713
TYPE: PR1
ORGANISM: Homo sapiens
US-10-171-311-113

Query Match 79.3%; Score 3560.5; DB 14; Length 1713;
Best Local Similarity 78.4%; Pred. No. 5.2e-283;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRNNGSGVVRLLPNDLEDKGYTSLFLQRPDLRENGTDEMFMVMTLGNDAKSDYIG 60
DB 771 MRNNGSGVVRLLPNDLEDKGYTSLFLQRPDSNENSGTETMFMVMTLGNDAKSDYIG 830
QY 61 MAVVDGQLTCVYNLGDREARVQIDVLTSESOBAVMDRVKFORIYOPAKLNTTKATSN 120
DB 831 MAVVDGQLTCVYNLGDREARVQIDVLTSESOBAVMDRVKFORIYOPAKLNTTKATSN 890
QY 121 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKGCIELDLNN 180
DB 891 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKGCIELDLNN 950
QY 181 VSLNFKTTEFLNTTVEPCRRRKESSDKNYFEGGYARIPTONAPFPNFIQTITQTV 240
DB 951 VSLNFKTTEFLNTTVEPCRRRKESSDKNYFEGGYARIPTONAPFPNFIQTITQTV 1010
QY 241 DRGLLFAENQDNFISLNIEDGNLWVRKYKLNSEPKKGIIRDITNDKDHSLITIGKQ 300
DB 1011 DRGLLFAENQDNFISLNIEDGNLWVRKYKLNSEPKKGIIRDITNDKDHSLITIGKQ 1070
QY 301 KRMWNNERSVRIEGLIPDFSTYLLGGLPIAIRERFNISTPAFOGCMKUKKTSGVNRL 360
DB 1071 KRMWNNERSVRIEGLIPDFSTYLLGGLPIAIRERFNISTPAFOGCMKUKKTSGVNRL 1130
QY 361 NDTFVGYTKKCSSEDMKLVRTASFSRGGQMSFTNLDVDSTDFOLSPFGFTQFQPSGTLINQ 420
DB 1131 NDTFVGYTKKCSSEDMKLVRTASFSRGGQMSFTNLDVDSTDFOLSPFGFTQFQPSGTLINQ 1190
QY 421 TRTSLLVLTLEDHIELSTSDSNIPTEKSGTMDGLHHVSVISDTSGLRLINDOVR 480
DB 1191 TRTSLLVLTLEDHIELSTSDSNIPTEKSGTMDGLHHVSVISDTSGLRLINDOVR 1250

QY 481 RNORLPSFNSMAQSLRLGGRBEGCISNVLYQRPSSQSEPEVLDLASKTKKQASIGGCSLN 540
DB 1251 NSKRLKHSSSRQSLRLGGSNFBEGCISNVLYQRLSLSPVLDLTNSLKRQVSLGGCSLN 1310
QY 541 KPPFLMLKSGTRFKTKTTFRINOLLOTPVAPSSVFWMD--ACSPLPKTOAHGALQ 599
DB 1311 KPPFLMLKSGTRFKTKTTFRINOLLOTPVAPSSVFWMD--ACSPLPKTOAHGALQ 1368
QY 600 FQDSPTSHLLKLPOLKLPSPQSLDIQTTSFKGLVFAAGTKQSLFLAYVADGVNRL 659
DB 1369 FQDITSHLLKLPOLKLPSPQSLDIQTTSFKGLVFAAGTKQSLFLAYVADGVNRL 1428
QY 660 GAGGKRLRSKERYHDKMHTVVGNGKARLVVDGLRAQBSGLPNSNTISPREQYLL 719
DB 1429 GTDGKKLTKSREKCNQDKMHTVVGNGKARLVVDGLRAQBSGLPNSNTISPREQYLL 1488
QY 720 GLPLSRKRLSPQHSFVGLCLDLPOLNSRPLDPSKARFVSPCLGSLKGLIYFSGGGHV 779
DB 1489 GSPSGKRLSPQHSFVGLCLDLPOLNSRPLDPSKARFVSPCLGSLKGLIYFSGGGHV 1548
QY 780 ILANSVSLGPELKLTFEIRPSRLTGLVLIHVSQSGQRLSYVMEAGKVTTSVSDAGSMT 839
DB 1549 VLAHSVLGPELKLTFEIRPSRLTGLVLIHVSQSGQRLSYVMEAGKVTTSVSDAGSMT 1608
QY 840 SVTPKQSLCDGQWHSVAVTIKQHILHL 866
DB 1609 SVTPKQSLCDGQWHSVAVTIKQHILHL 1635

RESULT 6

US-10-372-683-10
Sequence 10, Application US/10372683
Publication No. US20040009171A1
GENERAL INFORMATION:
APPLICANT: GERRITSEN, MARY E.
APPLICANT: PEALE JR., FRANKLIN V.
TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
FILE REFERENCE: P192881P1
CURRENT APPLICATION NUMBER: US/10/372,683
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 10/271,690
PRIOR FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: US 60/344,534
PRIOR FILING DATE: 2001-10-18
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 10
LENGTH: 1713
TYPE: PR1
ORGANISM: Homo sapiens
US-10-372-683-10

Query Match 79.3%; Score 3560.5; DB 15; Length 1713;
Best Local Similarity 78.4%; Pred. No. 5.2e-283;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRNNGSGVVRLLPNDLEDKGYTSLFLQRPDLRENGTDEMFMVMTLGNDAKSDYIG 60
DB 771 MRNNGSGVVRLLPNDLEDKGYTSLFLQRPDSNENSGTETMFMVMTLGNDAKSDYIG 830
QY 61 MAVVDGQLTCVYNLGDREARVQIDVLTSESOBAVMDRVKFORIYOPAKLNTTKATSN 120
DB 831 MAVVDGQLTCVYNLGDREARVQIDVLTSESOBAVMDRVKFORIYOPAKLNTTKATSN 890
QY 121 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKGCIELDLNN 180
DB 891 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKGCIELDLNN 950
QY 181 VSLNFKTTEFLNTTVEPCRRRKESSDKNYFEGGYARIPTONAPFPNFIQTITQTV 240
DB 951 VSLNFKTTEFLNTTVEPCRRRKESSDKNYFEGGYARIPTONAPFPNFIQTITQTV 1010
QY 241 DRGLLFAENQDNFISLNIEDGNLWVRKYKLNSEPKKGIIRDITNDKDHSLITIGKQ 300

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Db 1011 DRGLLFAENGDRFISINIEDGKLMVRYKLNSELPKERGVDALNNGRDHSIQIKIGLQ 1070
Qy 301 KRMINNERSVIREGIFDPSTYLLGIPAIHERNISTPAPGCKMLKXTSGVRL 360
Db 1071 KRMINVNDVNTIIDGVPFSTYLLGIPAIHERNISTPAPGCKMLKXTSGVRL 1130
Qy 361 NDTVGYTKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGFQTPQSGTLNMQ 420
Db 1131 NDTVGYTKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGFQTPQSGTLNMQ 1190
Qy 421 TRTSLLVTLDEGHIELSTDSNIPFKSPQTYMDGLLHVSVISDTSGRLIIDQVLR 480
Db 1191 TWTRNLQVTLDEGHIELSTDSGPIFKSPQTYMDGLLHVSVISDMSGRLIIDQVLR 1250
Qy 481 RNQRLBFSNAQSLRGGHFEGCISNVLYQPSQSPETLDAASKTKDASIGGCSLN 540
Db 1251 NSKRLKHIISSRSQSLRGGSNFECCISNVFQRLSPEVLDLTSNLSLKRVDVSLGGCSLN 1310
Qy 541 KPPLMLFKSPKRNKGRIFNVNQLMDAPQAT-RSTEAQODGRSCLPPLNTKASHRALQ 599
Db 1311 KPPLMLFKSSTRNKTKTFRINQLDPTVAPSRSVKWMOD-ACSPLEPTQANHALQ 1368
Qy 600 FGDSPSHLLKLPOELIKRSPQSLDIQTSPKGLVFAGTQDPLALYVADGRVVFAL 659
Db 1369 FGDIPSHLLKLPOELIKRSPQSLDIQTSPKGLVFAGTQDPLALYVADGRVVFAL 1428
Qy 660 GAGGKRLRLSKRYHDGKMTVYVGLNGSKALVYDGLRAQBSLPGNSTISPREOYTL 719
Db 1429 GTDGKRLRIKSKKENDGKMTVYVGHDEKGRVYDGLRARBSLPGNSTISIRAVYTL 1488
Qy 720 GLPLSRPKSLPOHSPFGCLRDPOLNKSPIDSPARPGVSPCLGSLKGIYFSGGSHV 779
Db 1489 GSPSPGPKSLPNTNSFVGCCKNFQDLSKPLVTPSSSGVSSCLGPLEKGIYFSEEGHV 1548
Qy 780 ILANSVSLGPELKLTFGIRPRLTGVLIVHVSQSGQSLSYMEAGKTYTSSVSDAGSVT 839
Db 1549 VLASHVTLGPEFLVFSIRPRLTGVLIVHVSQSGQSLCYLEAGKTYTASMDSGAGTST 1608
Qy 840 SITPKQSLCDGQMSVAVSIKORILHL 866
Db 1609 SVTPKQSLCDGQMSVAVSIKORILHL 1635

RESULT 7
US-10-603-725-6
; Sequence 6, Application US/10603725
; Publication No. US2004001465A1
; GENERAL INFORMATION:
; APPLICANT: Bouland, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1713
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-725-6

Query Match 79.3%; Score 3560.5; DB 15; Length 1713;
Best Local Similarity 78.4%; Pred. No. 5.2e-283;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

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Qy 121 KPRAPAYDLGEGSSNTLNLDPEDAVFYVGYPPDFELPSRLRFPYKGCIELDLNEN 180
Db 891 KPEPBGVYDMDGRKSNLNLDPEDAVFYVGYPPDFELPSRLRFPYKGCIELDLNEN 950
Qy 181 VLSIYNKTFPNTNTEVEBPCRRKESDKNYFEGTYABIPQPNAPFPNFIQTIQTV 240
Db 951 VLSIYNKTFPNTNTEVEBPCRRKESDKNYFEGTYABIPQPNAPFPNFIQTIQTV 1010
Qy 241 DRGLLFAENGDRFISINIEDGKLMVRYKLNSELPKERGVDALNNGRDHSIQIKIGLQ 300
Db 1011 DRGLLFAENGDRFISINIEDGKLMVRYKLNSELPKERGVDALNNGRDHSIQIKIGLQ 1070
Qy 301 KRMINNERSVIREGIFDPSTYLLGIPAIHERNISTPAPGCKMLKXTSGVRL 360
Db 1071 KRMINVNDVNTIIDGVPFSTYLLGIPAIHERNISTPAPGCKMLKXTSGVRL 1130
Qy 361 NDTVGYTKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGFQTPQSGTLNMQ 420
Db 1131 NDTVGYTKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGFQTPQSGTLNMQ 1190
Qy 421 TRTSLLVTLDEGHIELSTDSNIPFKSPQTYMDGLLHVSVISDTSGRLIIDQVLR 480
Db 1191 TWTRNLQVTLDEGHIELSTDSGPIFKSPQTYMDGLLHVSVISDMSGRLIIDQVLR 1250
Qy 481 RNQRLBFSNAQSLRGGHFEGCISNVLYQPSQSPETLDAASKTKDASIGGCSLN 540
Db 1251 NSKRLKHIISSRSQSLRGGSNFECCISNVFQRLSPEVLDLTSNLSLKRVDVSLGGCSLN 1310
Qy 541 KPPLMLFKSPKRNKGRIFNVNQLMDAPQAT-RSTEAQODGRSCLPPLNTKASHRALQ 599
Db 1311 KPPLMLFKSSTRNKTKTFRINQLDPTVAPSRSVKWMOD-ACSPLEPTQANHALQ 1368
Qy 600 FGDSPSHLLKLPOELIKRSPQSLDIQTSPKGLVFAGTQDPLALYVADGRVVFAL 659
Db 1369 FGDIPSHLLKLPOELIKRSPQSLDIQTSPKGLVFAGTQDPLALYVADGRVVFAL 1428
Qy 660 GAGGKRLRLSKRYHDGKMTVYVGLNGSKALVYDGLRAQBSLPGNSTISPREOYTL 719
Db 1429 GTDGKRLRIKSKKENDGKMTVYVGHDEKGRVYDGLRARBSLPGNSTISIRAVYTL 1488
Qy 720 GLPLSRPKSLPOHSPFGCLRDPOLNKSPIDSPARPGVSPCLGSLKGIYFSGGSHV 779
Db 1489 GSPSPGPKSLPNTNSFVGCCKNFQDLSKPLVTPSSSGVSSCLGPLEKGIYFSEEGHV 1548
Qy 780 ILANSVSLGPELKLTFGIRPRLTGVLIVHVSQSGQSLSYMEAGKTYTSSVSDAGSVT 839
Db 1549 VLASHVTLGPEFLVFSIRPRLTGVLIVHVSQSGQSLCYLEAGKTYTASMDSGAGTST 1608
Qy 840 SITPKQSLCDGQMSVAVSIKORILHL 866
Db 1609 SVTPKQSLCDGQMSVAVSIKORILHL 1635

RESULT 8
US-10-603-725-2
; Sequence 2, Application US/10603725
; Publication No. US2004001465A1
; GENERAL INFORMATION:
; APPLICANT: Bouland, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1724
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-725-2

Query Match 79.3%; Score 3560.5; DB 15; Length 1724;

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Qy 1 MRENGKSGVRYLPNDLJEDLKGYSLSLFLQRPDLRENGEDMFVWYLGKNDKSKYIG 60
Db 771 MRFRGKSGVRYLPNDLJEDLKGYSLSLFLQRPDSRENGEDMFVWYLGKNDKSKYIG 830
Qy 61 MAVVDGQLTCVYNLGDREABVOIDQVLTESBQEAANDRVYFORIYQPAKLYTKATSN 120
Db 831 MAVVDGQLTCVYNLGDREABVOIDQVLTESBQEAANDRVYFORIYQPAKLYTKATSN 890

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Best Local Similarity 78.4%; Pred. No. 5.3e-283; Matches 660; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRENGSGVAVLPNDLEDKGYTSLFLQRPDLRENGTDEMFMVYLGAKDASDYIG 60
Db 782 MRENGSGVAVLPNDLEDKGYTSLFLQRPDLRENGTDEMFMVYLGAKDASDYIG 641
QY 61 MAVVDQQLTCVYVLPGRBAVQIDQVLTSESGEAVMDRYKFORIYQPAKLNTKATSN 120
Db 842 MAVVDQQLTCVYVLPGRBAVQIDQVLTSESGEAVMDRYKFORIYQPAKLNTKATSN 901
QY 121 KKPAPAVYDLEGGSSNTLNLDEDAVFYVGYGPPDELSRLRFPYKGTIELDLNEN 180
Db 902 KKPAPAVYDLEGGSSNTLNLDEDAVFYVGYGPPDELSRLRFPYKGTIELDLNEN 961
QY 181 VLSLVNFKTFFNLNTEVEVERCRKRKESDKNYFEGTGYARIPTOPAPFPNFIOITQTV 240
Db 962 VLSLVNFKTFFNLNTEVEVERCRKRKESDKNYFEGTGYARIPTOPAPFPNFIOITQTV 1021
QY 241 DRGLFPAENQDNFISLNIEDGNLMVRYKLNSEPPKEKIRDTINDKHSILITIGKQ 300
Db 1022 DRGLFPAENQDNFISLNIEDGNLMVRYKLNSEPPKEKIRDTINDKHSILITIGKQ 1081
QY 301 KRWIVNRSVAVIBERIDPSTYVYIGPIAIRBNSTPAFQCMKRLKTTSGVAVL 360
Db 1082 KRWIVNRSVAVIBERIDPSTYVYIGPIAIRBNSTPAFQCMKRLKTTSGVAVL 1141
QY 361 NDTVGYTKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQSLFSGTQFQSGTLLNHQ 420
Db 1142 NDTVGYTKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQSLFSGTQFQSGTLLNHQ 1201
QY 421 TRTSLLVLTEDGHIELSTRDSNIPFKSPGYMDGLHHVSYISOTSGRLIIDQVLR 480
Db 1202 TRTSLLVLTEDGHIELSTRDSNIPFKSPGYMDGLHHVSYISOTSGRLIIDQVLR 1261
QY 481 RNORLPSFSAQOQLSLGGHEPGCTSNLYVORFQSPREVLDAKSTKKDASLGCSLN 540
Db 1262 RNORLPSFSAQOQLSLGGHEPGCTSNLYVORFQSPREVLDAKSTKKDASLGCSLN 1321
QY 541 KPEPLMLFKSPKPKFNKRIFFNVQMLQMDAPQAT-RSTEAMQDGRSCLPPLNTKASHRALQ 599
Db 1322 KPEPLMLFKSPKPKFNKRIFFNVQMLQMDAPQAT-RSTEAMQDGRSCLPPLNTKASHRALQ 1379
QY 600 FGDSPFSLHLKLPQELBLKRSQPSLDIQTTSKGLVFAGYTDSPLALYVADGRVAVL 659
Db 1380 FGDSPFSLHLKLPQELBLKRSQPSLDIQTTSKGLVFAGYTDSPLALYVADGRVAVL 1439
QY 660 GAGCKLRLRSKRYHDGKKHTVYFGLNGKALYVDGLPAORGSLPGNSTISIRAPVYL 719
Db 1440 GAGCKLRLRSKRYHDGKKHTVYFGLNGKALYVDGLPAORGSLPGNSTISIRAPVYL 1499
QY 720 GLPLSRKPKSLPOHSFVGLCLRDQLNSKPLDPSAPAFVSPCLGSGLEKGIYPSOGGSHV 779
Db 1500 GLPLSRKPKSLPOHSFVGLCLRDQLNSKPLDPSAPAFVSPCLGSGLEKGIYPSOGGSHV 1559
QY 780 ILANSVSLGBELKLTFSIRPSRLTGVLIHVSGSGQRLSYMEAGKVTTSVSSDAGSAYT 839
Db 1560 ILANSVSLGBELKLTFSIRPSRLTGVLIHVSGSGQRLSYMEAGKVTTSVSSDAGSAYT 1619
QY 840 SITPKOSLCDGQMHSAVAVSIKORILHL 866
Db 1620 SITPKOSLCDGQMHSAVAVSIKORILHL 1646

RESULT 9
US-10-106-698-5877
; Sequence 5877, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 5877
; LENGTH: 469
; TYPE: PR
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (47)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (65)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (436)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5877

Query Match 35.6%; Score 1599; DB 14; Length 469;
Best Local Similarity 65.9%; Pred. No. 1.7e-122; Matches 333; Conservative 55; Mismatches 82; Indels 30; Gaps 5;

QY 379 TASFSRGQMSFTNLDVSTDRFQSLFSGTQFQSGTLLNHQTRTSLLVLTEDGHIELS 438
Db 1 SASFSRGQMSFTNLDVSTDRFQSLFSGTQFQSGTLLNHQTRTSLLVLTEDGHIELS 60
QY 439 TRDSNIPFKSPGYMDGLHHVSYISOTSGRLIIDQVLRNRORLPSFSAQOQLSLG 498
Db 61 TRDSNIPFKSPGYMDGLHHVSYISOTSGRLIIDQVLRNRORLPSFSAQOQLSLG 120
QY 499 GGFHFGCTSNLYVORFQSPREVLDAKSTKKDASLGCSLNKPEPLMLFKSPKFNKGR 558
Db 121 GGFHFGCTSNLYVORFQSPREVLDAKSTKKDASLGCSLNKPEPLMLFKSPKFNKGR 180
QY 559 IFNVNQLQMDAPQAT-RSTEAMQDGRSCLPPLNTKASHRALQFGDPSFSLHLKLPQEL 617
Db 181 IFNVNQLQMDAPQAT-RSTEAMQDGRSCLPPLNTKASHRALQFGDPSFSLHLKLPQEL 238
QY 618 KERSQPSLDIQTTSKGLVFAGYTDSPLALYVADGRVAVLGAAGCKLRLRSKRYHDG 677
Db 238 KERSQPSLDIQTTSKGLVFAGYTDSPLALYVADGRVAVLGAAGCKLRLRSKRYHDG 298
QY 678 KHTVYFGLNGKALYVDGLPAORGSLPGNSTISIRAPVYIGSPSGKPSLPTNSFVG 737
Db 299 KHTVYFGLNGKALYVDGLPAORGSLPGNSTISIRAPVYIGSPSGKPSLPTNSFVG 358
QY 738 CLRDQLNSKPLDPSAPAFVSPCLGSGLEKGIYPSOGGSHVILANSVSLGBELKLTFSI 797
Db 358 CLRDQLNSKPLDPSAPAFVSPCLGSGLEKGIYPSOGGSHVILANSVSLGBELKLTFSI 418
QY 798 RPSRLTGVLIHVSGSGQRLSYMEAGKVTTSVSSDAGSAYTSITPKOSLCDGQMHSA 852
Db 418 RPSRLTGVLIHVSGSGQRLSYMEAGKVTTSVSSDAGSAYTSITPKOSLCDGQMHSA 852
QY 853 ---HSAVAVSI 859
Db 460 NVGHKTAHSV 469

RESULT 10
US-10-372-683-4
; Sequence 4, Application US/10372683
; Publication No. US20040009171A1

```

; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: PEALB JR., FRANKLIN V.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 4
; LENGTH: 1816
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-372-683-4

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Query Match      26.7%; Score 1198; DB 15; Length 1816;
Best Local Similarity 33.1%; Pred. No. 1.5e-88;
Matches 309; Conservative 161; Mismatches 373; Indels 90; Gaps 26;

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1 MRNKGSGVEVRLPNDLEDKGYTSLFL---QRPDLRENGGTEDMFVYVYAGNKDASK 56
229 MMTDGGSAVYHSTSHDDLKAFSLSLYKPKPKBELTE---TADQFLLYLSGSKNAXK 885
57 DYIGMAVVDQQLTCVYNLGDREAEVQIDOVLTSESGEAVMDRYKFORIYQAFKANTYKE 116
886 EYMGALIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAPFSYIKIRVGHGKVFLLVP 943
117 ATSNKPKAPAVYDLEGSSNTLNLDPEDAVFYGYGPPDFELSRIRFPYKGCIELDD 176
944 SLSTAEKRTIKKGEFSGDSDLDDLPEDVYFYGVGPSFKLPTSLNLGPGVCELELAT 1003
177 LNEENVSLYVFKTTPNLTTEVEPCRRRK-----EESDKNYFEGTGYARLPTQPN---A 227
1004 LNDVDSLVLNFKHLYNMDPSTVPCARDKLAFTOSRAASYFPGSGYAVVDITRRGKFG 1063
228 PPNFPIOTIOTYDRLGLLFAENQDNFISINIEDNLMVRY-----KLNSEPPKKGCI 280
1064 QVTRFDELVTRPADNGLILMNVGSMFRLERNGYLHVFDYDFGSSGRVHLEDTLAKA- 1122
281 RDTINDKDSILITIGLQKRMVNNERSVRI---EGEIPDSTYLLGIP-----I 331
1123 --QINDAKYHEIST-IYHNDKMTLVDRRVKSMDEKMKIPTDLYIGAPPEILQSR 1179
332 AIRRFNISTPAPFOGCKMNL---KKTSGVRLNDTVGTVKKCSBDWLVRTASFRGGM 388
1180 ALRAHLPLDI-NFRGCKMGFOFQKKDFNLLEQETILGVGCGCPEDSLISRAYFN--GQS 1236
389 SFTNLD-VPSIDRQLSFGQTFQPSGTLNHOQRTSLVLTLEDGHELESTRDSNPIIF 447
1237 FIASIQKISFPDGEFGFNRTLOPNGLIFYYAGSDVFSISLNGVIMDVK--GIKVO 1294
448 KSPETVMDGLAHVSVISDTSGLR--LIID-DQVLRNQRLLPSFSNAQOSLR---LGG-- 499
1295 SVDKQYNDGLSHF--VISSVSPTRYELIVDSRVGSKNPTGKLEQTAQSEKKFYFGSP 1352
500 -----GHEECISVAVVQFSQSPREVLDAKSKTKDASLQSGSLNPPMLPFKSKRF 554
1353 ISAOYAFPGICISAVYTRVDRVDEDFQRYTEKHTVTSLEYCEPIESSPLFLHKKKNL 1412
555 NKGRIFVNVQ--LMQAPQATSTRTEAWQDSSCLPIANT-----KASHRALQF 600
1413 SKPFASONKKGKSKDAP-----SWDPVALKLPENTPRNSHCHLSNRPRAIEHAUY 1465
601 GDSPTSHLLKLPBELLKPSQSLDQTTSPKGLVYVYAGKD--SFLALVYADGRVYA 658
1466 GGTNSHQBEPHEHLGDFGAKSOFISIRLTRSSHGMIFYVSDQENDMTPLFLAIGRLVYM 1525
659 LGAQGLKLRBSKRYHDKWHTVVFGLNGKARLVVDGLRAQSGSL-PGNSITSPREOV 717

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1526 FNVGHKKLRISQEKYNDGLMHDVIFIRERSGRLVIDGLVLEESLPTEATWIKXIGPI 1585
718 YLGLPLSRKXSLPQ-----HSFVGLRDPOLNKPLDPSARKGVSPCLGSLKGYFS 773
1586 YLGVAPGKRVKXVQINSITFSFGCLSNQLNAGSITSAQTSVTFCFPGMETGYFS 1645
774 OGGHVIANSVSLGPELKLTFIRPSRLTGLVLHVHSGOGRLSVYMEAKYVTSVSD 833
1646 TEGYVLDSEFNGILKFLAIEVRRSSGTLVHGSUNGEYTLNMGKQVLYKYNNG 1705
834 AGGSVTSITPKQSLCDQWHSVAVSIKORILHL 866
1706 IRDFSTSVTEKQSLCDGRWHRITVIRDSNVQVL 1738

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RESULT 11
US-10-363-616-457

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; Sequence 457, Application US/10363616
; Publication No. US20040044181A1

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; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 457
; LENGTH: 1823
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-363-616-457

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```

Query Match      26.5%; Score 1192; DB 15; Length 1823;
Best Local Similarity 33.5%; Pred. No. 4.7e-88;
Matches 312; Conservative 158; Mismatches 374; Indels 88; Gaps 28;

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1 MRNKGSGVEVRLPNDLEDKGYTSLFL---QRPDLRENGGTEDMFVYVYAGNKDASK 56
836 MMTDGGSAVYHSTSHDDLKAFSLSLYKPKPKBELTE---TADQFLLYLSGSKNAXK 892
57 DYIGMAVVDQQLTCVYNLGDREAEVQIDOVLTSESGEAVMDRYKFORIYQAFKANTYKE 116
893 EYMGALIKNDNLVYVYNLGTKDVEIPLDS--KPVSSWPAPFSYIKIRVGHGKVFLLVP 950
117 ATSNKPKAPAVYDLEGSSNTLNLDPEDAVFYGYGPPDFELSRIRFPYKGCIELDD 176
951 SLSTAEKRTIKKGEFSGDSDLDDLPEDVYFYGVGPSFKLPTSLNLGPGVCELELAT 1010
177 LNEENVSLYVFKTTPNLTTEVEPCRRRK-----EESDKNYFEGTGYARLPTQPN--A 227
1011 LNDVDSLVLNFKHLYNMDPSTVPCARDKLAFTOSRAASYFPGSGYAVVDITRRGKFG 1070
228 PPNFPIOTIOTYDRLGLLFAENQDNFISINIEDNLMVRYKLN--SEPPKKGIRDT--- 283
1071 QVTRFDELVTRPADNGLILMNVGSMFRLERNGYLHVFDYDFGSSGPVH--LEDTLKK 1128
284 --INDGKHSILITIGLQKRMVNNERSVRI---EGEIPDSTYLLGIP-----IA 332
1129 AQINDAKYHEIST-IYHNDKMTLVDRRVKSMDEKMKIPTDLYIGAPPEILQSR 1187
333 IRERFNISTPAPFOGCKMNL---KKTSGVRLNDTVGTVKKCSBDWLVRTASFRGGM 389
1188 LRAHLPLDI-NFRGCKMGFOFQKKDFNLLEQETILGVGCGCPEDSLISRAYFN--GQS 1244
390 FTMND-VPSIDRQLSFGQTFQPSGTLNHOQRTSLVLTLEDGHELESTRDSNPIIF 448
1245 IASIQKISFPDGEFGFNRTLOPNGLIFYYAGSDVFSISLNGVIMDVK--GIKVO 1302
449 SPTVMDGLAHVSVISDTSGLR--LIID-DQVLRNQRLLPSFSNAQOSLR---LGG--- 499
1303 VDKQYNDGLSHF--VISSVSPTRYELIVDSRVGSKNPTGKLEQTAQSEKKFYFGSP 1360

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QY 500 -----GHEGECISNLVVOFSSPEYLDIASXTKQDAIAGCCSLNKPEPLMFPSPKFN 555
Db 1361 SAQYANFTGCCISNAFYTRVDBDEVEDQRTTEKHTSLHYECPIESSLPFLHKKGKNTLS 1420
QY 556 KGRIFNVNQ--LMODAPQATRSTEAMODGRSLPEPLNT-----XASHRALQFG 601
Db 1421 KPKASQNKKGKSKDAP-----SWDEVALKLPERNTPRMSHCHLSNSPRAIEHAYQYG 1473
QY 602 DSPSHLLKLKPOELIKRPSQPSLDIOTTSFKGLVFNAGTGD--SFLALYADGRVVPAL 659
Db 1474 GTANSROBEFHKGDFPKASQPSIRILRTSRSHGMFYVSDSEBDFMTLPLAHGLVYMF 1533
QY 660 GAGGKCLRBSKERHHDGKMHVYVGLNAGKARLVVDDLRAQEGSL--GSGNSTISPRQEVY 718
Db 1534 NVGHKKLITRSQEKNDGIMHDVFIIRBSRSGRLYDGLRYLBSLPTEKATWKIKGFIY 1593
QY 719 LGLPLSRKPKSLPQ-----HSFVGLCLRDQLNLSKPLDPSAPFGVSPCLGSLKGIYPSQ 774
Db 1594 LGGVAPGQAVNVNQNSIYSPSGCLSNQLNGASITSAQYFPVSVPCEGEMETGYST 1653
QY 775 GGGHVIILANSVSLGPELKLTPSIRPRSLTGVLIVHGSQSGRSLSYVMEAGKVTTSVSSDA 834
Db 1654 EGGYVLDEISFNIGLKFEIAFEVPRSSSGTLVHGSYNGEILYAHMNGQYIVANNGI 1713
QY 835 GGSVTSITPRKSLCDQGWHSVAVSLKQKILHL 866
Db 1714 RDFSITSVPRKSLCDGRWHIRITVADNSVQDI 1745

```

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RESULT 12
US-10-408-765A-154
; Sequence 154, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boia D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154
; LENGTH: 1581
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-154

```

Query Match	26.5%	Score 1190	DB 16	length 1581
Best Local Similarity	33.2%	Pred. No. 5	48	
Matches	310	Conservative	161	Mismatches 372
			Indels	90
			Gaps	27
QY	1	MRFNKSGVEYRLPMDLEDIKGYTSLSTPL---	ORPDLREKGGTREDMFMTLGNKDKSK	56
DB	594	MMFDQSAVBSHRSRTSMDDKAFSLSLYMKPVRPELTB---	PADQITLTLGSKNNK	650
QY	57	DYIGNAVVDGOLTCVYNLGDBREAVQIDQVLTESESQEAVMDRVXFORIYQPAKNTYKE		116
DB	651	EYMGIAIKNDNLVYYVNLGDKQVEIPLDS--	KPVSSWPVAFSIVLEREGKGGKXFLTVP	708
QY	117	ATSNKPKAPAVYDLEGGSSNTLNLDDPEDAVFYGGYPPDPFSLRLRPPPKGCIETDD		176
DB	709	SLSTFAERKEFKKGFSQDSDSLDDLPBETLYYGGVPSNFTLPSNLPGVVGCIETLAT		768
QY	177	LNENLNLSTLYNFTTYNLNTTEVEPCRRK----	ESDKNYBEGGTYA--RIPTQPN--A	227

Dh	769	LNDVLSLXNFKHLVXNDPSTSVPCARDKLAFLQSRAA5FFDQSGAAYVRDITRRKFG	828
Qy	228	PFFNFIOITQTYDDRGILLFFAEKONDFISLNIEDGNLMRY-----KANSEPRKGI	280
Dh	829	QVTRFDEIVETPDNGILLMVNGSMFFRLBMRNGYLAHYFDQFSSGRVHLEETTLKA	887
Qy	261	RDITNDCKHSLITLTKLQKRMVINVNSVRH-----EGEIPDSTYLLGIP-----I	331
Dh	888	--QJNDKMYHEISI-IYHNDKMLLVDRHNVKSMONEKKIIPFTDIYIGAPELLQSR	944
Qy	332	AIRERFNISTPAFOGCKNKL---KTSGVVRLNDYVTVTKKCSHEDMLVTFASRGGOM	388
Dh	945	ALNRHLELDI-NFRGCKKGFQFOKQDNLLBQETTLGVGCGPBD5ISRAYFN--GQS	1001
Qy	389	SFTNLD-VPESTRFQLSFGQTFQPSGTLNHQTRISSLVLTLEDGHEIESTRDSNIPF	447
Dh	1002	FIASIQISFPDQEGEGFNFRLLQPNGLLEFYAAGSDVFSISLNGVIMDVK--GIKVVQ	1059
Qy	448	KSPETWDCILHNHVSISDTSGLR--LLID-DQYLRBNQGLBPSNMQOGLR--LIG--	499
Dh	1060	SVDKQYNDGSHF--VISSVSPTRYELLVDSRGSXNPTKGIETQJASEKFFFGSP	1117
Qy	500	-----GHFEGCISNVLQVRFQSQSEVLDLASKYTKQASIGCGSLNRPFLMLFKSPRF	554
Dh	1118	ISAGYANFTGISNAYFTRVDROVEVDPQRYTEKHTSLTYEGTESSPLEFLHKCKNL	1177
Qy	555	NKGEIFVNVQ--LMQDAPQATRSTEAWQGRSCPLINT-----KASHRALQF	600
Dh	1178	SKPRAQNKKGKQSKDAP-----SWDPVALKIPEBNTPRNSHCHLSNBPRAIEHAYQ	1230
Qy	601	GDSTSHLLKLPEBLLKPRSQSPSLDIQTTSPKGLVYYAGTKD--SFLALVYDGRVFA	658
Dh	1231	GGTJNSQOEFEHLGDEFGAKSOFISIRLTRSSHGMIFYVDOEBNDMTTLFLAGRLVYM	1290
Qy	659	LGAGGKKLRLRSKRYNDKXHTVFPGLNGCAKALVYDGLRAQEGSL-PGNSTSPREOV	717
Dh	1291	FNVGHKKLKLRSQEKYNDGLMHVDVIFRENSSGRLVLDGLRYLEBSLPRTYATKIKGPI	1350
Qy	718	YLAGPLSRKPKSLQO---HSFVQCLDPOLNSPKLDPSPARFVSPCLGSLBKGIYFS	773
Dh	1351	YLGVAVGKAVKXVQINSIYSFSSCLNLQJNGASISASQTFEVTQCFBSPMGTGYFS	1410
Qy	774	QGGGHVILANSVSLGPELKLTFSIRPSLFGVLIVHQSQSGQRLSVYMEAGKVTTSVSD	833
Dh	1411	TEGGYVULDESFNIGLFEFLAEFVRPSSSGTLVHGSHVGEYLVNVMKNGQVIVKXVNG	1470
Qy	834	AGGSVTSITPKQSLCDQGMHVSVAISIKORILHL	866
Dh	1471	IRDPSTVTPQOSLCDGRMHRITVIRDSNVQOL	1503

```

/ RESULT 13
/ US-10-239-058-2
/ Sequence 2, Application US/10299058
/ Publication No. US20030103975X1
/ GENERAL INFORMATION:
/ APPLICANT: JONES, JONATHAN C.R.
/ APPLICANT: GONZALES, MEREDITH
/ TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHelialIZATION
/ FILE REFERENCE: 1120-1-002 CIP
/ CURRENT APPLICATION NUMBER: US/10/299,058
/ CURRENT FILING DATE: 2002-11-18
/ PRIOR APPLICATION NUMBER: 09/706,235
/ PRIOR FILING DATE: 2000-11-03
/ PRIOR APPLICATION NUMBER: 60/163,159
/ PRIOR FILING DATE: 1999-11-03
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 1816
/ TYPE: PRT
/ ORGANISM: Homo sapien
/ FEATURE:

```


OTHER INFORMATION: X in position 1112 = Arg/Pro
US-10-299-058-2

Query Match	26.4%;	Score 1187;	DB 14;	Length 1816;
Best Local Similarity	-33.2%;	Pred. NO. 1.2e-87;		
Matches 310;	Conservative 160;	Mismatches 373;	Indels 90;	Gaps 27;

```

QY 1 MRPNKGSVEYRLPNDDLEDDLGYSLSLFL-----ORPDLRNGGGEDEMFVWYLLGNKQASK 56
Db 829 MMEFGQSVAVEHSHKTSMDDLBAFSTLSLYMKPVRKPELTLT---TADOFILYLSKNAKK 885
QY 57 DYIGMAVVDGOLTCVYNLGDREAREVOIDQVLTSESSEORAVNDRYKFORIYOPAKLTANYKE 116
Db 886 EYMGALIKNDLWVYVYNLGTQDVEIPLDS--KPSWSWAPYSYKLEBVGHGKGVPLTV 943
QY 117 ATSNKPKAPAVYDLEGGSSNTLLNIDPEDAVYVYGGVPPDELPBRLRFPFYKCCIBLDD 176
Db 944 SLSTSTAEKFPKKGSGFSGDSDILDLDEPDITVFVYGVGVSNFKLPTSLNLPFGVCLBIAT 10033
QY 177 LNEVNLISYNKKTENFNLTTEVEBPCRRK-----EEDJXNFEEGGVA--RIPTOPN--A 227
Db 1004 LNDVNLISYNKHLYNMDSTSVPCARBKALFOTGRASSTYFPDGSYAIVVDITRRKFG 10633
QY 228 PEPNFQITQTVTDRCGLLFAENODNFISLIEDGNLMVRY-----KLNSEPEKEXGI 280
Db 1064 QVTFEDIEVRFPANGLILLMVNGSMFRLMRNGYLHVFDPGSSGXVHLEDTLAKA- 11222
QY 281 RDTNDGKDSILITTGLOKRRMINNERSVRI---EGELPDSYTYLGGIP-----I 331
Db 1123 --QINDAKYHEISI-IYENDKKMLLVDRRHVKSMDNEKMKI PFDTIYIGAPELLQSR 1179
QY 332 AIRERFNISTAPGCKMNL---KKTSSVYVNLNTQVTKKCSBPMKLVNRASRGOM 388
Db 1180 ALRHLPLDIT-NFGCKMGKGFQOKKDNILQETELGVCYGCPEBSLSIRAYFN--GQS 1236
QY 389 SFTMLD-VPSYDRFOLSGFQTFOPSGTILNHORTSLSLTYLEBGLIELSTRDSNPIF 447
Db 1237 FIASIQKISFDPGEGFNFRITLQNGLLFFYASGSVDVFSISLNGVIMYVK--GIKVQ 1294
QY 448 KSPGTYMDGLLHVSVISDTSGLR--LLID-DQVLRNQRLLPSPNMQOSLR--LGG- 499
Db 1295 SVDRKQYNDGLSHF--VISVSAPTRIELIVDKSRVGSNKPTGAKIEQTQASKEKVFQGGP 1352
QY 500 -----GHEEGISNVLVGRFSGSPBYDLAKSKTYKQASLGGCSLNKPPMLMKSPGRF 554
Db 1353 ISAOYANPTGCSINAYFTRVDREVEBFOBYTEKVHTSLYCEPTLESSPFLHKKGNL 1412
QY 555 NKGRIFPNVNO--LMODAPQATRTTEAWODGRSCPLPLT-----KASHRALQF 600
Db 1413 SKPRASQNKKGKGSKDAP-----SWDPVALKLPERTTPRNSHCHLSNFRALIEHAYQ 1465
QY 601 GDSPTSHLLKLPOELLKPRSQSPSLDIQTTSPKGLVFFYAGTKD--SFLATLVADGRVVA 658
Db 1466 GGTANSRQEFHKLKQDFKXQSPSIRLATRSSHGMIFVVSQGBENDFWTLFLAIGRLVYM 1525
QY 659 LGAGGKRLKLSKERYHDGKHWTVYFGANGAKALVYDGLAAGBSL-PGNSITSPREQV 717
Db 1526 FNVGHKKKLKIKISOEYKXNDGLMHWDIYFIERSSGRLVYDGLVLBERSLPTATYKIKQPI 1585
QY 718 YLGLPLSRKPSLPO---HSFVGLCLRPOLNSKXLDPSARFGVSPCLGSLGKGIYFS 773
Db 1586 YLGGVAPBKAVKNQVINSIYFSGCLSMQJLNGASITASQTFSVTPCFEBSPEMETGIYFS 1645
QY 774 QGGGHVILANSVSLGPELKLTFPSIRPSLJTVLJHVGSQSQORLSVYMEAGKVTTSSD 833
Db 1646 TEGGVVVDDESFNIGLKEFELAFBYVPRSSGTLVGHGSHVNGEYLVNHHKNGQVIVKVNNG 1705
QY 834 AGGSVTSITPQKSLCDGQWHSVANYSIKRRIILH 866
Db 1706 IRDSTSVTPKQSLCDGRMHRITVYIRDSNVQOL 1738

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US-10-299-058-4
; Sequence 4, Application US/10299058
; Publication No. US20030103975A1
; GENERAL INFORMATION:
; APPLICANT: JONES, JONATHAN C.R.
; ADDRESSES: CONAIPS MEDICUTU

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FILE REFERENCE: 1720-1-002 CIP
CURRENT APPLICATION NUMBER: US/10/299,058
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/706,235
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: 60/163,199
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1816
TYPE: PRN
ORGANISM: Homo sapien
FEATURE:
OTHER INFORMATION: X in position 1112 = R/P
US-10-299-058-4

Query Match      26.4%; Score 1185; DB 14; Length 1816;
Best Local Similarity 33.2%; Pred. No. 1,7e-87;
Matches 310; Conservative 160; Mismatches 373; Indels 90; Gaps 27;

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Cy 57 DYIGMAVVDGQLTCVVM/GDREAEVQIDQVLTSESBOEAVMDRYKFORIYQFATLNTYKE 116
Db 886 EYMGALAKNDMLVYVYVNLGTQDVAEILPDS--KPYGSPAPAFSIYKIRGVGHGKVLTPV 943
Cy 117 ATSKKPKPAVAVYDLEGGSSNTLMLDPEDAVFYTGYPDPDFELSKLRFPPYKGCIELDD 176
Db 944 SLSTASBEKPLKKGEFSGDDSLDLDBEDVTFYVGVPVSNFKPLTSLNLPFGVCLBLAT 1003
Cy 177 LNEVNLSTYNKTFENATTEVEBCEBRK-----EESDKYFESGTGYA--RIPTQPN--A 227
Db 1004 LNNVYISLNNKHIYNNDPSTSVFCADKALFQTSRAASVYFDDSGYAVVADITRRKQFG 1063
Cy 228 PEPNFICTQTVDKGLLFAENODNFI SLNIEDGNLVRY-----KLNSEPPKEKGI 280
Db 1064 QVTFPFDIEVETRPADNGIILLMNVNMGSEFRLERNGYLVHVFDFGSSGXVILBDTLKKA- 11222
Cy 281 RDTINDGKDSILLTTCKLOKRMVNNBSVRI---EGEILFDSITYLGSI-----I 331
Db 1123 --QINDAKYHEISL-IYHNDKQMLVVDKRRVNSMDNEKAKIPTDIYIIGAPBELLQSR 1179
Cy 332 AIRERFNISTEFAFGCKAKNL---KKTSGVAVLNDTVGVTKKCSHEDMTLVRTASPSRGQM 388
Db 1180 ALRHLHPLDI-NFRGCKMKGPQFKQDKFNILLEGTEITLVGVGCGPDSILSRAYFN--QGS 1236
Cy 389 SFTNLD-VPSIDTRQLSFGQTFPPQSGTLNHOQRTSSLVLTEDGHIELSTRSNPIF 447
Db 1237 FLAIQKISLFPDGEFGGFPFTLOPNGLLFTYASGSVFSISLNDGVIYMDVK--GIKVVQ 1294
Cy 448 KSPGYMDGGLNHNVSIDSFGRL--LLID-DQVLRNRORPSPSNAAQSLR--LGG-- 499
Db 1295 SVDGQYNDGLSHF--VLSVSPTRYELIYDKSRGSGNPTPKGKIEQYDASKEKRYFGSGP 1352
Cy 500 ----GHPEGICSNVLVQRESQSPVILDLASKSTYKQASLGGCSLNRPPLMLFKSPKRF 554
Db 1353 ISAOYANFTGICISNAVYFTRVDRDVEVEDFORYTEKVTSLYECPILBESPLFLHKKGNL 1412
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Db 1413 SKPLASQNKKGKSKADP-----SNDPVALKPLPERNTPNNSGHLNSNRALIEHAYQY 1465
Cy 601 GDSPTSHLLKLPQELLKPRSQFSLDIQTSPKGLVFAVATKD--SFLATLVADGRVFA 658

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Db 1466 GGTANRROEFERHUKDGFKAQSOPISIRLRTSSHGIMFYVSDQENDFMTLFLAHGRLVYM 1525
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Db 1526 FNVGHKKLKRSEKINDIMHVIPIRERSSGRLVIDGLRIEELPPEBAWTKIKGPI 1585
QY 718 YLGLPLSRKRLPQ-----HSFVGLRDLPQLNSKPLDPSAPRGVSPCLGSLKGIYPS 773
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QY 774 QGGGHVILANSVLSGELKLTESIRPRSLTGVLIIHVSQSGQLSVYMEAKYTTVSSD 833
Db 1646 TREGYVLDSEFNIKGKFEIAPFVRPRSSSGTLVHGHSVGEYLVNHYMKGVIVKXNNG 1705
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Db 1706 IRDFTSVTPKOSLCDGRMHRITVIRDSNVQL 1738

RESULT 15
US-10-037-417-49
; Sequence 49, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Paturajan, Meera
; APPLICANT: Grose, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine B
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Billeman, Karen
; APPLICANT: Malvanek, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Eissen, Andrew J
; APPLICANT: Miller, Charles E
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12

; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 1634
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-037-417-49

Query Match 23.3%; Score 1045.5; DB 15; Length 1634;
Best Local Similarity 31.6%; Pred. No. 44e-76;
Matches 294; Conservative 159; Mismatches 367; Indels 109; Gaps 32;

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QY 61 MAVVDGQLTCVYNLDR-BAEVQIDQVLTSESQSAVMDRYKFORITYPAKLNTYKE--- 116
Db 736 VSLRDCKVMYVQLGABAPAVLISIDEDIGEQ-----PAVSLDRTLQFGHMSVTVBERQM 789
QY 117 --ATSNKDKAPAVYDLEGSSVTLNLPEDAVFYVGGYPPDFELPSRLRPPPYKGIETL 174
Db 790 IQETKGDVYAPGA---EG-----LNLKRPDDVFYVGGYPTFTPTPLIRPFPGYCIEM 841
QY 175 DDLNENVSLVYNFKTTPMINTTEVPCRRRKE-----SDKNYFEGTGYARIPTQPN-AP 228
Db 842 DTLNEBVSLVYFERTFPQDFAVDRPCARSKSTGDPWLTDSYLDGTGFARISPDQIST 901
QY 229 PPNFIQTITQTVDRGLPFAENQDNFISLNEEDGMLRYKLS-----EPP----- 275
Db 902 TTRFQDELRLVSYSGLVFFLKQSQFLCLAVQESLVLLYFGAELKKAVALQPPPPYTS 961
QY 276 KEKGIRDTINDKDSILITTKLOKRMIVNER---SVRLEGITPFGSTYYLAGI--- 329
Db 962 ASKAIQ-----VPLGSKRKVLVYERATYVSVEQDNLELADAYLLGSGVPPD 1010
QY 330 --PLAIRERFNISTPAFOGCMKLNK--KTSGVANLNDTVGVTKKCSBDMKLVRTASFSR 384
Db 1011 QLPPLRLRFP-TGGSVGRGVAVGKALGKYVDLKRLL-TTGVSACQADLLVGRAMTFHG 1068
QY 385 GG-QMSFTNLDVBPETDRFQLSFGQTQPSGTLNHOQTRSSLLVTEDEGHELESTDS 442
Db 1069 HGFRLRLALSNV-APLTGVNYSGFHSAODSLALYRRASPDGLCOVSLQGGVSLQLLRT 1127
QY 443 NIPFSPQTYMDGLHHVSVISDTSGLRLIYDQV--LRRNQRPSMSNAQOS---LR 496
Db 1128 EV---KTQAGFADGAPHYAFATSNATGWLIVDDQLQMKHRRGPPBELQRPBEPRL 1184
QY 497 LGG-----GHFEGCISNVLVQRFQSPDEVLDLASKSTKDKASIGGSLNKPPLMLFK 549
Db 1185 LGGLPESGTYVNFSGCISNVFQRLGQRYVFDLQONLGSVVST-GCA---PALQA-Q 1238
QY 550 SPKRNRKGRIFENVNOLMODAPQATSTEAQWQDGRSCPLPLTKASHRLAQEDSTSHL 609
Db 1239 TPGGLPRG-----LOATARKASRRSROPARNPACMLPPHILRTTRDYQFQSGSLSSH- 1289
QY 610 LKLPGELKKPRS--QFSIDIQTSPKGLVYAG---TDSFLLVAVADGRVVFALGAGSK 664
Db 1290 LRFVGLLAHRNWPBLSMHWLPRSSRGLLFARLRPGSPSLALFLSHGHVFAQEGIGLT 1349
QY 665 KLRLSKERYHDKMHTVVGILNGKARLVVDGLRA-QEG---SLPGNSTISPREQVYL 719
Db 1350 RLRAQSRQSRGRNHNKXSVREKRIILLYVDGAAWQEBGHRHQHQAENHQPITLFGV 1409
QY 720 GLPLSRKPKSLP-QHSFVGCLEDFOLNSKPLDPSAPRGVSPCLGSLKGIYPSQGGGH 778
Db 1410 GLPASHSKCLPVTVTGFSGCVCVRRLHGRPLGAPFRMGAVYPCIIIGPPEAGIFFPGSGGV 1469
QY 779 VILANSVLSGELKLTFSIRPRSLTGVLIIHG-SQSGQRLSVYMEAKYTTVSSDAGGS 837
Db 1470 ITLDPGATLPVGLGLEVRPLAVTGLIFHLGQARTPYLQIQVTEKQVLLRADDAGERF 1529
QY 838 VTSITPKOSLCDGQWHSVAVSIIKORILHL 866

Db 1530 STSVTRPSVLCDCGQWHRHIAVMKSGNVRL 1558

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Job time : 119.062 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:13:40 ; Search time 40.4378 Seconds
(without alignments)
1598.653 Million cell updates/sec

Title: US-10-817-423-2

Perfect score: 4491

Sequence: 1 MRFNGKSGVEVRLPNDLEDL.....LCDGQMSVAIVKIKRIHL 866

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB pep:*
2: /cgn2_6/prodata/1/iaa/5B COMB pep:*
3: /cgn2_6/prodata/1/iaa/6A COMB pep:*
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6: /cgn2_6/prodata/1/iaa/backfile1 pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4491	100.0	1694	4 US-09-560-385A-12	Sequence 12, Appl
2	4491	100.0	1725	4 US-09-560-385A-10	Sequence 10, Appl
3	3560.5	79.3	1693	4 US-09-560-385A-4	Sequence 4, Appl
4	3560.5	79.3	1693	4 US-09-560-385A-8	Sequence 8, Appl
5	3560.5	79.3	1713	3 US-08-600-982-24	Sequence 24, Appl
6	3560.5	79.3	1713	4 US-09-560-385A-24	Sequence 6, Appl
7	3560.5	79.3	1713	4 US-09-538-092-1359	Sequence 1359, Ap
8	3560.5	79.3	1713	5 PCT-US94-10261A-24	Sequence 24, Appl
9	3560.5	79.3	1724	4 US-09-560-385A-2	Sequence 2, Appl
10	1310	29.2	770	1 US-08-445-135-2	Sequence 2, Appl
11	1198	26.7	1792	4 US-09-561-818A-4	Sequence 4, Appl
12	1198	26.7	1800	4 US-09-561-818A-2	Sequence 8, Appl
13	1198	26.7	1816	4 US-09-561-818A-8	Sequence 10, Appl
14	1198	26.7	1824	4 US-09-561-818A-6	Sequence 6, Appl
15	1183	26.3	1792	4 US-09-561-818A-12	Sequence 12, Appl
16	1183	26.3	1816	4 US-09-561-818A-10	Sequence 10, Appl
17	1015.5	22.6	953	4 US-09-845-583A-4	Sequence 4, Appl
18	948	21.1	3635	4 US-09-845-583A-2	Sequence 2, Appl
19	925	20.6	3647	4 US-09-949-016-10932	Sequence 10932, A
20	534.5	11.9	1130	6 5444158-2	Patent No. 5444158
21	534.5	11.9	1130	6 5444158-2	Patent No. 5444158
22	530.5	11.8	3075	2 US-08-460-309-5	Sequence 5, Appl
23	530.5	11.8	3075	2 US-08-125-077-5	Sequence 5, Appl
24	526.5	11.7	1130	2 US-08-460-309-2	Sequence 2, Appl
25	526.5	11.7	1130	2 US-08-125-077-2	Sequence 2, Appl
26	526.5	11.7	3088	4 US-09-562-702A-8	Sequence 8, Appl
27	526.5	11.7	3089	4 US-09-562-702A-4	Sequence 4, Appl

28	526.5	11.7	3110	4 US-09-562-702A-2	Sequence 2, Appl
29	526.5	11.7	3110	4 US-09-562-702A-6	Sequence 6, Appl
30	526.5	11.7	3110	4 US-09-561-709B-7	Sequence 7, Appl
31	526.5	11.7	3110	4 US-09-917-254-86	Sequence 86, Appl
32	526.5	11.7	3110	4 US-09-949-016-5937	Sequence 5937, Ap
33	526.5	11.7	3111	2 US-08-460-309-4	Sequence 4, Appl
34	526.5	11.7	3111	2 US-08-125-077-4	Sequence 4, Appl
35	516.5	11.5	3084	4 US-09-562-702A-12	Sequence 12, Appl
36	516.5	11.5	3106	4 US-09-562-702A-10	Sequence 10, Appl
37	484.5	10.8	3070	4 US-09-961-403-7	Sequence 7, Appl
38	294	6.5	1384	4 US-09-949-016-7814	Sequence 7814, Ap
39	220.5	4.9	1384	4 US-09-949-016-6861	Sequence 6861, Ap
40	205	4.6	1384	4 US-08-826-134-2	Sequence 2, Appl
41	205	4.6	1384	4 US-09-949-016-6395	Sequence 6395, Ap
42	183	4.1	4391	4 US-10-006-011A-2	Sequence 2, Appl
43	180	4.0	705	4 US-10-006-011A-3	Sequence 3, Appl
44	176.5	3.9	1058	4 US-09-949-016-11457	Sequence 11457, A
45	174	3.9	1381	4 US-08-826-134-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-560-385A-12

Sequence 12, Application US/09560385A

Patent No. 6703363

GENERAL INFORMATION:

APPLICANT: Bouland, Arlet

TITLE OF INVENTION: Recombinant Laminin 5

FILE REFERENCE: 99-274-C

CURRENT APPLICATION NUMBER: US/09/560,385A

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 12

LENGTH: 1694

TYPE: PRT

ORGANISM: Rattus norvegicus

US-09-560-385A-12

Query Match

Best Local Similarity 100.0%; Pred. No. 0;

Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRFNGKSGVEVRLPNDLEDLKYTSLSLFLQRPDLRENGGTEDMFVYLGAKDASKDYIG	60
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QY	61	MAVVDQQLTCVYVNLGPREARVQIDVLTSESGEAVMDVKRPIYQFALNTTKATSN	120
DB	811	MAVVDQQLTCVYVNLGPREARVQIDVLTSESGEAVMDVKRPIYQFALNTTKATSN	870
QY	121	KPAPAVYDLEGGSSNTLNLDPEDAVFYVGGVPDPFELPSRLRFPYKGCIELDLLEN	180
DB	871	KPAPAVYDLEGGSSNTLNLDPEDAVFYVGGVPDPFELPSRLRFPYKGCIELDLLEN	930
QY	181	VLSLVFKTTFNLTVEVEPCRRKESDKNYEGTGARIPQPNAPFNFQITQTV	240
DB	931	VLSLVFKTTFNLTVEVEPCRRKESDKNYEGTGARIPQPNAPFNFQITQTV	990
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DB	991	DRLGLPFAKNDFISLNTBDGMLNRYKLNSEPPYKGRIRDTINDGKHSILITGKQ	1050
QY	301	KRWIMVNSRVVIEGIFDFTYVGGIPAIAREPNTSTPAFGCMKRLKKTSGVRL	360
DB	1051	KRWIMVNSRVVIEGIFDFTYVGGIPAIAREPNTSTPAFGCMKRLKKTSGVRL	1110
QY	361	NDTVGVTKKCSSEDMKLVRTASFSRGQMSFTNIDVSTDRFQLSFGRTFQPSGTLNHQ	420
DB	1111	NDTVGVTKKCSSEDMKLVRTASFSRGQMSFTNIDVSTDRFQLSFGRTFQPSGTLNHQ	1170

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QY 421 TRTSSLVLTLEBGIHELSTRDSNIPIFKSPGYMDGLHHVSVISDTSGLRLIIDQVLR 480
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QY 481 RNORLPSFSNAOQSLRLGGHFEBCISNVLYORFSGSPRYLDASSTKXDSIAGGCSLN 540
DB 1231 RNORLPSFSNAOQSLRLGGHFEBCISNVLYORFSGSPRYLDASSTKXDSIAGGCSLN 1290
QY 541 KPPFLMLFKSPKRFKGRIFNVNQMLQDAPQATRSTTEAMODGRSCPLPLNTKASHRALQF 600
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QY 601 GDSPTSHLLKLPOBLKPRSQPSLDIQTTSPPKGLVFYAGTKDSFLALYVADGRVVPALG 660
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QY 661 AGGKTLRLSKERYHDGKMTVVFGLNGGKARLVVDGLAQBESLPGNSTISPREQVYLQ 720
DB 1411 AGGKTLRLSKERYHDGKMTVVFGLNGGKARLVVDGLAQBESLPGNSTISPREQVYLQ 1470
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QY 841 ITPKOSLCDGQMHSAVSIKORILHL 866
DB 1591 ITPKOSLCDGQMHSAVSIKORILHL 1616

RESULT 2
US-09-560-385A-10
; Sequence 10, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Bouland, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-560-385A-10

Query Match 100.0%; Score 4491; DB 4; Length 1725;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 MAVVDGQLTCVYNLGDREAVQIDQVLTSESQDAVMRVKFORIYQPAKLNTYKATSN 120
DB 842 MAVVDGQLTCVYNLGDREAVQIDQVLTSESQDAVMRVKFORIYQPAKLNTYKATSN 901
QY 121 KPPAPAVYDLEGSSNTLNLDPEDAVFYVGYVPPDELPSTRLRFPYKGCIELDLNEN 180
DB 902 KPPAPAVYDLEGSSNTLNLDPEDAVFYVGYVPPDELPSTRLRFPYKGCIELDLNEN 961
QY 181 VLSLVNFKTFNLTTEVEPCRRRKESDKNVEGTCYARIPTQNPAPFPNFIOITQTV 240
DB 962 VLSLVNFKTFNLTTEVEPCRRRKESDKNVEGTCYARIPTQNPAPFPNFIOITQTV 1021
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DB 1082 KKMWINVERSVRIEGEIFDEFTYVLGGIPAIABERFNIPTAPQGCCKNLKKTSGVRL 1141
QY 361 NDTVGATKCSBDMKLVTAAPSRRGQMSFTNLDPVSTDRFQLSFGFOTPOPSGTLNMQ 420
DB 1142 NDTVGATKCSBDMKLVTAAPSRRGQMSFTNLDPVSTDRFQLSFGFOTPOPSGTLNMQ 1201
QY 421 TRTSSLVLTLEBGIHELSTRDSNIPIFKSPGYMDGLHHVSVISDTSGLRLIIDQVLR 480
DB 1202 TRTSSLVLTLEBGIHELSTRDSNIPIFKSPGYMDGLHHVSVISDTSGLRLIIDQVLR 1261
QY 481 RNORLPSFSNAOQSLRLGGHFEBCISNVLYORFSGSPRYLDASSTKXDSIAGGCSLN 540
DB 1261 RNORLPSFSNAOQSLRLGGHFEBCISNVLYORFSGSPRYLDASSTKXDSIAGGCSLN 1321
QY 541 KPPFLMLFKSPKRFKGRIFNVNQMLQDAPQATRSTTEAMODGRSCPLPLNTKASHRALQF 600
DB 1321 KPPFLMLFKSPKRFKGRIFNVNQMLQDAPQATRSTTEAMODGRSCPLPLNTKASHRALQF 1381
QY 601 GDSPTSHLLKLPOBLKPRSQPSLDIQTTSPPKGLVFYAGTKDSFLALYVADGRVVPALG 660
DB 1381 GDSPTSHLLKLPOBLKPRSQPSLDIQTTSPPKGLVFYAGTKDSFLALYVADGRVVPALG 1441
QY 661 AGGKTLRLSKERYHDGKMTVVFGLNGGKARLVVDGLAQBESLPGNSTISPREQVYLQ 720
DB 1441 AGGKTLRLSKERYHDGKMTVVFGLNGGKARLVVDGLAQBESLPGNSTISPREQVYLQ 1501
QY 721 LPLSRKPKSLPQHSFVGCRLDPOLNSKPLDSPARFVSPCLGSLKGIYFSGGGHYI 780
DB 1501 LPLSRKPKSLPQHSFVGCRLDPOLNSKPLDSPARFVSPCLGSLKGIYFSGGGHYI 1561
QY 781 LANSVSLGPELKLTFISIRPSRLTGVLHVGSQSGRLSYVMEAGKVTTSVSDAGSVTS 840
DB 1561 LANSVSLGPELKLTFISIRPSRLTGVLHVGSQSGRLSYVMEAGKVTTSVSDAGSVTS 1621
QY 841 ITPKOSLCDGQMHSAVSIKORILHL 866
DB 1621 ITPKOSLCDGQMHSAVSIKORILHL 1647

RESULT 3
US-09-560-385A-4
; Sequence 4, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Bouland, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1693
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-385A-4

Query Match 79.3%; Score 3560.5; DB 4; Length 1693;
Best Local Similarity 78.4%; Pred. No. 0;
Matches 660; Conservative 86; Mismatches 99; Indels 3; Gaps 2;

QY 1 MRFNGSGVEVRLPNDLELDKGYTSLSLFLQRPDLRENGGTEDMFVMTLGNKDSKDYIG 60
DB 751 MRFNGSGVEVRLPNDLELDKGYTSLSLFLQRPDLRENGGTEDMFVMTLGNKDSKDYIG 810
QY 61 MAVVDGQLTCVYNLGDREAVQIDQVLTSESQDAVMRVKFORIYQPAKLNTYKATSN 120
DB 811 MAVVDGQLTCVYNLGDREAVQIDQVLTSESQDAVMRVKFORIYQPAKLNTYKATSN 870

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[illegible]

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/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
/ STREET: 1420 Fifth Avenue
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98101-8100
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/600,982
/ FILING DATE: 02-SEP-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Shelton, Dennis K.
/ REGISTRATION NUMBER: 26,997
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 682-8100
/ TELEFAX: (206) 224-0779
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1713 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ DESCRIPTION: E170 protein as translated from sequence
/ of FIGURES 15A-15F, and as shown also in FIGURES
/ DESCRIPTION: 19A-19R
/ US-08-600-982-24

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Query Match 79.3%; Score 3560.5; DB 3; Length 1713;

Best Local Similarity 78.4%; Pred. No. 0; Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

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QY 1 MRFNGSGVEVRLPNDLEDLKGYTSLFLQRPDLRENGTDMFVMYLGNDASRDYIG 60
DB 771 MRFNGSGVEVRLPNDLEDLKGYTSLFLQRPDLRENGTDMFVMYLGNDASRDYIG 830
QY 61 MAVVDQQLTCVYNLGDREAEVQIDQVLTSESEQEAVMDRVKFORIYQPAKLNTYKATSN 120
DB 831 MAVVDQQLTCVYNLGDREAEVQIDQVLTSESEQEAVMDRVKFORIYQPAKLNTYKATSN 890
QY 121 KKPAAVYDLEGGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLNEN 180
DB 891 KKPAAVYDLEGGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLNEN 950
QY 181 VLSLVNFKTFTNLTTEVEPCRRRKESDKNYFEGTGVARIPQPNAPFNFYQTIQTTV 240
DB 951 VLSLVNFKTFTNLTTEVEPCRRRKESDKNYFEGTGVARIPQPNAPFNFYQTIQTTV 1010
QY 241 DRGLLFPANQDNFISLNIEDGNLWRYKLNSEPPYEKGIPTINDGKHSILITIGKIQ 300
DB 1011 DRGLLFPANQDNFISLNIEDGNLWRYKLNSEPPYEKGIPTINDGKHSILITIGKIQ 1070
QY 301 KRWMIINVERSVRIIEGIPDSTYYLGGIPAIRERNISTPAFOGCMKLLKKTSGVRL 360
DB 1071 KRWMIINVERSVRIIEGIPDSTYYLGGIPAIRERNISTPAFOGCMKLLKKTSGVRL 1130
QY 361 NDTVGVTKKCSBMDKLVRTASFRGGQMSFTNLDPVSTDRFQLSFGFQTFQPSGTLNMQ 420
DB 1131 NDTVGVTKKCSBMDKLVRTASFRGGQMSFTNLDPVSTDRFQLSFGFQTFQPSGTLNMQ 1190
QY 421 TRTSSLVLTLEDGHIILSTRDSNIPFKSPGTYMDGLLHHVSYISDTSGRLLLIDQVLA 480
DB 1191 TRTSSLVLTLEDGHIILSTRDSNIPFKSPGTYMDGLLHHVSYISDTSGRLLLIDQVLA 1250
QY 481 RNRRLRSFSAQOSLNLGGGHFEGCISNTLVORFSQSPFVLDAASKTKDASLGCSLN 540
DB 1251 RNRRLRSFSAQOSLNLGGGHFEGCISNTLVORFSQSPFVLDAASKTKDASLGCSLN 1310

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QY 541 KPPFLMLFKSPYKFKGRIFNVNQLOMDAPQAT-RSTEAMODGRCLPPLNTKASHRALQ 599
DB 1311 KPPFLMLKSGTRFKTKTRFNRNQLQDTVPVAPPSVAVWQD--ACSLPDKTQAHGHLQ 1368
QY 600 PDDSPSTSHLLKLPOELLKPRSQSLDIQTSSPKGLVYAGTQSPFLALVYADGVFVAL 659
DB 1369 PDDIPTSLLFKLPOLLLKPRSQFAVMDQTSSRGLVFHTGKSNFMALYLKSGRLVFLAL 1428
QY 660 GAGGKKLRIRSKERVHNDGWHVVFGLNGKRLVVDGRLAPEGSLPGNSTISPREQVTL 719
DB 1429 GNDGKKLRIRSKERKCNKNDGWHVVFHDEKGRLLVVDGRLAPEGSLPGNSTISRAPYTL 1488
QY 720 GLPLSRKPKSLPQHSFVGLTARDPOLNSKPLDPSARFVSPCLGSLLEKGIYFSQGGHY 779
DB 1489 GSPSPGKPKSLPTNSFVGLTKNFDLSDKPLVTPSSSPGVSSGLGSPLEKGIYFSREGHY 1548
QY 780 ILANSVSLGPELKLTPSIRPSRLTVLTHVGSQSORLSVTMEAGKVTTSVSSDAGSVT 839
DB 1549 VLAHSAVLGPBEKLVFSIRPRSLTGLIHIGSQPKHLCVYLEAGKVTASMDSGAGTST 1608
QY 840 SITPKOSLCDQGMHSAVASIKORILHL 866
DB 1609 SVTPKOSLCDQGMHSAVAITIKOHILHL 1635

```

RESULT 6
US-09-560-385A-6

```

/ Sequence 6, Application US/09560385A
/ Patent No. 6703363
/ GENERAL INFORMATION:
/ APPLICANT: Boucard, Arlet
/ TITLE OF INVENTION: Recombinant Lamtin 5
/ FILE REFERENCE: 99-274-C
/ CURRENT APPLICATION NUMBER: US/09/560,385A
/ CURRENT FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 1713
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-560-385A-6

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Query Match 79.3%; Score 3560.5; DB 4; Length 1713;

Best Local Similarity 78.4%; Pred. No. 0; Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

```

QY 1 MRFNGSGVEVRLPNDLEDLKGYTSLFLQRPDLRENGTDMFVMYLGNDASRDYIG 60
DB 771 MRFNGSGVEVRLPNDLEDLKGYTSLFLQRPDLRENGTDMFVMYLGNDASRDYIG 830
QY 61 MAVVDQQLTCVYNLGDREAEVQIDQVLTSESEQEAVMDRVKFORIYQPAKLNTYKATSN 120
DB 831 MAVVDQQLTCVYNLGDREAEVQIDQVLTSESEQEAVMDRVKFORIYQPAKLNTYKATSN 890
QY 121 KKPAAVYDLEGGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLNEN 180
DB 891 KKPAAVYDLEGGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLNEN 950
QY 181 VLSLVNFKTFTNLTTEVEPCRRRKESDKNYFEGTGVARIPQPNAPFNFYQTIQTTV 240
DB 951 VLSLVNFKTFTNLTTEVEPCRRRKESDKNYFEGTGVARIPQPNAPFNFYQTIQTTV 1010
QY 241 DRGLLFPANQDNFISLNIEDGNLWRYKLNSEPPYEKGIPTINDGKHSILITIGKIQ 300
DB 1011 DRGLLFPANQDNFISLNIEDGNLWRYKLNSEPPYEKGIPTINDGKHSILITIGKIQ 1070
QY 301 KRWMIINVERSVRIIEGIPDSTYYLGGIPAIRERNISTPAFOGCMKLLKKTSGVRL 360
DB 1071 KRWMIINVERSVRIIEGIPDSTYYLGGIPAIRERNISTPAFOGCMKLLKKTSGVRL 1130
QY 361 NDTVGVTKKCSBMDKLVRTASFRGGQMSFTNLDPVSTDRFQLSFGFQTFQPSGTLNMQ 420

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Db 1131 NDVGVATKCSSEMDKLVRSASFSRGQSLSTDLGPTDHLQASFGQTQPSGILLDHQ 1190
 QY 421 TRTSSLVLTLEDGHIESTRDSNIPFKSPGTMDGLHHVYSISDTSGRLIIDQVLR 480
 Db 1191 TWTRNLQVTLBEDGYIELSTSDSGPIFKSPQTYMDGLHHVYSISDMSGRLIIDQVLR 1250
 QY 481 RNORLPSFNAOQSLGCGHFGGCTSNVTVORFSGSPETLDLASKSTKDDALSGGCSLN 540
 Db 1251 NSRRLKHISSSRSOLRSGSNFEGCISNVFQRLISPEVLDLTSNLKRDVSLGGCSLN 1310
 QY 541 KPEPLMLFKSPKPKFNKGRIFNVNQLMODAPQAT-RSTEAMQDGRSCLPPLNTASHRALQ 599
 Db 1311 KPEPLMLKSTPFTNKTRINQLODTPVASPRSKWQD--ACSPLEKTOQNHGALQ 1368
 QY 600 FGDSPTSHLLKLPOELKPKRSQPSLDIQTSPKGLVFYAGTOSFLATLVADGRVFL 659
 Db 1369 FGDIPTSHLLFKLPQELKPKRSQPAVDMQTTSSRGVLFHTGTNKSFMALYLSKGRLVFAL 1428
 QY 660 GAGGKTLRLSKRYHDKMHTVYFGLNGSKARLVYDGLRAQSGSLPQNSTTIPREVVYL 719
 Db 1429 GTDGKTLRLSKRYHDKMHTVYFGLNGSKARLVYDGLRAQSGSLPQNSTTISIRAVYL 1488
 QY 720 GLPLSRKPKSLPOHSFVGCARDPOLNSKPLDSPARFVSPCLGSLKGIYSOGGSHV 779
 Db 1489 GSPSPGPKSLPFTNSFVGCARDPOLNSKPLDSPARFVSPCLGSLKGIYSOGGSHV 1548
 QY 780 ILANSVSLGPELKLTFESIRPSRLTGVLHHVSGSQGRLSYMEAGKVTTSVSSDAGSVT 839
 Db 1549 VLAHSVILGPEFLVFSIRPSRLTGVLHHVSGSQGRLSYMEAGKVTTSVSSDAGSVT 1608
 QY 840 SITPKOSLCDQWHSVAVSIKORILHL 866
 Db 1609 SVTPKOSLCDQWHSVAVSIKORILHL 1635

RESULT 7

US-09-538-092-1359
 ; Sequence 1359, Application US/09538092
 ; Patent No. 6753314
 ; GENERAL INFORMATION:
 ; APPLICANT: Menziesfield, Traci A.
 ; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
 ; FILE REFERENCE: 15966-542
 ; CURRENT APPLICATION NUMBER: US/09/538,092
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 60/127,352
 ; PRIOR FILING DATE: 1999-04-01
 ; PRIOR APPLICATION NUMBER: 60/178,965
 ; NUMBER OF SEQ ID NOS: 1387
 ; SOFTWARE: CuraParseFormat Version 0.9
 ; SEQ ID NO 1359
 ; LENGTH: 1713
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (0)..(0)
 ; OTHER INFORMATION: Polypeptide Accession Number Q16787
 US-09-538-092-1359

Query Match

Best Local Similarity 79.3%; Score 3560.5; DB 4; Length 1713;
 Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRFRGKSGVAVRLPNDLEDLKGYSLSLFLORPLRNGGHEMDFFVYVILGNKASRYIG 60
 Db 771 MRFRGKSGVAVRLPNDLEDLKGYSLSLFLORPNSRNGGHEMDFFVYVILGNKASRYIG 830
 QY 61 MAVVDGQLTCVYNLGDREAEVQIDQVLTESRSGEAWMDRVFQRIYQPAKNTYKKAETSN 120

Db 831 MAVVDGQLTCVYNLGDREAEVQIDQVLTESRSGEAWMDRVFQRIYQPAKNTYKKAETSN 890
 QY 121 KPAKAPVNDLEGGSSNTLNTLDEDAVFFVGVGPDPPELPSRLRPPRYGCIETLDLNTN 180
 Db 891 KPEPTGVYMDGNSNTLNTLDEDAVFFVGVGPDPPELPSRLRPPRYGCIETLDLNTN 950
 QY 181 VLSVNFKTTFNLTTEVERPCRRKESDKNYEGGVYARIPQPNAPFPNFLOTQVTV 240
 Db 951 VLSVNFKTTFNLTTEVERPCRRKESDKNYEGGVYARIPQPNAPFPNFLOTQVTV 1010
 QY 241 DRGLFPAENQDNFISLNTIEDGNLWRYKNSPEPKGIRDTINDKHSILITIGKLQ 300
 Db 1011 DRGLFPAENQDNFISLNTIEDGNLWRYKNSPEPKGIRDTINDKHSILITIGKLQ 1070
 QY 301 KRWIVNRSVARIIEEIPDFTYTGPIARREFPNSTPAPQCMKRLKTSQVYRL 360
 Db 1071 KRWIVNRSVARIIEEIPDFTYTGPIARREFPNSTPAPQCMKRLKTSQVYRL 1130
 QY 361 NDVGVATKCSSEMDKLVRTASFSRGQMSFTNLDVSTDRFQLSFGQTFQPSGTYLLNHQ 420
 Db 1131 NDVGVATKCSSEMDKLVRSASFSRGQSLSTDLGPTDHLQASFGQTQPSGILLDHQ 1190
 QY 421 TRTSSLVLTLEDGHIESTRDSNIPFKSPGTMDGLHHVYSISDTSGRLIIDQVLR 480
 Db 1191 TWTRNLQVTLBEDGYIELSTSDSGPIFKSPQTYMDGLHHVYSISDMSGRLIIDQVLR 1250
 QY 481 RNORLPSFNAOQSLGCGHFGGCTSNVTVORFSGSPETLDLASKSTKDDALSGGCSLN 540
 Db 1251 NSRRLKHISSSRSOLRSGSNFEGCISNVFQRLISPEVLDLTSNLKRDVSLGGCSLN 1310
 QY 541 KPEPLMLFKSPKPKFNKGRIFNVNQLMODAPQAT-RSTEAMQDGRSCLPPLNTASHRALQ 599
 Db 1311 KPEPLMLKSTPFTNKTRINQLODTPVASPRSKWQD--ACSPLEKTOQNHGALQ 1368
 QY 600 FGDSPTSHLLKLPOELKPKRSQPSLDIQTSPKGLVFYAGTOSFLATLVADGRVFL 659
 Db 1369 FGDIPTSHLLFKLPQELKPKRSQPAVDMQTTSSRGVLFHTGTNKSFMALYLSKGRLVFAL 1428
 QY 660 GAGGKTLRLSKRYHDKMHTVYFGLNGSKARLVYDGLRAQSGSLPQNSTTIPREVVYL 719
 Db 1429 GTDGKTLRLSKRYHDKMHTVYFGLNGSKARLVYDGLRAQSGSLPQNSTTISIRAVYL 1488
 QY 720 GLPLSRKPKSLPOHSFVGCARDPOLNSKPLDSPARFVSPCLGSLKGIYSOGGSHV 779
 Db 1489 GSPSPGPKSLPFTNSFVGCARDPOLNSKPLDSPARFVSPCLGSLKGIYSOGGSHV 1548
 QY 780 ILANSVSLGPELKLTFESIRPSRLTGVLHHVSGSQGRLSYMEAGKVTTSVSSDAGSVT 839
 Db 1549 VLAHSVILGPEFLVFSIRPSRLTGVLHHVSGSQGRLSYMEAGKVTTSVSSDAGSVT 1608
 QY 840 SITPKOSLCDQWHSVAVSIKORILHL 866
 Db 1609 SVTPKOSLCDQWHSVAVSIKORILHL 1635

RESULT 8

PCT-US94-10261A-24
 ; Sequence 24, Application PC/TUS9410261A
 ; GENERAL INFORMATION:
 ; APPLICANT: Carter, William G.
 ; APPLICANT: Gil, Susanna A.
 ; TITLE OF INVENTION: Epitigrin, an Epithelial Ligand for
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
 ; STREET: 1420 Fifeth Avenue
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101-8100
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10261A
FILING DATE: 02-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: E170 protein as translated from sequence of
DESCRIPTION: FIGURES 15A-15F, and as shown also in FIGURES 19A-19R
PCT-US94-10261A-24

Query Match 79.3%; Score 3560.5; DB 5; Length 1713;
Best Local Similarity 78.4%; Pred. No. 0;
Matches 680; Conservative 86; Mismatches 98; Indels 3; Gaps 2;

QY 1 MRNGSGVGVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMVMYLGNDKASRDYIG 60
DB 771 MRNGSGVGVRLPNDLEDKGYTSLFLQRPNSRENGGTENMVMYLGNDKASRDYIG 830
QY 61 MAVVDQQLTCVYNLDGREAEVQIDQVLTSESQEAVMDRVKFORIYQFANLTYTKATS 120
DB 831 MAVVDQQLTCVYNLDGREAEVQIDQVLTSESQEAVMDRVKFORIYQFANLTYTKATS 890
QY 121 KRPAPAVYDLEGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKGCIELDLNEN 180
DB 891 KRPETGVYDMDGNSTNLNLDPENVVFFVGYPPDFELPSRLRPPYKGCIELDLNEN 950
QY 181 VLSLVNFKTFNLTTEVEPCRRKESBDKNYFEGTGVARPTQPHAPITPFGQITIQTV 240
DB 951 VLSLVNFKTFNLTTEVEPCRRKESBDKNYFEGTGVARPTQPHAPITPFGQITIQTV 1010
QY 241 DRGLLFFAENQDNFISLINEDGNLMVRYKLNSEPPKEKIRDTINDKDSILITIGKLQ 300
DB 1011 DRGLLFFAENQDNFISLINEDGNLMVRYKLNSEPPKEKIRDTINDKDSILITIGKLQ 1070
QY 301 KRMWVNVRSVRIEGERIDFSTYYLGGIPAIIRERFNISTPAFQGCNKMLKKTSGVRL 360
DB 1071 KRMWVNVQNTIIDGVEVDFSTYYLGGIPAIIRERFNISTPAFQGCNKMLKKTSGVRL 1130
QY 361 NDTVGVTKKSEDMKLVRTASFSRGGMSFTNLDPSTDRFQLSFGQTQPSGTLNMQ 420
DB 1131 NDTVGVTKKSEDMKLVRTASFSRGGMSFTNLDPSTDRFQLSFGQTQPSGTLNMQ 1190
QY 421 TRTSSLVLTLEDGHIELSTRDSNIPFKSPGYMDGLLHHVSVISDPSGLRLIIDQVLR 480
DB 1191 TRTNRNLTLEDGHIELSTRDSNIPFKSPGYMDGLLHHVSVISDPSGLRLIIDQVLR 1250
QY 481 RNQRLPSFNAQSLRLGGHFGECISNVLVORFQSPPEVLDLASKSTYKDAISLGGCSLN 540
DB 1251 NSKRLKHISRSQSLRLGGHFGECISNVLVORFQSPPEVLDLASKSTYKDAISLGGCSLN 1310
QY 541 KRPFLMLFKSPKPKRINRVNQLMDAPQAT-RSTFAMQDGRSCIPPLNTQASHRALQ 599
DB 1311 KRPFLMLFKSTFNNKTKTRINQLQDTPVASRSVKWQD--ACSPFLKTPANHGALQ 1368
QY 600 FGDSPTSHLLLKXPOBELKPKRSOPSLDIOTSPKGLVFAVAGTQDSFLATLVADGRVVEAL 659
DB 1369 FGDIPTSHLLFKLPQELKPKRSOPFADVMQTTSSRGVLFHGTGNSEFALVLSKGRVLVAL 1428
QY 660 GAGGKKLRLSKRYHDKMHTVVFGLNGKARLVVDGLRAQEGSLPGNSTISPRREQVYL 719

DB 1429 GTDGGKKLRIKSKREKNCNDKMTVVFGHDEKGRLLVVDGLRARBGLPAGNSTISIRAPYLL 1488
QY 720 GLPLSRKPKSLPQHSFVGLCLNDPOLNSKPLDPSARFVSPCLAGSLKGYFSGGGHHV 779
DB 1489 GSPPGKPKSLPQHSFVGLCLNDPOLNSKPLDPSARFVSPCLAGSLKGYFSGGGHHV 1548
QY 780 ILANSVSLPELKLFTSIRPSRLTGLVILHVSQSGORSLVYMEAGKVTTSVSDAGSAYT 839
DB 1549 VLAHSVGLGPEFKLVFSIRPSRLTGLVILHVSQSGORSLVYMEAGKVTTSVSDAGSAYT 1608
QY 840 SITPKQSLCDGQMSVANSIKORIIHL 866
DB 1609 SITPKQSLCDGQMSVANSIKORIIHL 1635

RESULT 9
US-09-560-385A-2
Sequence 2, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Boufand, Ariel
TITLE OR INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560,385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1724
TYPE: PRT
ORGANISM: Homo sapiens
US-09-560-385A-2

QY 1 MRNGSGVGVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMVMYLGNDKASRDYIG 60
DB 782 MRNGSGVGVRLPNDLEDKGYTSLFLQRPNSRENGGTENMVMYLGNDKASRDYIG 841
QY 61 MAVVDQQLTCVYNLDGREAEVQIDQVLTSESQEAVMDRVKFORIYQFANLTYTKATS 120
DB 842 MAVVDQQLTCVYNLDGREAEVQIDQVLTSESQEAVMDRVKFORIYQFANLTYTKATS 901
QY 121 KRPAPAVYDLEGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKGCIELDLNEN 180
DB 902 KRPETGVYDMDGNSTNLNLDPENVVFFVGYPPDFELPSRLRPPYKGCIELDLNEN 961
QY 181 VLSLVNFKTFNLTTEVEPCRRKESBDKNYFEGTGVARPTQPHAPITPFGQITIQTV 240
DB 962 VLSLVNFKTFNLTTEVEPCRRKESBDKNYFEGTGVARPTQPHAPITPFGQITIQTV 1021
QY 241 DRGLLFFAENQDNFISLINEDGNLMVRYKLNSEPPKEKIRDTINDKDSILITIGKLQ 300
DB 1022 DRGLLFFAENQDNFISLINEDGNLMVRYKLNSEPPKEKIRDTINDKDSILITIGKLQ 1081
QY 301 KRMWVNVRSVRIEGERIDFSTYYLGGIPAIIRERFNISTPAFQGCNKMLKKTSGVRL 360
DB 1082 KRMWVNVQNTIIDGVEVDFSTYYLGGIPAIIRERFNISTPAFQGCNKMLKKTSGVRL 1141
QY 361 NDTVGVTKKSEDMKLVRTASFSRGGMSFTNLDPSTDRFQLSFGQTQPSGTLNMQ 420
DB 1142 NDTVGVTKKSEDMKLVRTASFSRGGMSFTNLDPSTDRFQLSFGQTQPSGTLNMQ 1201
QY 421 TRTSSLVLTLEDGHIELSTRDSNIPFKSPGYMDGLLHHVSVISDPSGLRLIIDQVLR 480
DB 1202 TRTNRNLTLEDGHIELSTRDSNIPFKSPGYMDGLLHHVSVISDPSGLRLIIDQVLR 1261
QY 481 RNQRLPSFNAQSLRLGGHFGECISNVLVORFQSPPEVLDLASKSTYKDAISLGGCSLN 540
DB 1262 NSKRLKHISRSQSLRLGGHFGECISNVLVORFQSPPEVLDLASKSTYKDAISLGGCSLN 1321


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Db      1099  --QINDAKTHEISI-IYHNDKMIILVDRRHVKSMDNEKKIIPFTDIYIGAPPEILQSR 1155
Qy      332  AIRERFNISTPAFOGCKNL---KKTSGVRLNDIVGTVCKCSEDMKLVRTASFSRGGOM 388
      1156  ALRAHLPLDI-NRRCMKGFQFOKXDPNLEQTEITIGVGCPEDELISRRAFTN--GQS 1212
Qy      389  SFTNLD-VSTDRFQLSFGFQFQPSGTLNHQTRTSSLVLTLEDGHIELSTRDSNIPF 447
      1213  FLASIOKISFFDFEGGFNFRITLQPNGLFYVASGSDVPSISLDNGTVIMDVK--GIKVQ 1270
Qy      448  KSPGTMDGLHHVVISIDTSGLR--LLID-DQVLRNRQRLPSFSNAOQSLR---LGG-- 499
      1271  SVDKQYNDGLSHF--VISSVSPTRYELVDKSRVGSKNPTKGIQGTQASEKKFYFGSP 1328
Qy      500  -----GHFEGCISNVLVORFSGQSEVLDLASKSTKDASLGCSLNKPPFLMFKSPKF 554
      1329  ISAOYANFPGCISNAFTVRDVEVDPRQRYTEKHNTSLYECPIESSPLFLHKKGNL 1388
Qy      555  NKGRIFNVNQ--LMODAPQATRSTEAMODGRSCLPLNT-----KASHRALQF 600
      1389  SKPKASQNKKGKSKDAP-----SMDPVALKLPERNTPRNSHCHLSNPRATIEHAQY 1441
Qy      601  GDSPTSHLLKLQBELKRSQFSLDIQTSPKGLVFIAGTKD--SFLALYVADGRVVA 658
      1442  GGTANRQROFELHKDPGAKSQFSIRLRTSSHGMIFYVSDQENDFMTLFLAHLRLVYM 1501
Qy      659  LGAGGKCLRLRKERYHDKMTTVFGLNGKARLVNDGLRAQESL-PGNSTISPREQV 717
      1502  FNVGHKKLIRSEKXNDGLMHDVIFIRERSGRLVIDGLRVLEBBLPTEATWIKGPI 1561
Qy      718  YLGLPLSRKPSLPQ---HSFVGLRDPQLNSKPLDSPARFVSPCLGSGLEKGIYPS 773
      1562  YLGVAAPGAVKXVQINSIYSPSGCLSNQLNGASITSQTPSVTPCEGPMETGYPS 1621
Qy      774  QGGHYILANSVSLGPELKLTFPSIRPSRLTGVLIHVGSQSGRLSVYMEAGKVTTSVSD 833
      1622  TBGGYVLDSEFNIGLKEPFAEFVRPRSSGTLVHGHSVNGEYLVNHMKNGQVIVKXNG 1681
Db      834  AGGSVTSITPKOSLCDQMHVAVSIKORILHL 866
Qy      1682  IRDFSTSVTPKOSLCDGRWHRITVIRDSNVQL 1714

RESULT 12
US-09-561-818A-8
; Sequence 8, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Korteemaa, Jarkko
; APPLICANT: Tryggvaeson, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1800
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-561-818A-8

Query Match      26.7%; Score 1198; DB 4; Length 1800;
Best Local Similarity 33.1%; Pred. No. 1,1e-109;
Matches 309; Conservative 161; Mismatches 373; Indels 90; Gaps 26;
Qy      1  MRPNKSGVVRLLPNDLEDKGYTSLFL---QSPDLRENGSTEDMFVYLGNDASK 56
      805  MNEDGSAVEVHSRTSMDLKAFTSLVYKPPVKPELBE--TADQFILVYSGXAKK 861
Db      57  DYTGMVNDGQLTCVYNNGLGRABEVQIDQVLTSESGEAMVYKQRIYQPAKMYTKE 116
      862  EYIGLAIKDNLVYVNLGTQVLEIPLDS--KPVSSMPAFYSIVKIERVGKHKGVFLVVP 919

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Qy      117  ATSNPKAPAVYDLEGGSSNTLLNIDPEDAVFYVGGYPPDFELPSRLNFPYKGCIELDD 176
      920  SLSTABEKFIKKGFSGDDSLDDDPEDTVYVGGVSNFPLPSLMLPGVGLCELAT 979
Db      177  LMENVLSTLYNFTTNNLTTEVEPCRRK-----ESDKNTEGEGYARIPQPN---A 227
      980  LNNVLSILNFGIINMDPSTSPCARDKLAFQSGRAASYFGSGVAVVDRDIPRRKFG 1039
Qy      228  PPNFPIQTIQTVDKGLLFFAENQDNFTSLNIEDNLWRY-----KLNSEPPKXGI 280
      1040  QVTRFDIEVRIPTADNGLILMNGSMFRLERKNGLYLVDFGSSGRVHLIEDTLKCA- 1098
Db      281  RDTINDKDHSLITITGLKQKMMINVERSVRI--EGEIPDFSTYVIGGIP-----I 331
      1099  --QINDAKTHEISI-IYHNDKMIILVDRRHVKSMDNEKKIIPFTDIYIGAPPEILQSR 1155
Qy      332  AIRERFNISTPAFOGCKNL---KKTSGVRLNDIVGTVCKCSEDMKLVRTASFSRGGOM 388
      1156  ALRAHLPLDI-NRRCMKGFQFOKXDPNLEQTEITIGVGCPEDELISRRAFTN--GQS 1212
Qy      389  SFTNLD-VSTDRFQLSFGFQFQPSGTLNHQTRTSSLVLTLEDGHIELSTRDSNIPF 447
      1213  FLASIOKISFFDFEGGFNFRITLQPNGLFYVASGSDVPSISLDNGTVIMDVK--GIKVQ 1270
Qy      500  -----GHFEGCISNVLVORFSGQSEVLDLASKSTKDASLGCSLNKPPFLMFKSPKF 554
      1329  ISAOYANFPGCISNAFTVRDVEVDPRQRYTEKHNTSLYECPIESSPLFLHKKGNL 1388
Qy      555  NKGRIFNVNQ--LMODAPQATRSTEAMODGRSCLPLNT-----KASHRALQF 600
      1389  SKPKASQNKKGKSKDAP-----SMDPVALKLPERNTPRNSHCHLSNPRATIEHAQY 1441
Qy      601  GDSPTSHLLKLQBELKRSQFSLDIQTSPKGLVFIAGTKD--SFLALYVADGRVVA 658
      1442  GGTANRQROFELHKDPGAKSQFSIRLRTSSHGMIFYVSDQENDFMTLFLAHLRLVYM 1501
Qy      659  LGAGGKCLRLRKERYHDKMTTVFGLNGKARLVNDGLRAQESL-PGNSTISPREQV 717
      1502  FNVGHKKLIRSEKXNDGLMHDVIFIRERSGRLVIDGLRVLEBBLPTEATWIKGPI 1561
Qy      718  YLGLPLSRKPSLPQ---HSFVGLRDPQLNSKPLDSPARFVSPCLGSGLEKGIYPS 773
      1562  YLGVAAPGAVKXVQINSIYSPSGCLSNQLNGASITSQTPSVTPCEGPMETGYPS 1621
Qy      774  QGGHYILANSVSLGPELKLTFPSIRPSRLTGVLIHVGSQSGRLSVYMEAGKVTTSVSD 833
      1622  TBGGYVLDSEFNIGLKEPFAEFVRPRSSGTLVHGHSVNGEYLVNHMKNGQVIVKXNG 1681
Db      834  AGGSVTSITPKOSLCDQMHVAVSIKORILHL 866
Qy      1682  IRDFSTSVTPKOSLCDGRWHRITVIRDSNVQL 1714

RESULT 13
US-09-561-818A-2
; Sequence 2, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Korteemaa, Jarkko
; APPLICANT: Tryggvaeson, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1816

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TYPE: PRT
ORGANISM: Homo sapiens
US-09-561-818A-2

Query Match 26.7%; Score 1198; DB 4; Length 1816;
Best Local Similarity 33.1%; Pred. No. 1.2e-109;
Matches 309; Conservative 161; Mismatches 373; Indels 90; Gaps 26;

1 MRPNKSGVAVRLPNDLJEDLKGYTSLFLP---QRDLRENGTEDEMPVYAGNDASK 56
229 MMDGSAVYHRTSMDDLKATSLSYMKPVPKPELRE---TADQFLIYGSNRAK 885
57 DYIGMAVVDGQLTCVYNLDGREAEVOIDQVLTSESSEAEVMDRYKFORIYQPAKANTKE 116
886 EYGLAIKNDNLVYVNLGTVKDEIPLDS--KPVSSWPAVFSYVKIERVKGKGVFLTP 943
117 ATSNKRAPAVYDLBEGSSNTLLNLPEDAVFYVGVGPPDELPRLPPYKCIETLD 176
944 SLSSTABEKRIKKGESGDSLLDLPEDVIFYVGVGVPSPFKLPTSLNLFPGVGLIAT 1003
177 LNEVLSLNFKTTFNLTTEVEPCRRK---EESDKYFEGTYARIPQPN---A 227
1004 LNDVLSLNFKTIYMDPSTSVPCARDKLAFTQSPAASTFFDGSQVAVVRDIPRGKFG 1063
228 PPNPFIQTITVDRLGILPFAENQDNFISINIEDGNLMVRY-----KINSEPKKGI 280
1064 QVTRFPIEVATPDNGILILMVGSMFRLMKNGLVHYFDGFSGGRVHLBDTLKA- 1122
281 RDTINDGKHSILITIGLQKRMWVNERSVRI---EGEIPDSTYLLGIP-----I 331
1123 --QINDAKTHEISI-IYHNDKMLVVDRLHVSMNKKKIPFTDIYIGAPPEILOSR 1179
332 AIRERFNISIPAFQCKNL---KTSGVRLNDVGVTKKCSBDMKLVFTASFSRGQM 388
1180 ALRAHPLDI-NRGCCKGQFOKOPONILEQETELGVGCEPDSLSIRAYFN--GQS 1236
389 SFTNLD-VPESTRFQLSFGQTFQPSGTLNMQTRSSLLVTLDEGHIELSTDSNPIF 447
1237 FIASIQKISFPDFEGGFNRTLOPNGLFYVAGSVFISLNDGVIMDVK--GIKQV 1294
448 KSPGTMGDLHNVYSIDTSGLR--LLID-DQVLRNQLRPFSSNAQSLR--LGC-- 499
1295 SVDKQVNDGISHF--YISSVSPRYELIYDKSRVGSNPKKIKIETQABEKKFYFGSP 1352
500 ----GHFEGCISNVLVQPSQSPVYLDAKSTKQDASIGGSLNKPPLMLFKSPKRF 554
1353 ISAQVAFNFTGCSINAFYTRVDREVEDPQRYTEKHTSLYECPIESSPLFLHKKGNL 1412
555 NKRIRFNVQ--LMQAPQATRSTAMQDGRSCLPLNT-----KASHRALQF 600
1413 SKPKAQNKKGKSKAP-----SWDPVALKLPENFTPRNSHCHLSNPRAIEHAYQ 1465
601 GDSPTSHLLKLPOELLKPRQSLDIQTSPKGLVYAGTKD--SFIALYVADGRVFA 658
1466 GGTANSRQEBEHLKDPGAKSQPSIRKTRSSHGMITYVSDQENDPMTLFLAHGRLVYM 1525
659 LAGAGKKLRLSKERYHDGKMTVVFGLNGKARLVVDGLRAQEGSL-PGNSTISPREQV 717
1526 FNVGHKKLKRISQEKYDGLMHDVIFIRERSGRLVLDGLRVLEBSLPTEATWTKIKGPI 1585
718 YLGLPLSRKPSLPQ---HSFVGLADPQNLSPKPLDPSARPVNSCLGSLKGIYFS 773
1586 YLDGVAAGKAVKVVQINSIYFSFGCLSNQLNGASITASQTSVTCFEGPMEWTGYFS 1645
774 OGGGHVILANSVSLGPELKLTFSPRLTGVLIHVHSGQSLSVYMEAGKVTYSVD 833
1646 TBGGVYVLDSEFNIGLKEFIAFVRPRSSGTLVHGSVNGEYLVANMKKGQVIVKYNNG 1705
834 AGGSVTSITPKOSLCDGQHTSVASIKORILHL 866
1706 IRDFSTSVTPKOSLCDGRMHRITIVIRDSNVQL 1738

RESULT 14
US-09-561-818A-6
Sequence 6, Application US/09561818A
Patent No. 6638907
GENERAL INFORMATION:
APPLICANT: Korteemaa, Jarkko
APPLICANT: Tyysvaara, Karl
TITLE OF INVENTION: Laminin 8 and Methods For Its Use
FILE REFERENCE: 99,274-D
CURRENT APPLICATION NUMBER: US/09/561,818A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 1824
TYPE: PRT
ORGANISM: Homo sapiens
US-09-561-818A-6

Query Match 26.7%; Score 1198; DB 4; Length 1824;
Best Local Similarity 33.1%; Pred. No. 1.2e-109;
Matches 309; Conservative 161; Mismatches 373; Indels 90; Gaps 26;

1 MRPNKSGVAVRLPNDLJEDLKGYTSLFLP---QRDLRENGTEDEMPVYAGNDASK 56
829 MMDGSAVYHRTSMDDLKATSLSYMKPVPKPELRE---TADQFLIYGSNRAK 885
57 DYIGMAVVDGQLTCVYNLDGREAEVOIDQVLTSESSEAEVMDRYKFORIYQPAKANTKE 116
886 EYGLAIKNDNLVYVNLGTVKDEIPLDS--KPVSSWPAVFSYVKIERVKGKGVFLTP 943
117 ATSNKRAPAVYDLBEGSSNTLLNLPEDAVFYVGVGPPDELPRLPPYKCIETLD 176
944 SLSSTABEKRIKKGESGDSLLDLPEDVIFYVGVGVPSPFKLPTSLNLFPGVGLIAT 1003
177 LNEVLSLNFKTTFNLTTEVEPCRRK---EESDKYFEGTYARIPQPN---A 227
1004 LNDVLSLNFKTIYMDPSTSVPCARDKLAFTQSPAASTFFDGSQVAVVRDIPRGKFG 1063
228 PPNPFIQTITVDRLGILPFAENQDNFISINIEDGNLMVRY-----KINSEPKKGI 280
1064 QVTRFPIEVATPDNGILILMVGSMFRLMKNGLVHYFDGFSGGRVHLBDTLKA- 1122
281 RDTINDGKHSILITIGLQKRMWVNERSVRI---EGEIPDSTYLLGIP-----I 331
1123 --QINDAKTHEISI-IYHNDKMLVVDRLHVSMNKKKIPFTDIYIGAPPEILOSR 1179
332 AIRERFNISIPAFQCKNL---KTSGVRLNDVGVTKKCSBDMKLVFTASFSRGQM 388
1180 ALRAHPLDI-NRGCCKGQFOKOPONILEQETELGVGCEPDSLSIRAYFN--GQS 1236
389 SFTNLD-VPESTRFQLSFGQTFQPSGTLNMQTRSSLLVTLDEGHIELSTDSNPIF 447
1237 FIASIQKISFPDFEGGFNRTLOPNGLFYVAGSVFISLNDGVIMDVK--GIKQV 1294
448 KSPGTMGDLHNVYSIDTSGLR--LLID-DQVLRNQLRPFSSNAQSLR--LGC-- 499
1295 SVDKQVNDGISHF--YISSVSPRYELIYDKSRVGSNPKKIKIETQABEKKFYFGSP 1352
500 ----GHFEGCISNVLVQPSQSPVYLDAKSTKQDASIGGSLNKPPLMLFKSPKRF 554
1353 ISAQVAFNFTGCSINAFYTRVDREVEDPQRYTEKHTSLYECPIESSPLFLHKKGNL 1412
555 NKRIRFNVQ--LMQAPQATRSTAMQDGRSCLPLNT-----KASHRALQF 600
1413 SKPKAQNKKGKSKAP-----SWDPVALKLPENFTPRNSHCHLSNPRAIEHAYQ 1465
601 GDSPTSHLLKLPOELLKPRQSLDIQTSPKGLVYAGTKD--SFIALYVADGRVFA 658
1466 GGTANSRQEBEHLKDPGAKSQPSIRKTRSSHGMITYVSDQENDPMTLFLAHGRLVYM 1525
659 LAGAGKKLRLSKERYHDGKMTVVFGLNGKARLVVDGLRAQEGSL-PGNSTISPREQV 717

```

Db      1526 FNVGHHKKLIRSOEKNYDGLMDVIFIRERSSGRLVIDGLRVLEESLPTEATWTKIGPI 1585
QY      718 YLGLPLSRKPSLPQ-----HSFVGCIRDPOLNKSPLDSPARPGVSPCLGSLKGIYFS 773
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1586 YLGGVAVPGAVKNVQINSISYFSGCLSNQLNGASITSAQTSVFPCBEGMEITGTYIS 1645
QY      774 QGGHVIILANSVSLGELKLTFSIRPSRLTGVLIVHGSQSGQRLSYMEAGKTTVSVD 833
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1646 TBGGYVVLDESFNIGKFEIAPFVRPRSSGTLVHGHSVNGEYLVHMKNGQYIVVNNNG 1705
QY      834 AGGSVTSITPKOSLCDGQMSVAVSIGORILHL 866
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1706 IRDFSTSVITPKOSLCDGRWHRTVIRDSNVQL 1738

RESULT 15
US-09-561-818A-12
; Sequence 12, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kotteesmaa, Jarkko
; TITLE OF INVENTION: Laminin 8 and Methode For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1792
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-12

Query Match      26.3%; Score 1183; DB 4; Length 1792;
Best Local Similarity 32.7%; Pred. No.3.6e-108;
Matches 304; Conservative 165; Mismatches 378; Indels 82; Gaps 26;

QY      1 MRENGSGVEVRLPNLLEDLKGYTSLPLQ---RPDLRENGGTEDMFVYVYLGNDKASXD 57
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      805 MMEFDGSAVEVHHKAVVDLAKFTSISLVKMPKAPRGAVVADQFVYVYLGSKAKKE 864
QY      58 YIGMAVVDGGLTCVYVNLGDBEAQVQIDQVLTSEBSQEAVMQVYKQRIYQPAKLYNTKEA 117
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      865 YMGIAIKNDLVVYVYVNMGMKDVIELDS--KPVSSWPAYFSIVKIERVGEHGVFLTVPS 922
QY      118 TSNKPPAPAVYDLEGSSNNTLNLDPEDAVFYVGVYPPDELPRLRFPYKGCIELDDL 177
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      923 LSTAEKPKTKKGEFAGDDSLDVTBEDVYFVGVYVANKLPASLNLPSYSCLELATL 982
QY      178 NENVLSLYNEKTFNLTTEVEPCRRRK-----EESDKYFEGTGYA--RIPTQPN--AP 228
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      983 NNDVLSLYNPKHLYNNDPSKVPKARDKLAFTQSRASAYFPDSSYAIVADITRRGKFGQ 1042
QY      229 FPNFTOTIOTTVDKGLLFPANODNFTISLNIEDGNLWRYKLN--SEBPKEKGIROT---- 283
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1043 VTRFDIEIRPADNGVLVLMVNGSMFESLEMRNGYLHVFDYDFGFSNGPVH--LEDTLAKKA 1100
QY      284 -INDGKHSILITIGLQKRMWVNVNERSVRI---EGEIFDFSTYYLGGIPILAIRERFNI 339
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1101 QINDAKYHEISI-ITYNDRKMLLVDRHVKSTONEKKKLPFTDIYIGAPQEVILQSRTL 1159
QY      340 STPA-----FOGCMKNL---KKTSGVVRLLNDIVGVTKKSEMDKLVRTASFSRQMSFT 391
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1160 RAHLPLDINPRGCMKGFQPKDFNLLEQETITLGVGCGPEDSLISRATFN--GQSFTA 1217
QY      392 NLD-VSTDRFQSLSPGQTFQPSGTLNHOQTTSLLVLTEDGHIELSTRDSNIPILFKSP 450
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1218 SIQKISFFPGFEGGFNRTLQPNGLLFYYTSGSDVFSISLDNGTVVMDVK--GIKVMSTD 1275
QY      451 GTYMDGLLHH-VSVIDTSGLRLIIDQVLRNRQRLPSFSNAQOS-----LRLGG----- 499
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1276 KQYHDGLPHFVVVISDTR--YELVVDKSRRLRGN--PTKGAKAQYOTTEKKFYFGGSPIS 1332

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```

QY      500 ---GHFEGCISNVLVQRESQSBVYDLASKSTKQDASLGCSLNKPPLMLFKSEKRPNK 556
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1333 PQYANFTGCSISNAVYPTRLDRDVEVEDFQRYSEKHTSLEYECPIESSPLFLHKKGKNSK 1392
QY      557 GRIFVYNQLMQDAP-----QATRSIEMQDGRSCLPLNTAQSRAALQFGGSP 604
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1393 PRTNQGKSKDAPSWDPIGLKFLERQKAPRDSH-----CHLSSSPRAIHHAYQYGGTA 1445
QY      605 TSHLLKLPOBELKERSQFSLDIOTTSFKGLVFYAGTKD--SPLALVYADGRVVPALGAG 662
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1446 NSROFHEHQDPRGKSQFAIRLKTTRSSHGMI FYVSDDEBNDFTLFLAHRGLVMEFVNG 1505
QY      663 GKGLRLSKERYHDKMHTVYVFGNLNGAKARLVVDGLRAQEGSL--PGNSTISPREQVYL-G 720
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1506 HKKLKIRSOEKNYDGLMDVIFIRERSSGRLVIDGLRVLEERLPPSGAAMKIKGPIYLG 1565
QY      721 LPLSRKPSL---PQHSFVGCIRDPOLNKSKPLDSPAARPGVSPCLGSLKGIYFSQGG 777
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1566 VAPGRAVKNVQITSVYSPSGCLGNQLNGASITSAQTSVFPCBEGMEITGTYFSTEGG 1625
QY      778 HVIILANSVSLGELKLTFSIRPSRLTGVLIVHGSQSGQRLSYMEAGKTTVSVDAGGS 837
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1626 YVVLDESFNIGKFEIAPFVRPRSSGTLVHGHSVNGEYLVHMKNGQYIVVNNNGVADF 1685
QY      838 VTSITPKOSLCDGQMSVAVSIGORILHL 866
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1686 STSVTPKQNLCDGRWHRTVIRDSNVQL 1714

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Search completed: February 22, 2005, 08:40:52
Job time : 44.4378 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:05:49 ; Search time 15.0758 Seconds

(without alignments)
3605.942 Million cell updates/sec

Title: US-10-817-423-4

Perfect score: 2940
Sequence: 1 MRFNGKSGVEVRLPNDLEDL.....MLFKSPKRFKGRIFVNLQ 565

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2439	83.0	1713	2 A55347	adhesive ligand ep
2	686	23.3	1816	1 S68960	laminin alpha-4 ch
3	681	23.2	3635	2 T10053	laminin alpha 5 ch
4	395	13.4	3712	2 S18253	laminin alpha-1 ch
5	302	10.3	3106	1 S53868	laminin alpha-2 ch
6	298.5	10.2	3672	2 T23433	hypothetical prote
7	298.5	10.2	3704	2 T37316	probable laminin a
8	294	10.0	1751	1 MMHJUH	laminin alpha-2 ch
9	280	9.5	3084	1 MMSA	laminin alpha-1 ch
10	270	9.2	3075	2 S14458	laminin alpha-1 ch
11	247	8.4	3102	2 T43281	laminin alpha chain
12	222.5	7.6	2823	2 F87908	protein T22A3.8 [1
13	222.5	7.6	2823	2 T23064	hypothetical prote
14	212.5	7.2	1438	2 A48216	neurexin III-alpha
15	212.5	7.2	1471	2 B48218	neurexin III-alpha
16	212.5	7.2	1578	2 T48216	neurexin III-alpha
17	199.5	6.8	1530	2 T45944	neurexin I-alpha
18	199	6.8	1507	2 A40228	neurexin I-alpha
19	175	6.0	1715	2 C40228	neurexin II-alpha
20	170	5.8	1283	2 T13799	neurexin IV - frut
21	160.5	5.5	1264	2 T19545	hypothetical prote
22	159	5.4	3707	2 S18252	heparan sulfate pr
23	153	5.2	4391	2 A38096	perlecan precursor
24	147.5	5.0	281	2 T33466	hypothetical prote
25	143.5	4.9	1955	1 AGCH	agrin precursor
26	140	4.8	1523	2 T13953	MEGF5 protein - ra
27	140	4.8	2610	2 T20968	hypothetical prote
28	138.5	4.7	1381	2 T31083	paranodin - rat
29	138	4.7	1025	2 T42626	secreted leucine-r

30	137.5	4.7	1385	2 T14158	neurexin IV - mouse
31	135.5	4.6	1328	2 T43060	agrin - electric r
32	128.5	4.4	3034	2 T14119	seven-pass transme
33	128	4.4	637	2 F83939	myo-inositol catab
34	128	4.4	1531	2 T42218	slit-1 protein hom
35	125	4.3	403	2 A26371	sex steroid-bindin
36	124.5	4.2	601	2 T22025	hypothetical prote
37	124.5	4.2	601	2 D89711	protein P40B10.4 [
38	124.5	4.2	673	2 A48089	growth arrest-spec
39	122	4.1	2325	2 A61208	chondroitin sulfat
40	121.5	4.1	935	2 A64608	exonuclease ABC c
41	121.5	4.1	2809	2 T30213	G-cadherin - sea u
42	120	4.1	757	2 T34362	hypothetical prote
43	120	4.1	768	2 B97725	outer membrane pro
44	119.5	4.1	627	2 A41609	dnar-type molecule
45	119.5	4.1	1417	2 AG2137	hypothetical prote

ALIGNMENTS

RESULT 1

A55347
adhesive ligand epiligrin, alpha-3 chain form A precursor - human
C/Species: Homo sapiens (man)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C/Accession: A55347
R/Ryan, M.C.; Tizard, R.; Vandevanter, D.R.; Carter, W.G.
J. Biol. Chem. 269, 22779-22787, 1994
A/Title: Cloning of the Lam3 gene encoding the alpha3 chain of the adhesive ligand epi
A/Reference number: A55347; PMID:94357926; PMID:8077230
A/Accession: A55347
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1713 <RYA>
A/Cross-references: UNIPROT:O16787; GB:U34155; NID:9551596; PID:9551597
C/Superfamily: laminin alpha-4 chain; laminin G repeat homology; laminin-type EGF-like
C/Keywords: alternative splicing
F/67-114/Domain: laminin-type EGF-like homology <LE2>
F/1392-1534/Domain: laminin G repeat homology <LG4>

Query Match	83.0%	Score 2439	DB 2	Length 1713
Best Local Similarity	81.9%	Pred. No. 5	9e-165	
Matches 463	Conservative 47	Mismatches 55	Indels 0	Gaps 0
QY	1	MRFNGKSGVEVRLPNDLEDLKGYSLSLFLQRPDLRENGTDMFWYLGKNDASXDYIG	60	
DB	771	MRFNGKSGVEVRLPNDLEDLKGYSLSLFLQRPNSRENGTDMFWYLGKNDASRDYIG	830	
QY	61	MAVVDGQLTCVNLGDBREAVQIDQVLTSEBSQAVMDRYKFORITYPALNTTKATSN	120	
DB	831	MAVVDGQLTCVNLGDBREAVQIDQVLTSEBSQAVMDRYKFORITYPALNTTKATSS	890	
QY	121	KPRAPAVYDLGGSSNTLNLDPEDAVFYVGYPPPELSRLRFPYKGCIELDDNEN	180	
DB	891	KPSTPGVYDMDGNSNTLNLDPENAVFYVGYPPPELSRLRFPYKGCIELDDNEN	950	
QY	181	VLSTLVNFKTFENLTTEVEPCRRRKESDKNVEGTYARIPQPNAPFNFIQTITTV	240	
DB	951	VLSTLVNFKTFENLTTEVEPCRRRKESDKNVEGTYARIPQPNAPFNFIQTITTV	1010	
QY	241	DRGLLFAENQDNFISLNTIDGNLAVRYKANSBPPEKGRIDTINDGKHSILITTKLQ	300	
DB	1011	DRGLLFAENQDNFISLNTIDGKLMVRYKANSBPPEKGRIDTINDGKHSIOLIKIGKLQ	1070	
QY	301	KRWMINNERSVRIEGEIPFESTYYIGAPIDAIRBNISTPAFOGCKMLKKTSGVRL	360	
DB	1071	KRWMINNERSVRIEGEIPFESTYYIGAPIDAIRBNISTPAFOGCKMLKKTSGVRL	1130	
QY	361	NDTVGVTKKCSBDKLVRTASFRGQMSFTNLDVPSIDRFSQSFQFOTQPSGTLTHQ	420	
DB	1131	NDTVGVTKKCSBDKLVRTASFRGQMSFTNLDVPSIDRFSQSFQFOTQPSGTLTHQ	1190	

QY 421 TRTSLLVLEDEGHIELSTRDSNIPFKSGPTMGLLHHVSYISPTSGRLIIDQVLR 480
 DB 1191 TWRRNQVLEDEYIEHSTSDSGPIFKSPQTMDDLHHVSYISNSGRLIIDQLLR 1250
 QY 481 RNORLPSFNAOGLSLGGHFEPCISNLYVRFPSQPEYLDLASKSTKDSLGCCSN 540
 DB 1251 NSGRLLHISSSKSLGSGNFEPCISNLYVRFQRLSLSPVLDLTSNLSKRDVSLGGCSLN 1310
 QY 541 KEPEMLFKSPKAFKNGRIYFNQOL 565
 DB 1311 KEPEMLFKSGTFRNKTPTRIINOL 1335
 RESULT 2
 S68960
 Laminin alpha-4 chain precursor - human
 N:Alternate names: laminin A4
 C:Species: Homo sapiens (man)
 C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
 C:Accession: S68960; S65926; S49149; S40150; I53516
 R:Richards, A.; Al-Imara, L.; Pope, F.M.
 Eur. J. Biochem. 238, 813-821, 1996
 A>Title: The complete cDNA sequence of laminin alpha-4 and its relationship to the other
 A:Reference number: S68960; PMID:96300249; PMID:8706685
 A:Accession: S68960
 A:Molecule type: mRNA
 A:Residues: 1-1816 <RIC>
 A:Cross-references: UNIPROT:Q16363; UNIPROT:Q14731; EMBL:X91171; NID:G1212962; PIDN:CAA6
 A:Experimental source: tissue type heart
 R:Vanhamen, A.; Salnio, K.; Saitola, H.; Tryggvason, K.
 FEBS Lett. 365, 183-188, 1995
 A>Title: Primary structure and expression of a novel human laminin alpha-4 chain.
 A:Reference number: I53516; PMID:95300971; PMID:7781776
 A:Accession: S65926
 A:Molecule type: mRNA
 A:Residues: 1142, 'P', 144-177, 'P', 179-490, 'Y', 492-1056, 'P', 1058-1816 <ITV>
 A:Cross-references: EMBL:S78569; NID:G1042081; PIDN:AA834635.1; PID:G1042082
 R:Richards, A.J.; Al-Imara, L.; Carter, N.; Levertha, M.; Lloyd, J.C.; Pope, F.M.
 submitted to the EMBL Data Library, December 1993
 A>Description: Localisation of the gene (LAMM4) to chromosome 6q21 and isolation of a p
 A:Reference number: S49149
 A:Accession: S49149
 A:Molecule type: mRNA
 A:Residues: 236-1816 <RI2>
 A:Cross-references: EMBL:X76939; NID:G509805; PIDN:CAA54258.1; PID:G509806
 R:Richards, A.J.; Al-Imara, L.; Carter, N.; Lloyd, J.C.; Pope, F.M.
 submitted to the EMBL Data Library, February 1993
 A>Description: Isolation of a partial cDNA encoding a protein homologous to laminin A. A
 A:Reference number: S40150
 A:Accession: S40150
 A:Molecule type: mRNA
 A:Residues: 1403-1541, 'S', 1543-1816 <RI3>
 A:Cross-references: EMBL:X70904; NID:G437804; PIDN:CAA50261.1; PID:G437805
 C:Genetics: GDB: LAMA4; LAMA3
 A:Gene: GDB: LAMA4; LAMA3
 A:Cross-references: GDB:203904; OMIM:600133
 A:Map position: 6q21-6q21
 C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
 C:Function:
 A>Description: Interact with cells and with other basement membrane proteins to promote
 C:Superfamily: laminin alpha-4 chain; laminin G repeat homology; laminin-type EGF-like h
 C:Keywords: basement membrane; cell binding; coiled coil; extracellular matrix; glycopro
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-1816/Product: laminin alpha-4 chain #status predicted <MAT>
 F:82-129/Domain: laminin-type EGF-like homology <LE1>
 F:132-184/Domain: laminin-type EGF-like homology <LE2>
 F:187-238/Domain: laminin-type EGF-like homology <LE3>
 F:241-265/Domain: laminin-type EGF-like homology <LE3>
 F:717-719/Region: cell attachment (R-G-D) motif
 F:662-1031/Domain: laminin G repeat homology <LG1>
 F:1068-1223/Domain: laminin G repeat homology <LG2>
 F:1252-1398/Domain: laminin G repeat homology <LG3>
 F:1488-1636/Domain: laminin G repeat homology <LG4>

F:1665-1816/Domain: laminin G repeat homology <LG5>
 F:104,215,308,458,524,550,571,574,631,639,735,751,754,780,803,1086,1281,1359,1411/Bindin
 F:266,269/Disulfide bonds: Interchain #status predicted
 Query Match 23.3%; Score 686; DB 1; Length 1816;
 Best Local Similarity 32.2%; Pred. No. 3.7e-40;
 Matches 194; Conservative 101; Mismatches 245; Indels 62; Gaps 21;
 QY 1 KEFNKSGVREYLPNDLELDKGYTSLSTL-----QRPDLRENGCTEDMFWMTLGNKDKSK 56
 DB 829 MAFDGSVAEVRHSKRSMDLKAFTLSLYMKPVPVPELTET---TADGFIYLGSKNAKK 885
 QY 57 DYIGNAVVDGQLTCYNNLGDRREAVQIDVLTSESOEAVMDRYEQRIRYOPAKLNTYKE 116
 DB 886 EYMGALIKNDNLVYYNLTGKQVEIPLDS--KPVSWPAYSIVIKIEVGRKHGKVFLLVP 943
 QY 117 ATSNKPKAPAVVDLEGGSSNTLLNDPEPDAPVYGVYPPDELPRLAPPPKGLIEDD 176
 DB 944 SLSSTAERKFKIKGFGSDSLDLDPDVTYVGVGVSNFGLPTSLMLPGFVGCLERAT 1003
 QY 177 LNEVTLSTYNFKTNTLNTTEVEPCRRK-----EESDKNVEGTYA--RIPTQPN--A 227
 DB 1004 LNDVYISLYNFHLYNMDSVSPCARDKLAFTQSRASYPFGSGYAVMDITRGKFG 1063
 QY 228 PPNPFYQITITQTVDRGLLFFAENQDNFSLNIEDGNLMVRY-----KLNSEPPKEGI 280
 DB 1064 QVTRPEDIKVRTPADNGLILIMVNGSMFRLERNGYLHVFDGFGSGRVHLEDTLKKA- 1122
 QY 281 RGTINDGDHSLITITGLQKRMVNNVERSVRI---EGEIPDSYTYLGCP-----I 331
 DB 1123 --QINDAKYHEISL--IYNDKMTILVDRRHAKSMNKKMIPFDIYIGAPPEILQSR 1179
 QY 332 AIRRFNISTPAFGCKMNL---KTSQVRLNDVTGATKCSBDMKLVRTASFSRGQM 388
 DB 1180 ALRAHLPLDI-NFRCKMGFGQKQDFYLBETITLGYGCPBSLISRAVFN--GQS 1236
 QY 389 SFTNLD-VPSTDRPLSFGFTQPSGTLLNHQTFTSSLLVTLDEGHIELSTRDSNIPF 447
 DB 1237 FIASIQKISFFGFGFGFRTIQNGLLIFVYASGSDFVSIIDNGYIMDVK--GIKQV 1294
 QY 448 KSPGYTMGLLHVHVIDTSGLR--LLID-DQVLRNQRPLSPFNAOGLR--LGG-- 499
 DB 1295 SVDKQYNGLSHF--VIVSSVPTREYELIVDSKRVSKNPTKGIQTQASEKKFYFGSP 1352
 QY 500 -----GHFEGCISNLYVRFPSQPEYLDLASKSTKDSLGCCSNLKPFLMFKSPKRF 554
 DB 1353 ISAQYANFPGCISNAYPTRVDRVDEVDPQRTTEKVTSLIECPLESSEPLFLHKKGNL 1412
 QY 555 NK 556
 DB 1413 SK 1414
 RESULT 3
 T10053
 Laminin alpha 5 chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C:Accession: T10053
 R:Miner, J.H.; Lewis, R.M.; Sanes, J.R.
 submitted to the EMBL Data Library, November 1997
 A:Reference number: Z16923
 A:Accession: T10053
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-3635 <MIN>
 A:Cross-references: UNIPROT:Q61001; EMBL:U37501; NID:G2599231; PID:G2599232
 C:Genetics:
 A:Gene: Lamas
 C:Keywords: basement membrane; cell binding; extracellular matrix
 F:1888-1939/Domain: laminin-type EGF-like homology <LE6>
 F:1942-1970/Domain: EGF homology <EGF>

3:273-330/Domain: lam1n1n-type EGF-like homology <LR0>
3:333-400/Domain: lam1n1n-type EGF-like homology <LR2>
3:541-584/Domain: lam1n1n-type EGF-like homology <LR3>
F:1776-2115/Domain: III <DOM3>
F:1776-1806/Domain: lam1n1n-type EGF-like homology [status atypical] <LR1>
F:1809-1856/Domain: lam1n1n-type EGF-like homology <LR2>
F:1859-1914/Domain: lam1n1n-type EGF-like homology <LR3>
F:1917-1967/Domain: lam1n1n-type EGF-like homology <LR4>
F:1970-2014/Domain: lam1n1n-type EGF-like homology <LR5>
F:2017-2061/Domain: lam1n1n-type EGF-like homology <LR6>
F:2064-2109/Domain: lam1n1n-type EGF-like homology <LR7>
F:2116-2697/Domain: I/II, heptad repeats <DOM2>
F:2698-3712/Domain: G <DOM5>
F:2698-2863/Domain: repeat G1 <RG1>
F:2864-3048/Domain: repeat G2 <RG2>
F:3049-3223/Domain: repeat G3 <RG3>
F:3209-3200/Domain: lam1n1n G repeat homology <LG3>
F:3539-3712/Domain: repeat G5 <RG5>
F:1847,1850,1943,2024,2136,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2850,2938

Query Match 13.4%; Score 395; DB 2; Length 3712;
Best Local Similarity 25.5%; Pred. No. 5,6e-19;
Matches 155; Conservative 105; Mismatches 236; Indels 110; Gaps 27;

QY 1 MRFNGSGVEVRLPNDELKGYTSLFLQRPDLRNGCTEDMFMVYIG--NKDASK-- 56
DB 2675 VNFPSRTLEHETPEKTKLMTRTLSTYFR---TTEBSG----FLLYGNNKTKAQKN 2727
QY 57 DYIGMAVDGGLTCVNNGDREABVQIDQVLTSSSQEAVMDRVKQRITYQPAKLNTYTE 116
DB 2728 DFVAWEIYNGPILITLTDGNGPERITSDKYADGMYQAVVDRMG----PNAKLTIRER 2782
QY 117 ATSNKPKAPAYVDEEG---SSNTLNLDPEDAVVYVGYP--PDFELPSRLFFPYKGC 171
DB 2783 L-----PNCDDVYEHKSGTLEBSQNLHYDKNSRLF-VGGYPSIDSPNAPDPLTNSFSG 2837
QY 172 IELDDLINENVLSTYNF-KTFPNLNTTEVEPCRRKRBSDKNYFEGCTGATLPTQPNAPF 229
DB 2838 IEDLTKIGDESGLWNFVYGGDNDQGARERDVLLKKKPYGLRPFKNGVQLNATSNLKS 2897
QY 230 PNFIQ---TIQTYDRGLFPAENQDNFSLINIEGNLMVVRKLNSEPPKKGIRPTIND 286
DB 2898 RSSIQFSFKADKDTNSNGLLFFPYGRDKHYMSLEMTDGLAFENISLGEQGVQSGSDRYND 2957
QY 287 GKDHISI-----LITIGLQKRMWINVERSVRIEGLIFDFSTYYLGGIPIALREBF 337
DB 2958 NQMKHKVQAEKRNKGLAKVDIV----ISRTAPLEADLELKKRLRLYCGHR---RL 3009
QY 338 NIS---TPAFQCGMKNLKKTSGVRLNDTV---GVTKKCSQEDMKLVRTASFSRGQMSFT 391
DB 3010 NTSISLQNFQGCIDNVINQGVVDLTRYVGGVEBGSAKSFVTSYAAPHYGLRMN 3069
QY 392 NLDVPSIDRFQLSGFGFTQPSGTLT---NHQTRSSLLVLTEDGHIELSTDSNPIFK 448
DB 3070 N--VSSDNNLHVLIFFKTPQNGVLFYANHD-QSSTIGLSLQDGLKLKNSMGSQSLVI-- 3124
QY 449 SPGYTMDGLT---HVASVDSPTSG-LRLLLDDQVLRNRQRLPSFSGNAQOSRLGGG--- 500
DB 3125 -----DRIILNDGEDHVVTVQHTQSEKRLIYVDV---DKRLIGS-----PQLILBSGDI 3172
QY 501 -----HFEQGISNLYVQFSGSPVTLDAKSTKQDASVGGCSLNK 541
DB 3173 FAGLPDNYRTPRNALASLAFVFGCISDVTY-----NBEIINFANSLEKKGNGINGC----- 3223
QY 542 PPFMLTK 549
DB 3224 PPHVLAAYR 3231

RESULT 5
SS3868
lam1n1n alpha-2 chain precursor - mouse

N/Alternate names: laminin M chain; merosin heavy chain
C/Species: Mus musculus (house mouse)
C/Date: 21-Aug-1998 #sequence revision 21-Aug-1998 #text_change 09-Jul-2004
A/Accession: I49077; S50829; I48655; S31576; S53868
R/Bernier, S.M.; Utsun, A.; Sugiyama, S.; Doi, T.; Polietina, C.; Yamada, Y.
Matrix Biol. 14, 447-455, 1995
A/Title: Cloning and expression of laminin alpha 2 chain (M-chain) in the mouse.
A/Reference number: I49077; PMID:95316259; PMID:7795883
A/Accession: I49077
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-3106 <RES>
A/Cross-references: UNIPROT:Q60675; EMBL:U12147; NID:9699109; PID:AA052165.1; PID:969921
R/Xu, H.; Wu, X.R.; Wewer, U.M.; Engvall, E.
Nature Genet. 8, 297-302, 1994
A/Title: Murine muscular dystrophy caused by a mutation in the laminin alpha-2 (Lama2) g
A/Reference number: S50829; PMID:95179178; PMID:7674173
A/Accession: S50829
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 64-281 <XUH>
A/Cross-references: GB:S75315; NID:9833929; PID:AA033573.1; PID:9833930
R/Chang, A.C.; Wedsworth, S.; Colligan, J.E.
J. Immunol. 151, 1789-1801, 1993
A/Title: Expression of merosin in the thymus and its interaction with thymocytes.
A/Reference number: I48655; PMID:93346725; PMID:8345183
A/Accession: I48655
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 2162-2204, 'D', 2206-2213, 'E', 2216-2279 <RE2>
A/Cross-references: EMBL:X69869; NID:953055; PID:CAA9502.1; PID:953056
C/Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C/Function:
A/Description: Interact with cells and with other basement membrane proteins to promote
C/Superfamily: laminin alpha-1 chain, laminin G repeat homology; laminin-type EGF-like h
C/Keywords: Basement membrane; calcium binding; coiled coil; extracellular matrix; glyco
F/1-22/Domain: signal sequence #status predicted <SIG>
F/23-3106/Product: laminin alpha-2 chain #status predicted <MAT>
F/283-337/Domain: laminin-type EGF-like homology <LE01>
F/340-407/Domain: laminin-type EGF-like homology <LE02>
F/410-462/Domain: laminin-type EGF-like homology <LE03>
F/465-511/Domain: laminin-type EGF-like homology <LE04>
F/514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>
F/720-750/Domain: laminin-type EGF-like homology <LE06>
F/753-800/Domain: laminin-type EGF-like homology <LE07>
F/803-858/Domain: laminin-type EGF-like homology <LE08>
F/861-911/Domain: laminin-type EGF-like homology <LE09>
F/914-960/Domain: laminin-type EGF-like homology <LE10>
F/963-1007/Domain: laminin-type EGF-like homology <LE11>
F/1010-1053/Domain: laminin-type EGF-like homology <LE12>
F/1102-1121/Domain: laminin-type EGF-like homology <LE13>
F/1123-1159/Domain: laminin-type EGF-like homology #status atypical <LE14>
F/1162-1171/Domain: laminin-type EGF-like homology #status atypical <LE15>
F/1376-1413/Domain: laminin-type EGF-like homology #status atypical <LE16>
F/1416-1462/Domain: laminin-type EGF-like homology #status atypical <LE17>
F/1465-1500/Domain: laminin-type EGF-like homology <LE18>
F/1523-1567/Domain: laminin-type EGF-like homology <LE19>
F/2166-2327/Domain: laminin G repeat homology <LG1>
F/2360-2520/Domain: laminin G repeat homology <LG2>
F/2546-2709/Domain: laminin G repeat homology <LG3>
F/2785-2933/Domain: laminin G repeat homology <LG4>
F/2960-3106/Domain: laminin G repeat homology <LG5>

Query Match 10.3%; Score 302; DB 1; Length 3106;
Best Local Similarity 22.1%; Pred. No. 1.8e-12;
Matches 131; Conservative 116; Mismatches 227; Indels 120; Gaps 30;

QY 32 RPDLRENG-----GTEDMFVMTYGNKASK--DYIGMAVVGQGLCVNLTGDRRA 79
DB 2155 RPIIKGSGYNNIVVHTAVADNLITLGLG--SAKPTIDFAIEKRGKSGSFLMTVSGVG 2211
QY 80 EVOIDOVLTSESGQEAVMRVRKFORIYQFAKLVYTKRATSNKPKA--PAVVDLEGSSSN 136

DB 2212 RVGFEDLTID-----DSWYRIEASRTGANGISV---RALDGPXAMWPFSTHVSPPGY 2264
QY 137 TLINLDPDPAVYGVGPPDELPRLRPFYKGIIEIDDLNENVLSTLYNRTFNMTT 196
DB 2265 TLIDVD-ANAMLPVGLTGKIKKADAVITFTFGMGSTTFDKNPTIGLMNPRE---KEG 2319
QY 197 EYEPCKRRRREESDCK---YFEGTYARLPTOPNAPFPPIOTI---QTYVDRGLLFPFAE 249
DB 2320 DCKGCTVBPQVDSBSGTLQFDGEGVALY-SRPRIKRYR-ISTWPKRPTPSSALMTWLA 2377
QY 250 NOD--NPISLNIEDGNLMVRYKLNSEPKKGIKIDTI-----NDGKHSILITGKLQKR 302
DB 2378 TFDLMDPMSVSLSDGHVKSVDLGS-----GMTSVSNQNMNDGKWKRA--FTLSRIQKQ 2429
QY 303 MNINV-----NERVRIEGLTFD-----STYLLGIP-----IARREPNISTAPFQ 345
DB 2430 ANISIVDIDSNQEEVNAVTSNGNFGDLKADDKTYFGGLPLKMLSMKAPPEVAVKFXS 2489
QY 346 GCMKRL---KKTSGVRLNDTVGVTKKSEDMKLVRTASFSRGG--QMSFTNLDPVSTDR 400
DB 2490 GGLKDIKISRTPIYNLISPDYGVTKGS--LENNVTYSFKPGGVLELAASIDVGT--- 2544
QY 401 FQLSFGPTPOPSTLL-----NHQRTSSLVLTLEDG---HIELSTRD-S 442
DB 2545 -RINLSFSTRNBSGILLGSGGTLTPPRKRKQTLQAYVALFLNKGRLVHLISGSTRMR 2603
QY 443 NPIPKSGTWDGLLHVSVISDTSGLRLIDQVLRNRQLPFSNAQ-QSLRLDGG- 500
DB 2604 KVIKPEPMLFHDGHEHVH-ERTRGIFTVOIDDRHIOVLEBPRIEVKGLFVGADP 2662
QY 501 -----HFGCISNVLVGRFSQSPVELDLASKTKDASIGGCSLNKP 542
DB 2663 PEFQSPPLRNTPAFQGCVMNLVINSIP-----MDPAQGLAFKNDIGCTYQKP 2711

RESULT 6
T23433
hypothetical protein K08C7.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T23433
R/Berks, M.
Submitted to the EMBL Data Library, March 1996
A/Reference number: Z19740
A/Accession: T23433
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-3672 <WTL>
A/Cross-references: UNIPROT:Q21313; EMBL:Z70286; PID:CAA94293.1; GSPDB:GN00022; CESP:K0
A/Experimental source: clone K08C7
C/genetic:8
A/gene: CESP:K08C7.3
A/map position: 4
A/introns: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 3
C/superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 10.2%; Score 298.5; DB 2; Length 3672;
Best Local Similarity 23.5%; Pred. No. 4.1e-12;
Matches 141; Conservative 106; Mismatches 233; Indels 121; Gaps 27;

QY 3 FNGKGVBEVRLPNDLEDLKGYSLSLPLQRPDLRENGTDEMFVMTYGNKCA----- 54
DB 2696 FEKGSIDLNTIPQRTYRRAAHADIFYRTR--QHG-----ILPFGNEREAVASRAVP 2748
QY 55 SDYIGMAVVDQGLCVNLTGDRRAEVOIDVLTSESGQEAVMRVRKFORIYQFAKLVNT 114
DB 2749 TADYVAARIEYGRPKITVDLGDPAVAVKLD-----TPVNDGLMRILNTERI-----GKT 2797
QY 115 KEATSNKPKAPAVYDLE---GSSNTLNLDPEDAVPVYGVGPPPELPRLRFPYKGC 171
DB 2798 VSVTLSPKNSVETAEATKSSVAGNKSVLINQOISRLPVGVPFARSISKDLVNDPVD 2857

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QY 172 IELDLINENVLSTYNFKTTFNLTTEVEBPGRARRKESDKNY--FEGNGYA-----R 220
DB 2858 IESLKLHGEPILGLMNSREKNTNVNGAQKKPKITDNADLVSLDGEGYTSYKPSHMNR 2917
QY 221 IPTQNPAPPNPFIQTITQTVDRGLLFFAENQDNFISLINEDGLMRYKLNSEPPREKGI 280
DB 2918 KATKISLSFLTF-----SPHGLLFVGRKDFMALLEISDGVKLSVDLGS-----GV 2964
QY 281 RDTI-----NCGKHSILITIGKLOKRMVNNERSVRIEGI----PDFT---YILG 327
DB 2965 GQWITSSSYNDQKMT--VSIYREKHVKIMIDGTEVLEGDVPGKDSMSYTEPLIYIG 3022
QY 328 GPIPIARERNISTPAFGQCMKLLKTSGVVRLND---TVGYTKCSBDKLVRTASF-S 383
DB 3023 GTPSGLSVTRTI--VPLRGICISVKLGSDNVDLSSHASKGVRSQC--PLHSVRYVSFLS 3078
QY 384 RGGQMSFTNLDVSTDRFOLSFQFOT---FQPSGTLINQRTSSLLVTL-EGGHLELT 439
DB 3079 DRTTASFNNTATERSD--VSTFTEFKTRSIROPSSLFTVNDDEDSVLSVINEGILTVIS 3137
QY 440 RD--SNIPFKSGFTVMDGLLHHVSVISDTSGRLIIDQVLRNRQLPSFSAQGSRL 497
DB 3138 GEDIALTEILASP-----DEKMHVYSIRKTYIIRIDAD-----SFSNEVARKIA 3183
QY 498 GGGH-----FEGCISNVLVQRFQSPREVLDLASKSTKXASLGCSL 539
DB 3184 DSNPDASFLSAFPGKSGRTSPVGCIGDVTL-----NGKLDPAN-SIKKISLNGCSL 3237
QY 540 N 540
DB 3238 S 3238

```

RESULT 7

```

T37316
probable laminin alpha chain - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37316
R:Joh, K.; Zhu, K.; Hedgecock, E.M.; Inoue, T.; Horii, K.
submitted to the EMBL Data Library, August 1998
A:Description: laminin alpha chain gene in the nematode C. elegans.
A:Reference number: Z21681
A:Accession: T37316
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3704 <JOB>
A:Cross-references: UNIPROT:P91904; EMBL:AB016806; PDB:BAJ2347.1
A:Experimental source: strain N2
A:Genetics:
A:Gene: epi-1
A:Map position: IV
A:Intons: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 3
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type BGF-like h

```

```

Query Match 10.2%; Score 298.5; DB 2; Length 3704;
Best local Similarity 23.5%; Pred. No. 4.1e-12;
Matches 141; Conservative 106; Mismatches 233; Indels 121; Gaps 27;

QY 3 FNKSGVEVRLPNDLBDKQYTSLSLELQRPDLRENGCTEDMVMVYGNDA----- 54
DB 2696 FEKSSLDLNIIPRVTRSAHAADISFYFRTE--QEHG-----IPLFPGNETAVGSRAPV 2748
QY 55 SKDYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTRESQCAVMDRVFQRIYOPAKLNTY 114
DB 2749 TADYVAARIEYGRPKITVDGDAPAVVKD-----TPVNDGMRRLNIRI-----GKT 2797
QY 115 KKAITSKPKAPAYDLE---GSSNTLANIDPDNAVYVGGYPPDELPRKLAPPPKGC 171
DB 2798 VSVTLKRPNSVETAEKTSVAGNKSVALNMQISRLFVGGVPSARISDILYNRDFVGD 2857
QY 172 IELDLINENVLSTYNFKTTFNLTTEVEBPGRARRKESDKNY--FEGNGYA-----R 220

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IDb 2858 IESLKLHGEPILGLMNSREKNTNVNGAQKKPKITDNADLVSLDGEGYTSYKPSHMNR 2917
QY 221 IPTQNPAPPNPFIQTITQTVDRGLLFFAENQDNFISLINEDGLMRYKLNSEPPREKGI 280
DB 2918 KATKISLSFLTF-----SPHGLLFVGRKDFMALLEISDGVKLSVDLGS-----GV 2964
QY 281 RDTI-----NCGKHSILITIGKLOKRMVNNERSVRIEGI----PDFT---YILG 327
DB 2965 GQWITSSSYNDQKMT--VSIYREKHVKIMIDGTEVLEGDVPGKDSMSYTEPLIYIG 3022
QY 328 GPIPIARERNISTPAFGQCMKLLKTSGVVRLND---TVGYTKCSBDKLVRTASF-S 383
DB 3023 GTPSGLSVTRTI--VPLRGICISVKLGSDNVDLSSHASKGVRSQC--PLHSVRYVSFLS 3078
QY 384 RGGQMSFTNLDVSTDRFOLSFQFOT---FQPSGTLINQRTSSLLVTL-EGGHLELT 439
DB 3079 DRTTASFNNTATERSD--VSTFTEFKTRSIROPSSLFTVNDDEDSVLSVINEGILTVIS 3137
QY 440 RD--SNIPFKSGFTVMDGLLHHVSVISDTSGRLIIDQVLRNRQLPSFSAQGSRL 497
DB 3138 GEDIALTEILASP-----DEKMHVYSIRKTYIIRIDAD-----SFSNEVARKIA 3183
QY 498 GGGH-----FEGCISNVLVQRFQSPREVLDLASKSTKXASLGCSL 539
DB 3184 DSNPDASFLSAFPGKSGRTSPVGCIGDVTL-----NGKLDPAN-SIKKISLNGCSL 3237
QY 540 N 540
DB 3238 S 3238

```

RESULT 8

```

MEMPHIS
laminin alpha-2 chain - human (fragment)
N:Alternate names: laminin M chain; merosin heavy chain
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C:Accession: PX0082; A35899; A38970; S14461
R:Horii, H.; Kanamori, T.; Mizuta, T.; Yamaguchi, N.; Liu, Y.; Nagai, Y.
J. Biochem. 116, 1212-1219, 1994
A:Title: Human laminin M chain: Epitope analysis of its monoclonal antibodies by immuno
A:Reference number: PX0082; MUID:95221315; PMID:7535762
A:Accession: PX0082
A:Molecule type: mRNA
A:Residues: 1-1751 <HOR>
A:Cross-references: UNIPROT:P24043
A:Experimental source: Placenta
R:Dirig, K.; Leiyo, I.; Argreaves, W.S.; Ruoslahti, E.; Engvall, E.
Proc. Natl. Acad. Sci. U.S.A. 87, 3264-3268, 1990
A:Title: Merosin, a tissue-specific basement membrane protein, is a laminin-like protei
A:Reference number: A35899; MUID:90238994; PMID:2185464
A:Accession: A35899
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'V', 623-1751 <EHRI>
A:Cross-references: EMBL:M59832
A:Accession: A38970
A:Molecule type: protein
A:Residues: 1368-1384; 1389-1406; 1593-1607 <EHR2>
A:Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in lacking 1599-'
submitted to the EMBL Data Library, December 1990
A:Description: The tissue-specific basement membrane protein merosin is a laminin-like i
A:Reference number: S14461
A:Molecule type: mRNA
A:Residues: 'V', 623-1264; 'R', 1266-1751 <LRI>
A:Cross-references: EMBL:M59832; NID:g187520; PDB:AAA63215.1; PID:g187521
C:Comment: This protein is a prominent component of the basement membrane that mediate
C:Genetics:
A:Gene: GDB:LAMA2; LAMM
A:Cross-references: GDB:132362; OMIM:156225
A:Map position: 6q22-6q23

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```

Y 464 ISDPSGRLLIDDOVLRNRQRLSPFSNAGSLRLG-----GG----- 500
Db 2596 VRNRKRVITTOYDE-----NSPVAKGLPELTREGKTIDISNLYIGSLPEDKATP 2642
Y 501 -----HREGGISNVLVQRFQSPPEVLDLASKSTKQDASLGCSLNKPPPLMLFK 549
Db 2643 MLKRRTSFHCIGKNVVL-----DAQLDFTHTATSEQVEYLDPTCLAEPMQSLHR 2692

RESULT 10
S14458
laminin alpha-1 chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S14458; S14663; A34961
R:Haaparanta, T.; Uitto, J.; Rosslahri, B.; Engvall, E.
Matrix 11, 151-160, 1991
A:Title: Molecular cloning of the cDNA encoding human laminin A chain.
A:Reference number: S14458; MUID: 91333420; PMID: 1714537
A:Accession: S14458
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-3075 <HAA>
A:Cross-references: UNIPROT:P25391
R:Nissinen, M.; Vuolteenaho, R.; Boot-Handford, R.; Kallunki, P.; Tryggvason, K.
Biochem. J. 276, 369-379, 1991
A:Title: Primary structure of the human laminin A chain. Limited expression in human ti
A:Reference number: S14663; MUID: 91264789; PMID: 2049067
A:Accession: S14663
A:Molecule type: mRNA
A:Residues: 1-227, 'PS', 230-251, 'MLP', 255-418, 'E', 420-518, 'L', 520-1022, 'V', 1024-1074, 'V'
A:Cross-references: EMBL:X85531; NID:8344225; PIND:CAA4418.1; PID:934226

```

Lab. Invest. 60, 772-782, 1989

A;Reference number: A34961; MUID:89280632; PMID:2733383
A;Accession: A34961

A/Status: not compared with conceptual translation
A/Molecule type: mRNA

A;Residues: 'W',2397-2745,'L',2747-3053,'L',3055-3072,'PSP',<OLS>
A;Note: the authors translated the codon AGA for residue 2692 as Pro

C;Genetics:
A:Gene: GDB:LAMA1; LAMA

A;Cross-references: GDB:120135; OMIM:150320
A;Map position: 18p11.32-18p11.22

C;superfamily: laminin alpha-1 chain; laminin 5 repeat homology; laminin-type EGF-like C;keywords: basement membrane; calcium binding; cell binding; coiled coil; disulfide bond

```
F;1-1//Domain: signal sequence #status predicted <SIG>
F;18-3075/Product: laminin alpha-1 chain #status predicted <MAT>
```

```
F;18-269/Domain: V1 <DOM6>
F;270-516/Domain: V <DOM5>
```

F:327-394/Domain: laminin-type EGF-like homology <LE2>

F;454-500/Domain: laminin-type BGF-1 like homology <LB4>

F;517-708/Domain: IVb <DO4B>
B;708-1158/Domain: T11b <DO3B>

F;709-739/Domain: laminin-type EGF-like homology #status atypical <LB6>
E:742-788/Domain: laminin-type EGF-like homology <LB7>

F;791-846/Domain: laminin-type EGF-like homology <LE8>
F:849-899/Domain: laminin-type EGF-like homology <LE9>

F;902-948/Domain: laminin-type EGF-like homology <LE10>
F;951-995/Domain: laminin-type EGF-like homology <LE11>

F;998-1041/Domain: laminin-type EGF-like homology <LB12>
F;1044-1087/Domain: laminin-type EGF-like homology <LB13>

F;11090-1109/Domain:	laminin-type EGF-like homology	#status	atypical	<LB15>
F;1111-1147/Domain: <td>laminin-type EGF-like homology <td>#status <td>atypical <td><LB15> </td></td></td></td>	laminin-type EGF-like homology <td>#status <td>atypical <td><LB15> </td></td></td>	#status <td>atypical <td><LB15> </td></td>	atypical <td><LB15> </td>	<LB15>

F;1130-1133/Domain: random-type B9-116 homologous to the acyl-CoA synthetase
F;1160-1361/Domain: IVA <DO4A>

F;1362-1400/Domain: laminin-type EGF-like homology #status atypical <LE17>

F:1403-1449/Domain: laminin-type EGF-like homology <LE18>
F:1452-1506/Domain: laminin-type EGF-like homology <LE19>
F:1509-1553/Domain: laminin-type EGF-like homology <LE20>
F:1554-2125/Domain: I/I, heptad repeats <DOM2>
F:2116-2120/Region: cell adhesion #status predicted
F:2126-3075/Domain: G <DOM>
F:2142-2300/Domain: laminin G repeat homology <LG1>
F:2329-2484/Domain: laminin G repeat homology <LG2>
F:2510-2676/Domain: laminin G repeat homology <LG3>
F:2534-2536/Region: cell attachment (R-G-D) motif
F:2739-2888/Domain: laminin G repeat homology <LG4>
F:2916-3073/Domain: laminin G repeat homology <LG5>
F:38,164,555,665,765,801,838,926,952,1045,1407,1579,1596,1678,1689,1717,1804,1894,1
rate (Asn) (covalent) #status predicted
F:297-305/Disulfide bonds: #status predicted

Query Match 9.2%; Score 270; DB 2; Length 3075;
Best Local Similarity 20.8%; Pred. No.3.3e-10; Indels 116; Gaps 26;
Matches 130; Conservative 116; Mismatches 262;

7 SGVEVRLPDLLEDKGY-----TSLSLFLQRPDLRENGGTEDEFWMTLGNKDS 55
2114 ASIKVAVSADRCIRAYQPISTNTNLTILNKTEP-----DNLFLIGSSTS 2164
56 KDYIGAAVVDGQLTCVYNGDREAEVQIDQVLTSESQEAWMRVKQRIYQAKLN--Y 113
2165 -DLAVEMRGRVAFPLMDLGSSTRLEFPDPFIDNRWMSI-----HVARFGNISLS 2216
114 TKRATSNKPKAPAVYDLEGGSSNTL-LNLDPEDAVFYGGYPPDFELPSLRPPKGC 172
2217 VEMSSNQ-KSPFKTSKSPCTANAVLDN--NSTLMFVGLGQIKSPAVKTHKGC 2272
173 ELDDLLENVLSLVNFKTTFNLNTTEVE-PCR---RRKESDKNVEFGTGYARIPTOPNA 227
2273 GBAFLNGKSGIGLWNY-----IERGKCRGCGSSQNDPSPFHDGSGSVVEKSLPA 2324
228 PPNPFIQTITTYDRGLLF--AENODNFI SLNIEGNTLVRYKLANSEPKKGIQDTIN 285
2325 TVTQIIMLFNTFSPNGLLYLGSYGYKDFLSIFLFGRVKVMIDLGSPTLLTIDR-RYN 2383
286 DGKDSILITIGLOKRMW---NNERSVRLEGRI-----FDPSTVYLLGIP1PA 332
2384 NGWYKIAQQRNKQGLAVIDAYNYSNKKTK-QGSETPGASSDLNRLDOP1YVGGILPSS 2442
333 IRRFNISTPAPQCGMKNLK-KTSGVRLNDIVGVTKKSEDKLVRTASFRSGQMSPT 391
2443 RYVRAGVTTKSFYCIKNLEISRTFDLANSYGVRKGL--LEPIRSYFLKGYIELP 2500
392 NLDVPESTRFQLSFGFQTFQPSGTL-----NHQRTSSLLVTLDEGHELEST 439
2501 PKSLSPSEEWLVTFP--TTNSSGIIILALAGDVEKRGDRREAHVPFPSVWLIGNIEVHY 2558
440 RDSN-----IPIKSP-GTYMDGLHHVSVISDTSGRLILIDQ---VLRRNRLSPFN 490
2559 NPQDGGIKRALHAFPTGTCDSQANSISLVNRNRITTVOLDNNPVEKMLGTLVESRT 2618
491 AQSGLRLG-----GHFSGCISNVLVQRFSSQPEVYLASKSTKKDASLGCG 537
2619 NVSNLVVGGIPBEGSGSLTMRSPFGCIKNLIF-----NLIELDRNSANGHQVDLDC 2673
538 SLNKKPPL-----MLFKSPKRP 554
2674 WLSERPKLAPDADSKLREPRAF 2697

RESULT 11
T43291
laminin alpha chain - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C/Accession: T43291
R/Zhu, X.; Kuo, G.; Joh, K.; Hall, D.H.; Wadsworth, V.K.; Hutter, H.; Vogel, B.E.; Huang
submitted to the EMBL Data Library, June 1998

A/Description: Expression, function and evolution of laminin alpha chains.
A/Reference number: 222397
A/Accession: T43291
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-3102 <ZHU>
A/Cross-References: UNIPROT:O45614; EMBL:AF074902; PDB:1AAC26793.1
A/Map position: 1
A/Note: lama1/2
C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 8.4%; Score 247; DB 2; Length 3102;
Best Local Similarity 22.1%; Pred. No.1.5e-08;
Matches 128; Conservative 108; Mismatches 210; Indels 134; Gaps 30;

50 GNKDSKDYIGAAVVDGQLTCVYNGDREAEVQIDQVLTSESQEA--MQRVKKRIYQ 107
2308 GRRTPSEHLAVEIKDKVAVVHMDIGSK-----KMTNSHPINYPVSNDRVTWYTHIDV 2361
108 FA---KLVNT---KEATSN--KPKAPAVYDLEGS--SNTLNLDPEDAVFYGGYPPDF 157
2362 LRIGAAVVLTVALKESYDGFPRGAPVSVFVNSKXDNISFNTIRGTTIDV---TDE 2418
158 ELPSRLRPPPYK---GCIBLDLENVLSLVNFKTTFNLNTTEVEPCRRRKESDXY 212
2419 TVASDIDGLTTHKFSIGVGLRIDEV---PLPLMSFST---TGECGATSPPKTSQRGH 2471
213 FEGCTYAHILPQPNAPFNPIQTITTYD-RGLLFF--AENODNFI SLNIEGNTLVRYK 269
2472 LFRDPFANVNSVSRTMSALTIVFNAPSNGLLFRGSEASGDVAIYLDGKVMFKIN 2531
270 INSEPKKEGIRDTINDKDSHI-LITIGLOKRMWVNNERSVR---IRGE---IFD 320
2532 LGGSVAELTSGNVYNDKKEHVKAIRTG---SEMYLVQVSDPADFNVTIIGENTALNIE 2588
321 PSTYLLGIP1PAI-RERF-NISTPAPQCGMKNLK-----KTSGVRLN 361
2589 NENHYVAGVPMTLNKEVFGDINMNGFICILTVKPSQVGBLDDHPHESQGTDCSQVS 2648
362 DTVGTYKKCSBWKLVRTASFRSGQMSPTNLDVSTSRPOLSPGFQFQSGTLLNQT 421
2649 ---GVYDK-----ITGPKPGYLLTKGISDINSSTF--ASFRRRENGTILVYQS 2694
422 RTSSLLVTLTED-----GHI-----ELSTRDSNIP1FSPGTYMDGLLH 460
2695 KLOK--VGRKDEDDGKGYIAFLRGYLVLFHFGDASR--KEVYTFRSHHPYNDQYHA 2751
461 VSVISDTSGRLILIDQVLRNRQL--PSFSNAQSLRLG-----GHF 502
2752 VEMERNKGKIIIVKVDKEIGSQSLSDTSVGTTSGRILIGFSDLDLKPNNIEIP1TSFF 2811
503 EGCISNVLV--VQRFSSQPEVYLASKSTKKDASLGCGSLN 540
2812 IGCISDVFLNMRVSLAP-----KHNAQICMSMD 2842

RESULT 12
P67908
Protein T22A3.8 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: P67908
R:anonymous, The C. elegans Sequencing Consortium.
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see webites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ele
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: P67908
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-2823 <STO>

A:Cross-references: UNIPROT:O45614; GB:chr_1; PIDN:CAA15432.1; PID:g3924779; GSPDB:GN0019; CESP:R1McMurray, A.
A:Accession: E87908
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2823 <Str2>
A:Cross-references: GB:chr_1; PIDN:CAA03385.1; PID:g3924881; GSPDB:GN00019; CESP:R1McMurray, A.
C:Gene: T22A3.8
A:Map position: 1
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 7.6%; Score 222.5; DB 2; Length 2823;
Best Local Similarity 21.7%; Pred. No. 7e-07;
Matches 119; Conservative 102; Mismatches 205; Indels 123; Gaps 28;

QY	50	GKNDASKDYIGMAVNDQLTCCVNLGDRFAEVDQVLTSESQEAIV-MDRYKFGRIYQ	107
DB	2308	GRTPGSEHLAVEIRDGRVVVHMDIGSGK-----KMTNSHPINVPENDRTVWHIDV	2361
QY	108	PA---KLNT---KEATSN--KPKAPAVYDLEGG--SNTLNLDPEDAVFYGGYPPDP	157
DB	2362	LRIGNAVNLVALKESYDGGKPRGAPVSVFVGNKSDNSIFNTIPGETTIDVG---TDE	2418
QY	158	BLPSRLRPPEYK-----GCTELDDLNENVLSLVNKKTFPNTLTFEVRPRRRKESDXY	212
DB	2419	TVASDGLTTHKSGIVGLRIDEV---PLPLMSPEST---TGECEGATSPPKTSQGH	2471
QY	213	FRGTGARLPTQGNAPFPNFIQTITQTVWD-RGLLFF--AEQDNFISLNIEDGNLWVRK	269
DB	-2472	LPRDGFANVMSVSERTMSALTVIPNAPSNGLLYFRSGEASGDVAIYLDGKVMFKIN	2531
QY	270	LNSEPRKEGIRDTINDGKHSI-LITIGLKQKRMVNVNERSVR---IEGE---IFD	320
DB	2532	LGGSVAELTSGQVNVNDGKEHTVAIRTG---SEWYLVQVSDPADRFNVITGENTALNIE	2588
QY	321	FSYTYIGLPIAL-RERF-NISTPAFGCMQNLK-----XTSGVRLN	361
DB	2589	NENHYVAGVPMTLNKEVFGDINMGFIICILITVPSQVGEILDLDHPHSQGTIDGCSQVS	2648
QY	362	DTVGVTKKCSBDKVLVTAFSFRSGQMSFTMLDVPSTDRFOLSPFGQTFQPSGTLINHOT	421
DB	2649	---GVTDK-----IIGPKPGYLLTKRISIDNSSTF--AFSFRTEBNGTLYVQGS	2694
QY	422	KTSSLIVLTED-----GH1-----ELSTRDSNIPFVSPGYMDGLHH	460
DB	2695	KLQK--VSKRDSBDGKGYIAFYLFGRYLVLHPKDASSR--KEVVTFRSHHPYNDQVHA	2751
QY	461	VGVISDTSGRLRLDDQVLRNRQL---PFSMAQGSRLGG-----GHF	502
DB	2752	VFMERNGKLTISVXVDKREIGDSQSLSDETSVGTTSGRLILGFSDDLKPPNNEIPTSEF	2811
QY	503	EGCISNVLV	511
DB	2812	IGCISDVFL	2820

RESULT 13
T23064
hypothetical protein T22A3.8 - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23064; T25096
R:Barlow, K.
submitted to the EMBL Data Library, October 1997
A:Reference number: Z19669
A:Accession: T23064
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-2823 <WIL>
A:Cross-references: UNIPROT:O45614; EMBL:AL008585; PIDN:CAA15432.1; GSPDB:GN00019; CESP:R1McMurray, A.
submitted to the EMBL Data Library, October 1996

A:Reference number: Z19980
 A:Accession: T25096
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-2823 <WT>
 A:References: EMBL:Z81125, PIDN:CA803385.1; GSPDB:GN00019; CESP:T22A3.8
 A:Experimental source: clone T22A3
 C:Genetics:
 A:Gene: CESP:T22A3.8
 A:Map position: 1
 A:introns: 45/1; 282/2; 312/3; 416/2; 1255/3; 1329/3; 1418/3; 1776/2; 1988/2; 2760/2
 C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
 Query Match 7.6%; Score 222.5; DB 2; Length 2823;
 Best Local Similarity 21.7%; Fred. No. 7e-07;
 Matches 119; Conservative 102; Mismatches 205; Indels 123; Gaps 28;
 QY 50 GNKASKQYIGMAVVDGGLTCVYNLGDREARVQIDQVTESESGAV--MDRVKFORLYQ 107
 DB 2308 GRFPOPSHLAVERIDKRVVVMHDIGSK-----KMTTSHPIPVNSDRVMTYHIDV 2361
 QY 108 PA---KLYNT---KEATSN--KPAKAVYDDEGGS--SNTLLNDPDAVEVYGGYPPDF 157
 DB 2362 LRIGNAVVLTALESYDGGFKPGAPVSVGNSKDNISFNITPGETTIDVG---TDR 2418
 QY 158 ELPSRLRPPEYK---GCIEDLLENVSLVNFKTTFNLTTEVEPCRRKRKESDKY 212
 DB 2419 TVASDITGLTHKFGIVGRLIDEV--PLPLMSFEST---TGCCEGATSPPKTSQRGH 2471
 QY 213 FEGCYAIAIPQPNAPFPNFIQTITQTVD-RGLLFF--AENQDNFISLINDGMVRYK 269
 DB 2472 LFRDGFANVSVSERTMSALTIVFNAPSPNGLLYFRGSEASGDVALYINDGKMFYKIN 2531
 QY 270 LNSEPPKCKGIRDTINDGKHSI-LITIGKLOKMMIVNERSVR---IEGE---IFD 320
 DB 2532 LGGGSVALTELTYQNYINDGKHETVKAIRTG---SEMYLQVDSADBRFNTVITGENTALNIE 2588
 QY 321 FSTYLLGGIPIAI-RERF-NISTPAQGCMLNK-----KTSGVRLN 361
 DB 2589 NENHVAGVPTWLNKEVAGDINMNGFICILTVKPSQVGLDLDPHEHSGKTDGCSQVS 2648
 QY 362 DTGVTGKCKSDMKLVRASFSGGQMSFTMLDVPSTDRPQLSRGFQFQSGTLLNQT 421
 DB 2649 ---GVTDK-----IIGFKPGGYLTKGISIDNSTF--ASFRTRENSHTLVYQSS 2694
 QY 422 RTSSLVLTLAD-----GHI-----ELSTRDSNIPFESKPGTYMDGLLHH 460
 DB 2695 KLQK--VSKRSDSDGKGYIAFYLERGLVLVHPKDAISR--KEVVTFRSSHPIYNDGQVHA 2751
 QY 461 VSVISDTSGLRLIIDQVLRNRQL---PSFSNAQQSILRG-----GHP 502
 DB 2752 VFMERNGKIISVKVDKKEIGDSQSLSDETSVGTTSGRLILGFSDDLKPNNKEIPTTSFF 2811
 QY 503 EGCISNVLV 511
 DB 2812 IGCISDVPL 2820
 RESULT 14
 A88216
 neurexin III-alpha secreted type 1 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Dec-2002
 A:Accession: A48216; B48216
 R:Unkaryov, Y.A.; Suedhof, T.C.
 PROC. Natl. Acad. Sci. U.S.A. 90, 6410-6414, 1993
 A:Title: Neurexin IIIalpha: extensive alternative splicing generates membrane-bound and
 A:Reference number: A48216; MUID:93342001; PMID:8341647
 A:Molecule type: mRNA
 A:Residues: 1-1438 <USH>
 A:Cross-References: GB:LI4851

A/Accession: B48216
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1368,1372-1438 <US2>
A/Cross-references: GB:L14851
C/Genetics:
A/Introns: 1372/1
C/Superfamily: neurexin; EGF homology
C/Keywords: alternative splicing; brain; cell surface component; duplication; extracellular
F:1-27/Domain: signal sequence #status predicted <Sig>
F:202-234/Domain: EGF homology <EGF>
F:651-683/Domain: EGF homology <EGF1>

Query Match 7.2%; Score 212.5; DB 2; Length 1438;
Best Local Similarity 20.6%; Pred. No. 1.3e-06;
Matches 118; Conservative 72; Mismatches 185; Indels 199; Gaps 26;
QY 36 RENGTEDEMFVWYLGKNDKSKDYIGMAVVDGQLTCVYNLGD----- 76
DB 295 QRRG-----LILHTGK---SADYVNLALKDGAVSLVINIGSGAPFAIVEPVNGKENDNAM 346
QY 77 -----REAEOIDOVLTSESQEAVMRVKQRIYQFAKNTYTKATSNNKPKAPAV 127
DB 347 HDVKYTRNLKQVTVISVDGILTT-----GYOE----- 374
QY 128 YDEGGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKCI----- 173
DB 375 -----DYTMLG---SDDFYVGGSPSTADLPSPVNNFMGCLKEVYVKNNDIRLELS 424
QY 174 -LDDIANENVLSLYN---FKTTPNLTTEVEPCRRKESDKNYFEGTGARIPTQPNAPF 229
DB 425 RLARIQDTKMKLYGEVVFKE---NVATLDPI-----NFEPEAYISLPKNTKRM 472
QY 230 PNFQITQTTVDRLGLFPA-----ENOD-----NFISLIEBGNLWRYKLNSEPP 275
DB 473 GSISDFRTTEPNGLLFTHGKPKQERKDVRSQKTKVDFFAVELDGNLYLIDMGSGIT 532
QY 276 KEGGIRDTINDKDSHILITIGLQKRMWNNERSVRI---EGEIPDF-STYYLGAP 330
DB 533 KVKATQKANDGEWYH--VDIQDRSGTISVNSRPTFTASGESILDLBGDMYLGGLP 590
QY 331 IAIREFNISTP-----AFQCMKUL-----KTSGVRLNDTVGYTKCS--- 371
DB 591 ---ENRAGILPTELTMTAMLNHYGVCIRDLFIDGRSKNIRQLAEQONAGVYKSSCSRMS 647
QY 372 -----EDMK-----LVRTAS-FSRGGMSFTNLDP--- 396
DB 648 AKQCDYPCKNNAVCCKDGNRFTCDCTGTGWGRTCEBASILSYDGSN-YMKVIMPMVM 706
QY 397 STDRFQLSFGFQTFQPSGTLNHOQRTS--SLVLTLEDGHIELSTRDSNIP-----FKSP 450
DB 707 HTAEADVSPRFMSQRAYGLVATTSRDSADTLRLDLGGRVLMVNLDCIRINCNSKGP 766
QY 451 GTYM-----DGLAHVYSIDTSGRLILDDQV 478
DB 767 ETLVAGQKLNDEMHTVVRERKSLKLTVDVDDV 800

RESULT 15
B48216
neurexin III-alpha membrane-bound type 3 precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-May-1994 #sequence _revision 26-May-1994 #text_change 09-Dec-2002
C/Accession: B48218; C48218
R:Ushkaryov, Y.A.; Suedhof, T.C.
Proc. Natl. Acad. Sci. U.S.A. 90, 6410-6414, 1993
A/Title: Neurexin IIIalpha: extensive alternative splicing generates membrane-bound and
A/Reference number: A48216; WUID:93342001; PMID:8341647
A/Accession: B48218
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1471 <USH>
A/Cross-references: GB:L14851

A/Accession: C48218
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1368,1372-1471 <US2>
A/Cross-references: GB:L14851
C/Genetics:
A/Introns: 1372/1
C/Superfamily: neurexin; EGF homology
C/Keywords: alternative splicing; brain; cell surface component; duplication; receptor;
F:1-27/Domain: signal sequence #status predicted <Sig>
F:202-234/Domain: EGF homology <EGF>
F:651-683/Domain: EGF homology <EGF1>

Query Match 7.2%; Score 212.5; DB 2; Length 1471;
Best Local Similarity 20.6%; Pred. No. 1.3e-06;
Matches 118; Conservative 72; Mismatches 185; Indels 199; Gaps 26;
QY 36 RENGTEDEMFVWYLGKNDKSKDYIGMAVVDGQLTCVYNLGD----- 76
DB 295 QRRG-----LILHTGK---SADYVNLALKDGAVSLVINIGSGAPFAIVEPVNGKENDNAM 346
QY 77 -----REAEOIDOVLTSESQEAVMRVKQRIYQFAKNTYTKATSNNKPKAPAV 127
DB 347 HDVKYTRNLKQVTVISVDGILTT-----GYOE----- 374
QY 128 YDEGGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKCI----- 173
DB 375 -----DYTMLG---SDDFYVGGSPSTADLPSPVNNFMGCLKEVYVKNNDIRLELS 424
QY 174 -LDDIANENVLSLYN---FKTTPNLTTEVEPCRRKESDKNYFEGTGARIPTQPNAPF 229
DB 425 RLARIQDTKMKLYGEVVFKE---NVATLDPI-----NFEPEAYISLPKNTKRM 472
QY 230 PNFQITQTTVDRLGLFPA-----ENOD-----NFISLIEBGNLWRYKLNSEPP 275
DB 473 GSISDFRTTEPNGLLFTHGKPKQERKDVRSQKTKVDFFAVELDGNLYLIDMGSGIT 532
QY 276 KEGGIRDTINDKDSHILITIGLQKRMWNNERSVRI---EGEIPDF-STYYLGAP 330
DB 533 KVKATQKANDGEWYH--VDIQDRSGTISVNSRPTFTASGESILDLBGDMYLGGLP 590
QY 331 IAIREFNISTP-----AFQCMKUL-----KTSGVRLNDTVGYTKCS--- 371
DB 591 ---ENRAGILPTELTMTAMLNHYGVCIRDLFIDGRSKNIRQLAEQONAGVYKSSCSRMS 647
QY 372 -----EDMK-----LVRTAS-FSRGGMSFTNLDP--- 396
DB 648 AKQCDYPCKNNAVCCKDGNRFTCDCTGTGWGRTCEBASILSYDGSN-YMKVIMPMVM 706
QY 397 STDRFQLSFGFQTFQPSGTLNHOQRTS--SLVLTLEDGHIELSTRDSNIP-----FKSP 450
DB 707 HTAEADVSPRFMSQRAYGLVATTSRDSADTLRLDLGGRVLMVNLDCIRINCNSKGP 766
QY 451 GTYM-----DGLAHVYSIDTSGRLILDDQV 478
DB 767 ETLVAGQKLNDEMHTVVRERKSLKLTVDVDDV 800

Search completed: February 22, 2005, 08:19:38
Job time : 18.0758 secs

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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:07:29 ; Search time 95.5943 Seconds
(without alignments)
3026.590 Million cell updates/sec

Title: US-10-817-423-4

Perfect score: 2940

Sequence: 1 MRFNGKSGVRLPNDLEDL.....MLFKSPKRRFKRIENVNQL 565

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2940	100.0	1725	2	P70570	P70570 ratius norv
2	2704	92.0	3333	2	LM43_MOUSE	Q61789 mus musculu
3	2441	83.0	1668	2	Q6VU69	Q6VU69 homo sapien
4	2441	83.0	3277	2	Q6VU67	Q6VU67 homo sapien
5	2439	83.0	3333	2	Q6VU68	Q6VU68 homo sapien
6	2439	83.0	1713	2	LM43_HUMAN	Q16787 homo sapien
7	2439	83.0	1806	2	Q96TG0	Q96TG0 homo sapien
8	2439	83.0	3333	2	Q76B14	Q76B14 homo sapien
9	2224.5	75.7	1725	2	Q867A1	Q867A1 canis famli
10	712	24.2	3695	2	LM45_HUMAN	O15230 homo sapien
11	712	24.2	3695	2	Q8TD8	Q8TD8 homo sapien
12	685	23.3	1816	2	LM44_HUMAN	O16363 homo sapien
13	685	23.3	1254	2	Q91V70	Q91V70 mus musculu
14	685	23.3	1816	2	LM44_MOUSE	P97927 mus musculu
15	681	23.2	1524	2	Q6ZQX1	Q6ZQX1 mus musculu
16	681	23.2	3718	2	LM45_MOUSE	Q61001 mus musculu
17	492.5	16.8	6770	2	Q9BT3	Q9BT3 homo sapien
18	395	13.4	3712	2	LM4 DROME	O00174 drosophila
19	395	13.4	3712	2	Q9VRW0	Q9VRW0 drosophila
20	359	12.2	3616	2	Q7PP9	Q7PP9 anopheles g
21	326	11.1	794	2	Q8R37	Q8R37 mus musculu
22	302	10.3	3106	2	LM42_MOUSE	Q60675 mus musculu
23	298.5	10.2	1518	2	Q21442	Q21442 caenorhabdi
24	298.5	10.2	3672	2	LM42_CAEEL	Q21313 caenorhabdi
25	298.5	10.2	3704	2	P919F4	P91904 caenorhabdi
26	294	10.0	3110	2	LM42_HUMAN	P24043 homo sapien
27	285.5	9.7	858	2	Q8R15	Q8R15 mus musculu
28	280	9.5	3084	2	LM41_MOUSE	P19137 mus musculu
29	270	9.2	3075	1	LM41_HUMAN	P25391 homo sapien
30	247	8.4	3102	2	O45614	O45614 caenorhabdi
31	219.5	7.5	1247	2	Q7PT06	Q7PT06 anopheles g

32	216	7.3	1392	2	Q81UE3	Q81UE3 homo sapien
33	213.5	7.3	1541	1	NX3A_HUMAN	Q94C00 homo sapien
34	213	7.2	3375	2	Q81P51	Q81P51 drosophila
35	212.5	7.2	1203	2	Q6Z056	Q6Z056 mus musculu
36	212.5	7.2	1587	2	Q6P9K9	Q6P9K9 mus musculu
37	207.5	7.1	1363	2	NX1A_CHICK	Q9DD00 gallus gall
38	204.5	7.0	1514	2	NX1A_RAT	Q63372 ratius norv
39	200	6.8	1530	2	Q8CHE6	Q8CHE6 mus musculu
40	199.5	6.8	1530	1	NX1A_BOVIN	Q80Y87 bos taurus
41	198	6.7	1176	2	Q80Y87	Q80Y87 mus musculu
42	197	6.7	1560	2	Q18291	Q18291 caenorhabdi
43	196	6.7	1477	1	NX1A_HUMAN	Q9ULB1 homo sapien
44	196	6.7	3367	2	Q9XZC9	Q9XZC9 drosophila
45	195.5	6.6	747	2	Q7Z5W6	Q7Z5W6 homo sapien

ALIGNMENTS

RESULT 1	PRELIMINARY;	PRT;	1725 AA.
P70570	P70570		
AC	P70570;		
DT	01-FEB-1997 (TrEMBLrel. 02, Created)		
DT	01-FEB-1997 (TrEMBLrel. 02, Last sequence update)		
DE	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Laminin-5 alpha 3 chain.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_Taxid=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97081969; PubMed=8923212;		
RA	Baker S.E., Hopkinson S.B., Fitchman M., Andreason G.L., Frasier F.,		
RA	Plopper G., Quaranta V., Jones J.C.R.,		
RT	"Laminin-5 and hemidesmosomes: role of the alpha 3 chain subunit in		
RT	hemidesmosome stability and assembly."		
RL	U. Cell Sci. 109:2509-2520 (1996).		
DR	EMBL; U61261; AAB17053.1; .		
DR	HSP; P35070; 11P0.		
DR	GO; GO:0005606; C:laminin-1; IEA.		
DR	GO; GO:0005102; F:receptor binding; IEA.		
DR	GO; GO:0005198; F:structural molecule activity; IEA.		
DR	GO; GO:0030155; P:regulation of cell adhesion; IEA.		
DR	GO; GO:0030334; P:regulation of cell migration; IEA.		
DR	GO; GO:0045995; P:regulation of embryonic development; IEA.		
DR	InterPro; IPR008985; Cona_1like_1ec_g1.		
DR	InterPro; IPR006209; EGF_Like.		
DR	InterPro; IPR002049; Laminin_EGF.		
DR	InterPro; IPR001791; Laminin_G.		
DR	InterPro; IPR009254; Laminin_I.		
DR	InterPro; IPR010307; Laminin_II.		
DR	InterPro; IPR003129; TSP_N.		
DR	Pfam; PF02210; Laminin_G_2; 4.		
DR	Pfam; PF06008; Laminin_I; 1.		
DR	Pfam; PF06009; Laminin_II; 1.		
DR	SMART; SM00180; EGF_Lam; 2.		
DR	SMART; SM00282; LamG; 5.		
DR	PROSITE; PS00022; EGF_1; 1.		
DR	PROSITE; PS01186; EGF_2; 1.		
DR	PROSITE; PS01248; LAMININ_TYPE_EGF; 2.		
DR	PROSITE; PS50025; LAM_G_DOMAIN; 5.		
KW	Laminin EGF-like domain.		
SO	SEQUENCE 1725 AA; 190392 MW; 02EE43B33E72B0FB CRC64;		
Query Match	100.0%;	Score 2940;	DB 2; Length 1725;
Best Local Similarity	100.0%;	Pred. No. 2.7e-191;	
Matches 565;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1 MRFNGKSGVRLPNDLEDLKGYTSLPLFQRLRENGGTEDMFVYTLGNKQASXDYIG 60		

Db	762	MFENKSGVREVRLLPNDLBDLKGKTSLSLFLQRDLAENGGTEBDMFMYLGNDAASDXYIG	841
Qy	61	MAVVDGQLTCVYNLGDREAREVQIDQVLTSESSEGEAVMDRYKFORITIQPAKLNTKEATSN	120
Db	842	MAVVDGQLTCVYNLGDREAREVQIDQVLTSESSEGEAVMDRYKFORITIQPAKLNTKEATSN	901
Qy	121	KPKAAVVDLEGSSNTLLNLPEDAVFVYGGVPPDFELPSRLRPPPYKCIELDLNEN	180
Db	902	KPKAAVVDLEGSSNTLLNLPEDAVFVYGGVPPDFELPSRLRPPPYKCIELDLNEN	961
Qy	181	VLSLNFKTTFNLTTEVAPCRRRKESDQNTFEGTGVARIPTOPNAPPNFIQTITQTV	240
Db	962	VLSLNFKTTFNLTTEVAPCRRRKESDQNTFEGTGVARIPTOPNAPPNFIQTITQTV	102
Qy	241	DGLLFPANQNPTSLNIEDGNLWRYLNLNSPPEKGIKRTDINGKXHSILITIGKIQ	300
Db	1022	DGLLFPANQNPTSLNIEDGNLWRYLNLNSPPEKGIKRTDINGKXHSILITIGKIQ	108
Qy	301	KEMINVERSVRIEGEIPDFSTYYLGGIPIAIRERFNI STPAFGCMKLLKTSGVNL	360
Db	1082	KEMINVERSVRIEGEIPDFSTYYLGGIPIAIRERFNI STPAFGCMKLLKTSGVNL	114
Qy	361	NDTVGYTKKCSDDMLVRTASPSRGQMGFTNLDVSTDRPOLSRFGQTFQSGEGLLNQ	420
Db	1142	NDTVGYTKKCSDDMLVRTASPSRGQMGFTNLDVSTDRPOLSRFGQTFQSGEGLLNQ	120
Qy	421	TRTSSLVLVEBGEHELSTRDSNIPFKPSPGTMDGLHHVSYISPTSGRLIIDQVLR	480
Db	1202	TRTSSLVLVEBGEHELSTRDSNIPFKPSPGTMDGLHHVSYISPTSGRLIIDQVLR	126
Qy	481	RNQRLPSPFNAAQOSLRLGGGHEGCGISNVLVORFOSPEVLDIASKSTKXDAISGCSIN	540
Db	1262	RNQRLPSPFNAAQOSLRLGGGHEGCGISNVLVORFOSPEVLDIASKSTKXDAISGCSIN	132
Qy	541	KPPFLMLFPKSPKRFNKGRIENNQL	565
Db	1322	KPPFLMLFPKSPKRFNKGRIENNQL	1346
RESULT 2			
LMA3_MOUSE			
ID	LMA3_MOUSE	STANDARD:	PRT: 3333 AA.
AC	O61789: O08751; O61788; O61966; Q9JHQ7;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DS	Laminin alpha-3 chain precursor (Nicein alpha subunit).		
GN	Name=Lama3;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE OF 1-58 FROM N.A., AND SEQUENCE OF 32-38.		
RX	MEDLINE=21818471; PubMed=11829758; DOI=10.1042/0264-6021.3620213;		
RA	Garbe J.H., Gehring W., Mann K., Trippel R., Sasaki T.,		
RT	"Complete sequence, recombinant analysis and binding to laminins and		
RT	eluphated ligands of the N-terminal domains of laminin alpha3B and		
RT	alpha3 chains.";		
RL	Biochem. J. 362:213-221 (2002).		
RN	[2]		
RP	SEQUENCE OF 1-726 FROM N.A.		
RC	STRAIN=ICR.		
RX	MEDLINE=97296337; PubMed=9151674; DOI=10.1083/jcb.137.3.685;		
RA	Winer J.H., Patton B.L., Lentz S.I., Gilbert D.D., Snider W.D.,		
RT	Jenkins N.A., Copeland N.G., Sames J.R.;		
RT	"The laminin alpha chains: expression, developmental transitions, and		
RT	chromosomal locations of alpha1-5, identification of heterotrimeric		
RT	laminins 8-11, and cloning of a novel alpha3 isoform.";		
RL	J. Cell Biol. 137:685-701 (1997).		
RN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORM A), AND SEQUENCE OF 716-3284 FROM N.A.		
RP	(ISOFORM B).		

CC STRPAIN-BALB/C; TISSUE=Lung;
RX MEDLINE=95394948; PubMed=7665604; DOI=10.1074/jbc.270.37.21820;
RA Galliano M.-F., Aberdam D., Aguzzi A., Ortonne J.-P., Meneguzzi G.;
RT "Cloning and complete primary structure of the mouse laminin alpha 3
RT chain. Distinct expression pattern of the laminin alpha 3A and alpha
RT 3B chain isoforms";
RL J. Biol. Chem. 270:21820-21826(1995).
RN [4]
RN REVISIONS.
RP Aberdam D.;
RA Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
RL [5]
RP SEQUENCE OF 1767-2485 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94281750; PubMed=8012114;
RA Aberdam D., Galliano M.-F., Mattei M.-G., Pisanì-Spadafora A.,
RA Ortonne J.-P., Meneguzzi G.;
RT "Assignment of mouse nicein genes to chromosomes 1 and 18";
RL Mamm. Genome 5:229-233(1994).
RN [6]
RP SEQUENCE OF 1767-2485 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94363405; PubMed=8081888;
RA Aberdam D., Aguzzi A., Baudoin C., Galliano M.-F., Ortonne J.-P.,
RA Meneguzzi G.;
RT "Developmental expression of nicein adhesion protein (laminin-5)
RT subunits suggests multiple morphogenic roles";
RL Cell Adhes. Commun. 2:115-129(1994).
CC -1 FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -1 FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
CC via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-
CC 6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
CC phosphorylation of p125-PAK and p80, (3) differentiation of
CC keratinocytes (by similarity).
CC -1 SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The alpha-3 chain is a subunit of laminin-5
CC (epiligrin/kalinin/nicein), and possibly also a component of
CC laminin-6 (k-laminin) and laminin-7 (KS-laminin).
CC -1 SUBCELLULAR LOCATION: Extracellular; found in the basement
CC membranes (major component).
CC -1 ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=G61789-1; Sequence=Displayed;
CC Name=A;
CC IsoId=G61789-2; Sequence=VSP_003038, VSP_003039;
CC -1 TISSUE SPECIFICITY: Basal membrane of the upper alimentary tract
CC and urinary and nasal epithelia, salivary glands and teeth (both
CC variants). Isoform A is predominantly expressed in skin, hair
CC follicles and developing neurons of the trigeminal ganglion.
CC Isoform B was found in bronchi, alveoli, stomach, intestinal
CC crypts, whisker pads, CNS, telencephalic neuroectoderm, thalamus,
CC Rathke's pouch and periventricular subependymal germinal layer.
CC -1 DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -1 DOMAIN: Domains IV and G are globular.
CC -1 SIMILARITY: Contains 15 laminin EGF-like domains.
CC -1 SIMILARITY: Contains 5 laminin G-like domains.
CC -1 SIMILARITY: Contains 1 laminin N domain.
CC -1 SIMILARITY: Contains 1 laminin N-terminal domain.
CC -----
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CC -----

DR EMBL: AJ293592; CAB9254.2; -

DR EMBL: U86353; AAC5179.1; -

DR EMBL: X84014; CAAS6837.1; -

DR EMBL: X84013; CAAS6836.1; ALT_FRAME.

DR EMBL: L20478; AAA68091.1; -

DR HSSP: P02468; INPE.

DR MGD; MGT.99909; Lama3.

DR GO; GO:0005604; C:Basement membrane; IDA.

DR InterPro: IPR008985; Cona_like_1ec_g1.

DR InterPro: IPR006209; EGF_like.

DR InterPro: IPR008979; Gal_bind_like.

DR InterPro: IPR009030; Grow_fac_recept.

DR InterPro: IPR008212; Lam_N2.

DR InterPro: IPR000034; Laminin_B.

DR InterPro: IPR002049; Laminin_EGF.

DR InterPro: IPR001791; Laminin_G.

DR InterPro: IPR009254; Laminin_I.

DR InterPro: IPR010307; Laminin_II.

DR InterPro: IPR008211; Laminin_N.

DR InterPro: IPR003129; TSP_N.

DR Pfam: PF00052; Laminin_B; 1.

DR Pfam: PF00053; Laminin_G; 10.

DR Pfam: PF00054; Laminin_I; 3.

DR Pfam: PF06008; Laminin_II; 1.

DR Pfam: PF06009; Laminin_III; 1.

DR Pfam: PF00055; Laminin_N; 1.

DR PRINTS: PR00011; EGF_LAMININ.

DR ProDom: PD003031; Laminin_B; 1.

DR PROSITE: PS00023; EGF_1; 10.

DR PROSITE: PS01166; EGF_2; 1.

DR PROSITE: PS00025; LAM_G_DOMAIN; 5.

DR PROSITE: PS01244; LAMININ TYPE EGF; 10.

DR Alternative splicing; Basement membrane; Cell adhesion; Coiled coil;

KM Direct protein sequencing; Extracellular matrix; Glycoprotein;

KW Laminin EGF-like domain; Repeat; Signal.

FT SIGNAL 1 31

FT CHAIN 32 3333 Laminin alpha-3 chain.

FT DOMAIN 32 294 Laminin N-terminal (domain VI).

FT DOMAIN 295 725 Domain V.

FT DOMAIN 296 350 Laminin EGF-like 1.

FT DOMAIN 353 420 Laminin EGF-like 2.

FT DOMAIN 423 464 Laminin EGF-like 3.

FT DOMAIN 468 530 Laminin EGF-like 4.

FT DOMAIN 533 576 Laminin EGF-like 5.

FT DOMAIN 582 625 Laminin EGF-like 6.

FT DOMAIN 628 678 Laminin EGF-like 7.

FT DOMAIN 681 725 Laminin EGF-like 8.

FT DOMAIN 725 1262 Laminin domain IV 1 (domain IV B).

FT DOMAIN 1263 1464 Domain III B.

FT DOMAIN 1310 1353 Laminin EGF-like 9.

FT DOMAIN 1354 1403 Laminin EGF-like 10.

FT DOMAIN 1404 1454 Laminin EGF-like 11.

FT DOMAIN 1455 1464 Laminin EGF-like 12 (N-terminal).

FT DOMAIN 1465 1653 Laminin domain IV (domain IV A).

FT DOMAIN 1654 1821 Domain III A.

FT DOMAIN 1654 1686 Laminin EGF-like 12 (C-terminal).

FT DOMAIN 1687 1733 Laminin EGF-like 13.

FT DOMAIN 1734 1786 Laminin EGF-like 14.

FT DOMAIN 1787 1821 Laminin EGF-like 15 (incomplete).

FT DOMAIN 1822 2388 Domain II and I.

FT DOMAIN 2389 2590 Laminin G-like 1.

FT DOMAIN 2591 2759 Laminin G-like 2.

FT DOMAIN 2766 2926 Laminin G-like 3.

FT DOMAIN 2986 3150 Laminin G-like 4.

FT DOMAIN 3157 3330 Laminin G-like 5.

FT DOMAIN 1854 1983 Coiled coil (Potential).

FT DOMAIN 2015 2060 Coiled coil (Potential).

FT DOMAIN 2091 2168 Coiled coil (Potential).

FT DOMAIN 2214 2241 Coiled coil (Potential).

FT DOMAIN 2321 2386 Coiled coil (Potential).

FT SITE 2277 2279 Cell attachment site (Potential).

FT DISULFID 1310 1317 By similarity.

FT DISULFID 1312 1324 By similarity.

FT DISULFID 1326 1335 By similarity.

FT DISULFID 1338 1351 By similarity.

FT DISULFID 1354 1369 By similarity.

FT DISULFID 1366 1376 By similarity.

FT DISULFID 1378 1387 By similarity.

FT DISULFID 1390 1401 By similarity.

FT DISULFID 1404 1416 By similarity.

FT DISULFID 1426 1434 By similarity.

FT DISULFID 1437 1452 By similarity.

FT DISULFID 1467 1496 By similarity.

FT DISULFID 1689 1703 By similarity.

FT DISULFID 1706 1715 By similarity.

FT DISULFID 1718 1731 By similarity.

FT DISULFID 1734 1746 By similarity.

FT DISULFID 1736 1755 By similarity.

FT DISULFID 1757 1766 By similarity.

FT DISULFID 1769 1784 By similarity.

FT DISULFID 1822 1822 Interchain (Probable).

FT DISULFID 1825 1825 Interchain (Probable).

Query Match 92.0%; Score 2704; DB 1; Length 3333;

Best Local Similarity 92.2%; Pred. No. 8.3e-175;

Matches 521; Conservative 15; Mismatches 29; Indels 0; Gaps 0;

QY 1 MRFNGSGVVRLLPNLDELKGYTSLFLQRPDLRENGTDMFYNTLGNKASXDYIG 60

DB 2390 MRFNGSGVVRLLPNLDELKGYTSLFLQRPDLRENGTDMFYNTLGNKASXDYIG 2449

QY 61 MAVVDQGLTCVNLGSRBAVQIDVLTSEESQEAAMDVKRQRIYQFALNTKRTSN 120

DB 2450 MAVVDQGLTCVNLGSRBAVQIDVLTSEESQEAAMDVKRQRIYQFALNTKRTSN 2509

QY 121 KPRAPAYDLEGGSSNTLNLDPEDAVFYVGGPPDFELPSRLRFPYKGCIELDLNEN 180

DB 2510 KPRAPAYDLEGGSSNTLNLDPEDAVFYVGGPPDFELPSRLRFPYKGCIELDLNEN 2569

QY 181 VLSLYNFKTTFNLTTEVEPCRRKESDKNVEGTGYARIPIQPNAPFPNFIQTQTV 240

DB 2570 VLSLYNFKTTFNLTTEVEPCRRKESDKNVEGTGYARIPIQPNAPFPNFIQTQTV 2629

QY 241 DRGLTFPABNDPFIPLNTEEDNLNRYKLNSEPPKRGIRDTNCKHSLITGKQ 300

DB 2630 DRGLTFPABNDPFIPLNTEEDNLNRYKLNSEPPKRGIRDTNCKHSLITGKQ 2689

QY 301 KRWMINVNSVRLEGRIPISTYTGIPAIIRERFNIPTPAFGCMKUKTSGVRL 360

DB 2690 KRWMINVNSVRLEGRIPISTYTGIPAIIRERFNIPTPAFGCMKUKTSGVRL 2749

QY 361 NDTVGYTKKCEDMKLVRTASFSRQGMSTNLDPVSTDRFQSLFGFTQPSGTLNHQ 420

DB 2750 NDTVGYTKKCEDMKLVRTASFSRQGMSTNLDPVSTDRFQSLFGFTQPSGTLNHQ 2809

QY 421 TRTSSILVYTEDGHILSTDSNIPFKSGTMDGLHNVYSISDSSGRLLIDQVLR 480

DB 2810 TRTSSILVYTEDGHILSTDSNIPFKSGTMDGLHNVYSISDSSGRLLIDQVLR 2869

QY 481 RNRRLSPSNAQOSSLRGGHFPGCTSNVYVORFSQSPVLDLASKSTKQDASIGGCSLN 540

DB 2870 RNRRLSPSNAQOSSLRGGHFPGCTSNVYVORFSQSPVLDLASKSTKQDASIGGCSLN 2929

QY 541 KPPEFLMLFKSPKRFNKRIFNVQL 565

DB 2930 KPPEFLMLFKSPKRFNKRIFNVQL 2954

RESULT 3

Q6VU69 PRELIMINARY; PRT; 1668 AA.

AC Q6VU69;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

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DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE Laminin alpha 3 splice variant a.
GN Name=LAMA3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
RA McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
RA Coleman-Campbell C.M., Mellerio J.B., Ashton G.S.,
RA Dopping-Hepenstal P.J., Bady R.A., Jamil T., Phillips R.J.,
RA Shabbir S.G., Haroon T.S., Khurehd K., Moore J.B., Page B.,
RA Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
RA McGrath J.A.;
RT "An unusual N-terminal deletion of the laminin (alpha)3a isoform leads
RT to the chronic granululation tissue disorder laryngo-oncho-cutaneous
RT syndrome."
RL Hum. Mol. Genet. 12:2395-2409(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA McLean W.H.I.;
RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY327114; AAQ72569.1; -.
DR GO; GO:0005606; C:lamatin-1; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR GO; GO:0030334; P:regulation of cell migration; IEA.
DR GO; GO:0045995; P:regulation of embryonic development; IEA.
DR InterPro; IPR001844; Chapman Cpn60.
DR InterPro; IPR008985; Cona_1like_1ec_g1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00053; Laminin_EGF; 1.
DR Pfam; PF02210; Laminin_G_2; 4.
DR Pfam; PF06008; Laminin_I; 1.
DR Pfam; PF06009; Laminin_II; 1.
DR SMART; SM00180; EGF_Lam; 2.
DR SMART; SM00282; LamG; 5.
DR PROSITE; PS00226; CHAPERONINS_CPN60; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW Laminin EGF-like domain.
SQ
SEQUENCE 1668 AA; 184053 MW; 9EB5F5FC45637645C CRC64;

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Query Match      83.0%; Score 2441; DB 2; Length 1668;
Best Local Similarity 81.9%; Pred. No. 2,7e-157;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

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QY 1 MRNNGSGVAVRPLNDLEDKGTTSLSLFLQRPDLKNGTEDMFWYTLGNKASADYIG 60
DB MRNNGSGVAVRPLNDLEDKGTTSLSLFLQRPDSRNGCTEMFWYTLGNKASADYIG 785
QY 726 MAVVDGQLTCVNYLADREAEVQIDQVLTSSSQBAWMDRYKFORIQPAFLANTYTKATSN 120
DB MAVVDGQLTCVNYLADREAEVQIDQVLTSSSQBAWMDRYKFORIQPAFLANTYTKATSN 845
QY 61 MAVVDGQLTCVNYLADREAEVQIDQVLTSSSQBAWMDRYKFORIQPAFLANTYTKATSN 180
DB MAVVDGQLTCVNYLADREAEVQIDQVLTSSSQBAWMDRYKFORIQPAFLANTYTKATSN 845
QY 121 KPRAPAVYDLGGSSNTLNTLDPEDAVFYVGYPPDFELPSRLFPFYKGCIELDLINEN 180
DB KPRAPAVYDLGGSSNTLNTLDPEDAVFYVGYPPDFELPSRLFPFYKGCIELDLINEN 905
QY 846 KPETPGYDMDGNSNTLNTLDPENYVFFYVGYPPDPKPLSRSLSPFYKGCIELDLINEN 905
DB KPETPGYDMDGNSNTLNTLDPENYVFFYVGYPPDPKPLSRSLSPFYKGCIELDLINEN 905
QY 181 VLSLNYFKTFTNTTTEVEPCRRRKESSDKNYFEGTGYARIPTQPNAPFPNFIQTITTY 240
DB VLSLNYFKTFTNTTTEVEPCRRRKESSDKNYFEGTGYARVPTQPNAPFPNFIQTITTY 965

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QY 241 DRGLFPANODNFISLNEIDGNLMVRYKLNSBPPEKGRIDTINDGDSILITIGLQ 300
DB DRGLFPANODNFISLNEIDGNLMVRYKLNSBPPEKGRIDTINDGDSILITIGLQ 1025
QY 301 KKMWINNERSVRIEGLIFDFSTYLLGGIPIAIRERFNIISPPAGOCMKNLKTTSGVRL 360
DB KKMWINNERSVRIEGLIFDFSTYLLGGIPIAIRERFNIISPPAGOCMKNLKTTSGVRL 1085
QY 361 NDTGVVTKKCSHDMVLVTASPSRGGMSFTNLDPVPSIDRQLSTGPTPTPQSGTLLHQ 420
DB NDTGVVTKKCSHDMVLVTASPSRGGMSFTNLDPVPSIDRQLSTGPTPTPQSGTLLHQ 1145
QY 421 TTSLSLVTLEEGHIELSTRDSNIPFSPGTYMDGLAHVYSISDTSGRLTIDQVLR 480
DB TTSLSLVTLEEGHIELSTRDSNIPFSPGTYMDGLAHVYSISDTSGRLTIDQVLR 1205
QY 481 RNQRLSPSMAQSLRLGGHFECCISNVLVQPSQSPFVLDLASKSTKQASLGGCSLN 540
DB RNQRLSPSMAQSLRLGGHFECCISNVLVQPSQSPFVLDLASKSTKQASLGGCSLN 1265
QY 541 KPPFLMLFKSPRFRKGRIFNVNOL 565
DB KPPFLMLFKSGTRFKKTYFRINOL 1290
QY 1266 KPPFLMLFKSGTRFKKTYFRINOL 1290

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RESULT 4

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ID Q6VU67 PRELIMINARY; PRT; 3277 AA.

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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE Laminin alpha 3 splice variant b2.
GN Name=LAMA3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
RA McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
RA Coleman-Campbell C.M., Mellerio J.B., Ashton G.S.,
RA Dopping-Hepenstal P.J., Bady R.A., Jamil T., Phillips R.J.,
RA Shabbir S.G., Haroon T.S., Khurehd K., Moore J.B., Page B.,
RA Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
RA McGrath J.A.;
RT "An unusual N-terminal deletion of the laminin (alpha)3a isoform leads
RT to the chronic granululation tissue disorder laryngo-oncho-cutaneous
RT syndrome."
RL Hum. Mol. Genet. 12:2395-2409(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA McLean W.H.I.;
RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY327116; AAQ72571.1; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005606; C:lamatin-1; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR GO; GO:0030334; P:regulation of cell migration; IEA.
DR GO; GO:0045995; P:regulation of embryonic development; IEA.
DR InterPro; IPR001844; Chapman Cpn60.
DR InterPro; IPR008985; Cona_1like_1ec_g1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR008979; EGF_bind_1like.
DR InterPro; IPR006210; IKGf.
DR InterPro; IPR00034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.

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DR InterPro: IPR010307; Laminin II.
 DR InterPro: IPR008211; Laminin N.
 DR InterPro: IPR003129; TSP N.
 DR Pfam: PF00052; Laminin B; 1.
 DR Pfam: PF00053; Laminin EGF; 8.
 DR Pfam: PF02210; Laminin G; 2; 4.
 DR Pfam: PF06008; Laminin_I; 1.
 DR Pfam: PF06009; Laminin_II; 1.
 DR Pfam: PF00055; Laminin_N; 1.
 DR PRINTS: PR00011; EGF_LAMININ.
 DR ProDom: PD003031; Laminin_B; 1.
 DR SMART: SM00181; EGF; 8.
 DR SMART: SM00180; EGF_Lam; 14.
 DR SMART: SM00281; Lamb; 1.
 DR SMART: SM00282; Lamb; 5.
 DR SMART: SM00136; Lamnt; 1.
 DR PROSITE: PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE: PS00022; EGF 1; 12.
 DR PROSITE: PS01186; EGF 2; 1.
 DR PROSITE: PS01248; LAMININ_TYPB_EGF; 13.
 DR PROSITE: PS50025; LAM_G_DOMAIN; 5.
 DR Laminin EGF-like domain.
 SQ SEQUENCE 3277 AA; 360209 MW; 3ACFPE9983571228 CRC64;

Query Match 83.0%; Score 2441; DB 2; Length 3277;
 Best Local Similarity 81.9%; Pred. No. 6.9e-157;
 Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRFNGSGVVRRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYILGNKQASKDYIG 60
 DB 2335 MRFNGSGVVRRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYILGNKQASRYIG 2394
 QY 61 MAVVDGQLTCVYNLGDREAEVQIDVLTESQEAANDRYKFORIYQPAKLNTKATSN 120
 DB 2395 MAVVDGQLTCVYNLGDREAEVQIDVLTESQEAANDRYKFORIYQPAKLNTKATSS 2454
 QY 121 KPRAPANYDLEGSSNTLNLDPDPAVYVYGGYPPDELSRLRFPYKCIETLDLEN 180
 DB 2455 KPRAPANYDLEGSSNTLNLDPDPAVYVYGGYPPDELSRLRFPYKCIETLDLEN 2514
 QY 181 VLSLYNFKTFLNLTTEVEPCRRKESDKNYFEGTVAHLPQNPAPFNFIQTIQTV 240
 DB 2515 VLSLYNFKTFLNLTTEVEPCRRKESDKNYFEGTVAHLPQNPAPFNFIQTIQTV 2574
 QY 241 DRGLLFAENQDNFISLNIIDGMLVYKLNSEBPKEKGRDITNDKSHIITIGKQ 300
 DB 2575 DRGLLFAENQDNFISLNIIDGMLVYKLNSEBPKEKGRDITNDKSHIITIGKQ 2634
 QY 301 KRWMINNERSVRLKEGIFDPSTYLLGIPAIIRERNISTPAVQGCMLKKTSSVYRL 360
 DB 2635 KRWMINNERSVRLKEGIFDPSTYLLGIPAIIRERNISTPAVQGCMLKKTSSVYRL 2694
 QY 361 NDVTVGTVKKSDEMKLVRTASFSRGGMSFTNIDVPSDFRQSLRFGFOTPSGTLINHQ 420
 DB 2695 NDVTVGTVKKSDEMKLVRTASFSRGGMSFTNIDVPSDFRQSLRFGFOTPSGTLINHQ 2754
 QY 421 TRTSLSLVLTEDGHIETSDSNIPKFSFGTYMDGLHNVSVISDTSGLRLTIDDOVLR 480
 DB 2755 TRTSLSLVLTEDGHIETSDSNIPKFSFGTYMDGLHNVSVISDTSGLRLTIDDOVLR 2814
 QY 481 RNQRLPFSNAQSLRIGGHPFECINVLVQFSQSPVYIDLASKTKDASIGGCSLN 540
 DB 2815 RNQRLPFSNAQSLRIGGHPFECINVLVQFSQSPVYIDLASKTKDASIGGCSLN 2874
 QY 541 KPEFLMFKSPKRNKGRIFENVOL 565
 DB 2875 KPEFLMFKSPKRNKGRIFENVOL 2899

RESULT 5
 Q6VU68
 ID Q6VU68 PRELIMINARY; PRT; 3333 AA.
 AC Q6VU68;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Laminin alpha 3 splice variant b1.
 SN Name=IAMA3;
 SN Name=IAMA3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxId=9606;
 RX SEQUENCE FROM N.A.
 RX MEDLINE=2833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
 RA McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
 RA Dopping-Hepenstal P.V., Bady R.A., Jamali T., Phillips R.J.,
 RA Shabbir S.G., Haroon T.S., Khurshid K., Moore J.B., Page B.,
 RA Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
 RA McGrath J.A.;
 RT "An unusual N-terminal deletion of the laminin (alpha)3a isoform leads
 to the chronic granulation tissue disorder laryngo-oncho-cutaneous
 RT syndrome";
 RT Hum. Mol. Genet. 12:2395-2409(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA McLean W.H.I.;
 RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RU EMBL: A1327115; AAC72570.1; -;
 DR GO: GO:0005578; Extracellular matrix (sensu Metazoa); IEA.
 DR GO: GO:0005606; Cytoskeleton; IEA.
 DR GO: GO:0005102; Receptor binding; IEA.
 DR GO: GO:0005198; Structural molecule activity; IEA.
 DR GO: GO:0030155; Proliferation of cell adhesion; IEA.
 DR GO: GO:0030334; Regulation of cell migration; IEA.
 DR GO: GO:0045995; Regulation of embryonic development; IEA.
 DR InterPro: IPR001844; Chaprin Cpn60.
 DR InterPro: IPR008985; ConA like_1ec_g1.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR008979; Gal_bind_like.
 DR InterPro: IPR006210; IEGF.
 DR InterPro: IPR000304; Laminin_B.
 DR InterPro: IPR002049; Laminin_EGF.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR009254; Laminin_I.
 DR InterPro: IPR010307; Laminin_II.
 DR InterPro: IPR008211; Laminin_N.
 DR InterPro: IPR003129; TSP_N.
 DR Pfam: PF00052; Laminin_B; 1.
 DR Pfam: PF00053; Laminin_EGF; 8.
 DR Pfam: PF02210; Laminin_G; 2; 4.
 DR Pfam: PF06008; Laminin_I; 1.
 DR Pfam: PF06009; Laminin_II; 1.
 DR Pfam: PF00055; Laminin_N; 1.
 DR PRINTS: PR00011; EGF_LAMININ.
 DR ProDom: PD003031; Laminin_B; 1.
 DR SMART: SM00181; EGF; 8.
 DR SMART: SM00180; EGF_Lam; 14.
 DR SMART: SM00281; Lamb; 1.
 DR SMART: SM00282; Lamb; 5.
 DR SMART: SM00136; Lamnt; 1.
 DR PROSITE: PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE: PS00022; EGF 1; 12.
 DR PROSITE: PS01186; EGF 2; 1.
 DR PROSITE: PS01248; LAMININ_TYPB_EGF; 13.
 DR PROSITE: PS50025; LAM_G_DOMAIN; 5.
 DR Laminin EGF-like domain.
 SQ SEQUENCE 3333 AA; 366646 MW; 9F99AFA4988BF27D0 CRC64;

Query Match 83.0%; Score 2441; DB 2; Length 3333;
 Best Local Similarity 81.9%; Pred. No. 7.1e-157;
 Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;
 QY 1 MRFNGSGVVRRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYILGNKQASKDYIG 60

Db 2391 MRPNGSGVAVRLPNDLEDKGTSLSLFLQRPNSRNGENTEMFMVLTGKNDASRDYIG 2450
 QY 61 MAVVDQGLTCVYNIADREARVQIDQVLTSESGQAVMDRVKFORIYQFAMNTYKATSN 120
 Db 2451 MAVVDQGLTCVYNIADREARVQIDQVLTSESGQAVMDRVKFORIYQFAMNTYKATSN 2510
 QY 121 KPRAPAVYDLEGSSNTLLNLPEDNAVPPYVGGYPPPELPRLRFPFYKCIETLDLNN 180
 Db 2511 KPEPVPYDMDGNSNTLLNLPENVPYVGGYPPPELPRLRFPFYKCIETLDLNN 2570
 QY 181 VLSLVNFKTTPNNTTEVEPCRRRKEESDKNVEGQVARIPIQPAAPPNFQITQTV 240
 Db 2571 VLSLVNFKTTPNNTTEVEPCRRRKEESDKNVEGQVARIPIQPAAPPNFQITQTV 2630
 QY 241 DRGLLFFAENODNFISLNTEDGNMRYKLNSEPPKRGIDRTINDGKHSILITIGKQ 300
 Db 2631 DRGLLFFAENODNFISLNTEDGNMRYKLNSEPPKRGIDRTINDGKHSILITIGKQ 2690
 QY 301 KRMWIVNERSVRIEGBIIPDFSTYYIGIPIAIRFPNISTPAFQCMKRLKKTSGVRL 360
 Db 2691 KRMWIVNERSVRIEGBIIPDFSTYYIGIPIAIRFPNISTPAFQCMKRLKKTSGVRL 2750
 QY 361 NDVVGATKCSSEDMKLVRTASFSRGGOMFTNLDPVSTDRFQSLSPGFQFPQSGTLLNHQ 420
 Db 2751 NDVVGATKCSSEDMKLVRTASFSRGGOMFTNLDPVSTDRFQSLSPGFQFPQSGTLLNHQ 2810
 QY 421 TRTSSLVLTLEDGHIETSDSNIPFKSPGYMDGLMHRVYSIDTSGRLIIDQVLR 480
 Db 2811 TRTSSLVLTLEDGHIETSDSNIPFKSPGYMDGLMHRVYSIDTSGRLIIDQVLR 2870
 QY 481 RNORLPSFSAQSLRLGGHFGCISNVLVQRFSSPEVLDIASSTKXKSLGSCSIN 540
 Db 2871 NSRKLRIHSSRSQSLRLGGHFGCISNVLVQRFSSPEVLDIASSTKXKSLGSCSIN 2930
 QY 541 KPEFLMLFKSPKFKNGRIFFNVOL 565
 Db 2931 KPEFLMLFKSPKFKNGRIFFNVOL 2995
 QY 565 KPEFLMLFKSPKFKNGRIFFNVOL 565
 Db 2995 KPEFLMLFKSPKFKNGRIFFNVOL 2995

RESULT 6

LMA3_HUMAN STANDARD; PRT; 1713 AA.
 ID LMA3_HUMAN STANDARD; PRT; 1713 AA.
 AC Q16787; Q13679; Q13680;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE laminin alpha-3 chain precursor (Epiligrin 170 kDa subunit) (E170)
 GN (Nuclein alpha subunit).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Keratinocytes;
 RX MEDLINE=94357926; PubMed=8077230;
 RA Ryan M.C., Tizard R., Vandevanter D.R., Carter W.G.;
 RT "Cloning of the lama3 gene encoding the alpha 3 chain of the adhesive
 RT ligand epiligrin. Expression in wound repair.";
 RL J. Biol. Chem. 269:22779-22787 (1994).
 RN [2]
 RP SEQUENCE OF 1-1331 FROM N.A. (ISOPFORMS A AND B).
 RX MEDLINE=96163880; PubMed=8586427;
 RA Vidal F., Baudoin C., Miguel C., Galliano M.-F., Christiano A.M.,
 RA Uitto J., Ottome J.-P., Meneguzzi G.;
 RT "Cloning of the laminin alpha 3 chain gene (LAMA3) and identification
 RT of a homozygous deletion in a patient with Herlitz junctional
 RT epidermolysis bullosa.";
 RL Genomics 30:273-280 (1995).
 RN [3]
 RP DISEASE.
 RX PubMed=12915477; DOI=10.1093/hmg/ddg234;

RA Irwin McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Melleiro J.E., Ashton G.S.,
 RA Dopping-Hepenstall P.J.H., Bady R.A.J., Jamlin T., Phillips R.J.,
 RA Shabir S.G., Haeon T.S., Khurshid K., Moore J.E., Page B.,
 RA Darling J., Acheron D.J., Van Steensel M.A.M., Munro C.S.,
 RA Smith P.J.D., McGrath J.A.;
 RT "An unusual N-terminal deletion of the laminin alpha3a isoform leads
 RT to the chronic granulation tissue disorder laryngo-oncho-cutaneous
 RT syndrome.";
 RL Hum. Mol. Genet. 12:2395-2409 (2003).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
 CC via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-
 CC 6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
 CC phosphorylation of p125-Fak and p80, (3) differentiation of
 CC keratinocytes.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end. The alpha-3 chain is a subunit of laminin-5
 CC (epiligrin/kalium/nicein), and possibly also a component of
 CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Bient-Alternative splicing; Named isoforms=2;
 CC Name=A;
 CC IsoId=Q16787-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=Q16787-2; Sequence=VSP_003037;
 CC Note-incomplete sequence;
 CC -1- TISSUE SPECIFICITY: Skin; respiratory, urinary, and digestive
 CC epithelia and in other specialized tissues with prominent
 CC secretory or protective functions. Epithelial basement membrane,
 CC and epithelial cell tongue that migrates into a wound bed. A
 CC differential and focal expression of the alpha-3 chain is observed
 CC in the CNS.
 CC -1- INDUCTION: Laminin-5 is up-regulated in wound sites of human skin.
 CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact
 CC with other laminin chains to form a coiled coil structure.
 CC -1- DOMAIN: Domain G is globular.
 CC -1- DISEASE: Defects in LAMA3 are a cause of junctional epidermolysis
 CC bullosa gravis (JEB) [MIM:226700]; also known as junctional
 CC epidermolysis bullosa Herlitz-Pearson type. JEB is a blistering
 CC disorder in skin that is characterized by a separation of basal
 CC cells from the basement membrane due to a decreased number of
 CC hemidesmosomes. Laminin-5 is missing from the basement membrane of
 CC patients with the gravis form of epidermolysis bullosa.
 CC -1- DISEASE: Defects in LAMA3 are the cause of laryngoonychocutaneous
 CC syndrome (LOCS) [MIM:245660]. LOCS is an autosomal recessive
 CC epithelial disorder confined to the Punjab Muslim population. The
 CC condition is characterized by cutaneous erosions, nail dystrophy
 CC and exuberant vascular granulation tissue in certain epithelia,
 CC especially conjunctiva and larynx.
 CC -1- SIMILARITY: Contains 3 laminin EGF-like domains.
 CC -1- SIMILARITY: Contains 5 laminin G-like domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; I34155; AAA59483.1; -
 DR EMBL; X85107; CAA59428.1; -
 DR EMBL; X85108; CAA59429.1; -
 DR PIR; A55347; A55347.

DR HSSP; P02468; INPE.
 DR Genew; HGNC:6483; LAMA3.
 DR MIM; 608085; -.
 DR MIM; 226700; -.
 DR MIM; 245660; -.
 DR GO; GO:0005604; C:basement membrane; TAS.
 DR GO; GO:0008544; P:epidermal differentiation; TAS.
 DR InterPro; IPR008985; Cna1-like_1ec_g1.
 DR InterPro; IPR006209; EGF-like_recept.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR009254; Laminin_I.
 DR InterPro; IPR003037; Laminin_II.
 DR InterPro; IPR003129; TSP_N.
 DR Pfam; PF00053; Laminin_EGF; 2.
 DR Pfam; PF00054; Laminin_G; 2.
 DR Pfam; PF06008; Laminin_I; 1.
 DR Pfam; PF06009; Laminin_II; 1.
 DR PROSITE; PS00023; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01248; LAMININ_TYRP_EGF; 2.
 DR PROSITE; PS50025; LAM G DOMAIN; 5.
 KM Alternative splicing; Basement membrane; Cell adhesion; Coiled coil;
 KM Epidermolysis bullosa; Extracellular matrix; Glycoprotein;
 KM Laminin EGF-like domain; Repeat; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 1713
 FT DOMAIN 46 201
 FT DOMAIN 67 113
 FT DOMAIN 114 166
 FT DOMAIN 167 185
 FT DOMAIN 186 769
 FT DOMAIN 770 971
 FT DOMAIN 978 1140
 FT DOMAIN 1147 1307
 FT DOMAIN 1366 1530
 FT DOMAIN 1537 1710
 FT DOMAIN 231 327
 FT DOMAIN 396 548
 FT DOMAIN 594 621
 FT DOMAIN 702 765
 FT DOMAIN 1686 1713
 FT DISULFID 67 76
 FT DISULFID 69 83
 FT DISULFID 86 95
 FT DISULFID 98 111
 FT DISULFID 114 126
 FT DISULFID 116 135
 FT DISULFID 137 146
 FT DISULFID 149 164
 FT DISULFID 202 202
 FT DISULFID 205 205
 FT SITE 658 660
 FT CARBOHYD 542 542
 FT CARBOHYD 645 645
 FT CARBOHYD 745 745
 FT CARBOHYD 882 882
 FT CARBOHYD 964 964
 FT CARBOHYD 1108 1108
 FT CARBOHYD 1131 1131
 FT CARBOHYD 1325 1325
 FT CARBOHYD 1477 1477
 FT CARBOHYD 1667 1667
 FT VARSPLIC 1 45
 FT FT 5 5
 FT CONFLICT 123 125
 FT CONFLICT 481 481

IT CONFLICT 754 754 R -> L (in Ref. 2).
 IT CONFLICT 969 969 E -> Q (in Ref. 2).
 IT CONFLICT 1052 1052 D -> A (in Ref. 2).
 IT CONFLICT 1184 1184 G -> A (in Ref. 2).
 SQ SEQUENCE 1713 AA; 189304 MW; 45E9BE1017B60D3 CXC64;
 Query Match 83.0%; Score 2439; DB 1; Length 1713;
 Best Local Similarity 81.9%; Pred. No. 3,8e-157;
 Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;
 QY 1 MRENGSGVVRLLPNLDELKGYTSLFLQRPDLRNGSTDMFVNTLGNKASKDYIG 60
 DB 771 MRENGSGVVRLLPNLDELKGYTSLFLQRPDLRNGSTDMFVNTLGNKASKDYIG 830
 QY 61 MAVVDQLTCVYMLGPREAEVQIDVLTSESEBAVMDRKRRIQAPALNTKATSN 120
 DB 831 MAVVDQLTCVYMLGPREAEVQIDVLTSESEBAVMDRKRRIQAPALNTKATSN 890
 QY 121 KPRAPAVYDLGGSSNTLNLADPEDAVFYGYGPPDFELPSRLRFPYKGCIELDLNEN 180
 DB 891 KPRTPGVYDMGKNSNTLNLADPENAVFYGYGPPDFELPSRLRFPYKGCIELDLNEN 950
 QY 181 VLSLVNFKTFFNLNTEVEPCRRRKESSDKNYEGTGYARIPQNPAPFENFQTIQTV 240
 DB 951 VLSLVNFKTFFNLNTEVEPCRRRKESSDKNYEGTGYARIPQNPAPFENFQTIQTV 1010
 QY 241 DRGLLTPAENQDNFISLNIHDKMLNRYKLNSEPPREKGIKIDITNGKHSILITGKIQ 300
 DB 1011 DRGLLTPAENQDNFISLNIHDKMLNRYKLNSEPPREKGIKIDITNGKHSILITGKIQ 1070
 QY 301 KRMWVNVSRVIBSGIFPFSTYYIGTPIAIRFPNISTPAPFGCMKMLKKTSGVRL 360
 DB 1071 KRMWVNVSRVIBSGIFPFSTYYIGTPIAIRFPNISTPAPFGCMKMLKKTSGVRL 1130
 QY 361 NDTVGYTKKCSBDKLVRTASFSRGGQMSFTNLDVSTGRFQSPGFQPSGTLNLHQ 420
 DB 1131 NDTVGYTKKCSBDKLVRTASFSRGGQMSFTNLDVSTGRFQSPGFQPSGTLNLHQ 1190
 QY 421 TRTSLLVTEDEGHILSTDSNIPFKSGPTMDGLLHVSVYISDTSGRLIDDOVLR 480
 DB 1191 TRTSLLVTEDEGHILSTDSNIPFKSGPTMDGLLHVSVYISDTSGRLIDDOVLR 1250
 QY 481 RNORLPFSNAOQSLGLGGHPEGCSNLYVORFSSQSPETLDLASKSTKDKASIGGCSLN 540
 DB 1251 RNORLPFSNAOQSLGLGGHPEGCSNLYVORFSSQSPETLDLASKSTKDKASIGGCSLN 1310
 QY 541 KPPEFLMFKSPKRFNKRIFNVNQL 565
 DB 1311 KPPEFLMFKSPKRFNKRIFNVNQL 1335
 RESULT 7
 ID 096TGO PRELIMINARY; PRT; 1806 AA.
 AC 096TGO;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DB Alpha 3B chain of laminin-5 (Fragment).
 GN Name=LAMA3;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Aberdam D., Vidal, Baudoin, Miguel, Otrone, Meneguzzi;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X84900; CA459325.1; -.
 DR HSSP; P02468; INPE.
 DR GO; GO:0005606; C:laminin-1; IBA.
 DR GO; GO:0005102; F:receptor binding; IBA.
 DR GO; GO:0005198; F:structural molecule activity; IBA.

DR GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR GO; GO:0030334; P:regulation of cell migration; IEA.
DR GO; GO:0045995; P:regulation of embryonic development; IEA.
DR InterPro; IPR001844; Chaprinin Cpn60.
DR InterPro; IPR008985; ConA_like_1ec_g1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00052; Laminin_B; 1.
DR Pfam; PF00053; Laminin_EGF; 2.
DR Pfam; PF02210; Laminin_G_2; 4.
DR Pfam; PF06008; Laminin_I; 1.
DR Pfam; PF06009; Laminin_II; 1.
DR ProDom; PD003031; Laminin_B; 1.
DR SMART; SM00180; EGF_Lam; 2.
DR SMART; SM00281; Lamb; 1.
DR SMART; SM00282; LamG; 5.
DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW Laminin EGF-like domain.
FT NON TER 1 1
SQ SEQUENCE 1806 AA; 199411 MW; EF94CDE2A52B93 CRC64;

Query Match 83.0%; Score 2439; DB 2; Length 1806;
Best Local Similarity 81.9%; Pred. No. 4.1e-157;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRFNKGSGVEVRLPNLDELKGYTSLSLFLQRPDLRENGGTREMPVMTLGNKQASRDYIG 60
DB 864 MRFNKGSGVEVRLPNLDELKGYTSLSLFLQRPNSRNGGTREMPVMTLGNKQASRDYIG 923
QY 61 MAVVDQGLTCVYMLGDRREAVQIDVLTSESOEAVMDRVKFORIYQFAKNTYTKATSN 120
DB 924 MAVVDQGLTCVYMLGDRREAVQIDVLTSESOEAVMDRVKFORIYQFAKNTYTKATSN 983
QY 121 KPPAPAVYDIEGSSNTLNLDPEDAVFYVGYPPPELPSRLRPPTYKGCIELDLNEN 180
DB 984 KPPAPAVYDIEGSSNTLNLDPEDAVFYVGYPPPELPSRLRPPTYKGCIELDLNEN 1043
QY 181 VLSVYFKTPTNLTTEVERECRRKESDKNYEGGYARIPQOPNAPFNFIQTITQTV 240
DB 1044 VLSVYFKTPTNLTTEVERECRRKESDKNYEGGYARIPQOPNAPFNFIQTITQTV 1103
QY 241 DRGLTFPAENQDNFISLNIEDGNLMVRYKLSNBPYKRGIRDTINDGKHSILITIGKIQ 300
DB 1104 DRGLTFPAENQDNFISLNIEDGNLMVRYKLSNBPYKRGIRDTINDGKHSILITIGKIQ 1163
QY 301 KRMWIVNERSVRIEGEIPDFSTYYIAGPIAIRERFNISTPAFGCMKMLKKTSGVRL 360
DB 1164 KRMWIVNERSVRIEGEIPDFSTYYIAGPIAIRERFNISTPAFGCMKMLKKTSGVRL 1223
QY 361 NDTVGATKCKSEBWKLVRTASFSGQMSFTINDVSTDRFQLSRFGQTFQSGTILANQ 420
DB 1224 NDTVGATKCKSEBWKLVRTASFSGQMSFTINDVSTDRFQLSRFGQTFQSGTILANQ 1283
QY 421 TRTSLLVLTLEDGHEISTSDSNIPFESPGTYMDGLLHHVSYISPTSGLRLLIDDOVR 480
DB 1284 TRTSLLVLTLEDGHEISTSDSNIPFESPGTYMDGLLHHVSYISPTSGLRLLIDDOVR 1343
QY 481 RNORLPSFSAQOSLRIGGHEGCTISNVLVQFSGSEVVLDAASKTKKDAAGGCSIN 540
DB 1344 RNORLPSFSAQOSLRIGGHEGCTISNVLVQFSGSEVVLDAASKTKKDAAGGCSIN 1403
QY 541 KPPFLMLFKSPKPKFKGRIFNNQOL 565
DB 1404 KPPFLMLFKSPKPKFKGRIFNNQOL 1428

RESULT 8

ID Q76E14 PRELIMINARY; PRT; 3333 AA.

AC Q76E14; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Laminin alpha 3b chain.
GN Name=LAMA3

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RT [1]

RP SEQUENCE FROM N.A.
RA Kariya Y., Yasuda C., Nakashima Y., Ishida K., Tsubota Y.,
RA Miyazaki K.;
RT "Characterization of laminin 5B and NH2-terminal proteolytic fragment
RT of its alpha3b chain: promotion of cellular adhesion, migration, and
RT proliferation.";
RL J. Biol. Chem. 279:24774-24784(2004).

DR EMBL; AB107369; BAD13428.1; -;
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005606; C:laminin-1; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0030155; P:regulation of cell adhesion; IEA.
DR GO; GO:0030334; P:regulation of cell migration; IEA.
DR GO; GO:0045995; P:regulation of embryonic development; IEA.
DR InterPro; IPR001844; Chaprinin Cpn60.
DR InterPro; IPR008985; ConA_like_1ec_g1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR008211; Laminin_N.
DR InterPro; IPR003129; TSP_N.

DR Pfam; PF00052; Laminin_B; 1.
DR Pfam; PF00053; Laminin_EGF; 8.
DR Pfam; PF02210; Laminin_G_2; 4.
DR Pfam; PF06008; Laminin_I; 1.
DR Pfam; PF06009; Laminin_II; 1.
DR Pfam; PF00055; Laminin_N; 1.
DR PRINTS; PR00011; EGF/LAMININ.
DR ProDom; PD003031; Laminin_B; 1.
DR SMART; SM00180; EGF; 8.
DR SMART; SM00181; EGF_Lam; 14.
DR SMART; SM00281; Lamb; 1.
DR SMART; SM00282; LamG; 5.
DR SMART; SM00136; LamT; 1.
DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; 12.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 13.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW Laminin EGF-like domain.

SQ SEQUENCE 3333 AA; 366616 MW; 6F99AF4D4B99FCB0 CRC64;
Query Match 83.0%; Score 2439; DB 2; Length 3333;
Best Local Similarity 81.9%; Pred. No. 9.7e-157;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRFNKGSGVEVRLPNLDELKGYTSLSLFLQRPDLRENGGTREMPVMTLGNKQASRDYIG 60
DB 2391 MRFNKGSGVEVRLPNLDELKGYTSLSLFLQRPNSRNGGTREMPVMTLGNKQASRDYIG 2450
QY 61 MAVVDQGLTCVYMLGDRREAVQIDVLTSESOEAVMDRVKFORIYQFAKNTYTKATSN 120


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Db 2451 MAVVDGQLTCVYNLGDREAEIQVDQILTKSETKEAAMDVKFQRIYQFARLNTYKATSS 2510
QY 121 KPRAPAVYDLGGSSNTLNLDPEDAVFYVGGYPPDELSRLRPPYKGCIELDLNEN 180
Db 2511 KPEPVGVDMDGRNSNTLNLDPENNVFVYGGYPPDELSRLRPPYKGCIELDLNEN 2570
QY 181 VLSLYNFKTFTNLTTEVEPCRRKESDKNYFEGTGYARIPTQPNAPFPNFIOITQTV 240
Db 2571 VLSLYNFKTFTNLTTEVEPCRRKESDKNYFEGTGYARIPTQPNAPFPNFIOITQTV 2630
QY 241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEBPKEGIRDTINDKHSILITGKLQ 300
Db 2631 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEBPKEGIRDTINDKHSILITGKLQ 2690
QY 301 KRWMINVNSVRIEGEIPDPSTYYLGIPAIARERNISTPAPOGCKMLKKTSGVRL 360
Db 2691 KRWMINVNDVNTIIDGVFDPSTYYLGIPAIARERNISTPAPOGCKMLKKTSGVRL 2750
QY 361 NDVTGYTKKSEBMDKLVRTASFSRGGOMSFNTLDVPTDRFOLSFGFOTPOSGTLNHQ 420
Db 2751 NDVTGYTKKSEBMDKLVRTASFSRGGOMSFNTLDVPTDRFOLSFGFOTPOSGTLNHQ 2810
QY 421 TRTSLLVLTLEDGHIELSTDSNIPFKSPGYMDGLHVSYSIDTSGLRLIDQVLR 480
Db 2811 TWTRNLQVLTLEDGHIELSTDSNIPFKSPGYMDGLHVSYSIDTSGLRLIDQVLR 2870
QY 481 RNQRLPSFNAQSLRGSGHFECCISNVLVORFSGSEVLDLASKSTKQDASLGCSLN 540
Db 2871 NSRKLKHISSRSQSLRGSGHFECCISNVLVORFSGSEVLDLASKSTKQDASLGCSLN 2930
QY 541 KPPELMLFKSPKRPKNKRIFNVNQ 565
Db 2931 KPPELMLFKSTLRNKTKTRINQL 2955

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RESULT 9

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ID 0867A1 PRELIMINARY; PRT; 1725 AA.
AC 0867A1;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Laminin alpha 3 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Placentalia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Spirito F., Capri A., Guagnere E., Ottome J.-P., Meneguzzi G.,
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF236865; AAL54876.1; -.
DR HSSP; P11209; IG2C.
DR GO; GO:0005066; C:laminin-1; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0030343; P:regulation of cell adhesion; IEA.
DR GO; GO:0030344; P:regulation of cell migration; IEA.
DR GO; GO:0045995; P:regulation of embryonic development; IEA.
DR Interpro; IPR006985; Cona_like_1ec_g1.
DR Interpro; IPR006208; EGF_Like.
DR Interpro; IPR002049; Laminin_EGF.
DR Interpro; IPR001791; Laminin_G.
DR Interpro; IPR009254; Laminin_I.
DR Interpro; IPR010307; Laminin_II.
DR Interpro; IPR003129; TSP_N.
DR Pfam; PF00053; Laminin_EGF; 2.
DR Pfam; PF02210; Laminin_G_2; 4.
DR Pfam; PF06008; Laminin_I; 1.
DR Pfam; PF06009; Laminin_II; 1.
DR SMART; SM00180; EGF Dom; 2.
DR SMART; SM00282; LamG; 5.

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DR PROSITE; PS00022; EGF 1; 1.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS01248; LAMININ TYPE EGF; 2.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
FW Laminin EGF-like domain.
PT NON TER 1725 1725
SQ SEQUENCE 1725 AA; 191053 MW; DF1EB0E1FB5134C CRC64;

Query Match 75.7%; Score 2224.5; DB 2; Length 1725;
Best Local Similarity 75.0%; Pred. No. 1.0e-142;
Matches 423; Conservative 60; Mismatches 80; Indels 1; Gaps 1;

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QY 1 MRENGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTDMFVYLGKNDKADYIG 60
Db 782 MRENGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGTDMFVYLGKNDKADYIG 841
QY 61 MAVVDGQLTCVYNLGDREAEIQVDQILTKSETKEAAMDVKFQRIYQFARLNTYKATSN 120
Db 842 MAVVDGQLTCVYNLGDREAEIQVDQILTKSETKEAAMDVKFQRIYQFARLNTYKATSS 901
QY 121 KPRAPAVYDLGGSSNTLNLDPEDAVFYVGGYPPDELSRLRPPYKGCIELDLNEN 180
Db 902 KPRAPAVYDLGGSSNTLNLDPEDAVFYVGGYPPDELSRLRPPYKGCIELDLNEN 961
QY 181 VLSLYNFKTFTNLTTEVEPCRRKESDKNYFEGTGYARIPTQPNAPFPNFIOITQTV 240
Db 962 VLSLYNFKTFTNLTTEVEPCRRKESDKNYFEGTGYARIPTQPNAPFPNFIOITQTV 1021
QY 241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEBPKEGIRDTINDKHSILITGKLQ 300
Db 1022 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEBPKEGIRDTINDKHSILITGKLQ 1081
QY 301 KRWMINVNSVRIEGEIPDPSTYYLGIPAIARERNISTPAPOGCKMLKKTSGVRL 360
Db 1082 KRWMINVNSVRIEGEIPDPSTYYLGIPAIARERNISTPAPOGCKMLKKTSGVRL 1141
QY 361 NDVTGYTKKSEBMDKLVRTASFSRGGOMSFNTLDVPTDRFOLSFGFOTPOSGTLNHQ 420
Db 1142 NDVTGYTKKSEBMDKLVRTASFSRGGOMSFNTLDVPTDRFOLSFGFOTPOSGTLNHQ 1201
QY 421 TRTSLLVLTLEDGHIELSTDSNIPFKSPGYMDGLHVSYSIDTSGLRLIDQVLR 480
Db 1202 TRTSLLVLTLEDGHIELSTDSNIPFKSPGYMDGLHVSYSIDTSGLRLIDQVLR 1260
QY 481 RNQRLPSFNAQSLRGSGHFECCISNVLVORFSGSEVLDLASKSTKQDASLGCSLN 540
Db 1261 RNQRLPSFNAQSLRGSGHFECCISNVLVORFSGSEVLDLASKSTKQDASLGCSLN 1320
QY 541 KPPELMLFKSPKRPKNKRIFNVNQ 564
Db 1321 KPPELMLFKSTLRNKTKTRINQL 1344

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RESULT 10

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ID LMA5_HUMAN STANDARD; PRT; 3695 AA.
AC O15230; Q8WZ77; Q9H1PL;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Laminin alpha-5 chain precursor.
GN Name=LMA5; Synonyms=KIAA0533, KIAA1907;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,

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RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.B., Connor R.E., Corby N.R.,
 RA Coulson A., Cowille G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafton D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jokusch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Levesajohn M.H., Leverhulme M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McElroy K., McMurray A.A.,
 RA Milne S.A., Mistry A.D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prachalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.B., Sehra H.K., Showkseen R., Sims S.,
 RA Stuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.W.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilmshurst L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.,
 RT "The DNA sequence and comparative analysis of human chromosome 20.",
 RL Nature 414:865-871(2001).
 [2]
 RP SEQUENCE OF 197-1934 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=21456161; PubMed=11572484;
 RA Nagase T., Kikuno R., Ohara O.,
 RT "Prediction of the coding sequences of unidentified human genes. XXI.
 RT The complete sequences of 60 new cDNA clones from brain which code for
 RT large proteins.",
 RL DNA Res. 8:179-187(2001).
 [3]
 RP SEQUENCE OF 2051-3695 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98280545; PubMed=9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.,
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.",
 RL DNA Res. 5:31-39(1998).
 [4]
 RP SEQUENCE OF 2743-3695 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97415425; PubMed=9271224; DOI=10.1016/S0014-5793(97)00686-8;
 RA Durkin M.E., Loeschel F., Mattei M.-G., Gilpin B.J., Albrechtsen R.,
 RA Wever U.M.,
 RT "Tissue-specific expression of the human laminin alpha5-chain, and
 RT mapping of the gene to human chromosome 20q13.2-13.3 and to distal
 RT mouse chromosome 2 near the locus for the ragged (Ra) mutation.",
 RL PNAS Lett. 411:296-300(1997).
 [5]
 RP EXPRESSION IN RETINA.
 RX MEDLINE=20422761; PubMed=10964957;
 RA Libby R.T., Champiand M.-F., Claudepierre T., Xu Y., Gibbons E.P.,
 RA Koch M., Burgeson R.R., Hunter D.D., Brunken W.J.,
 RT "Laminin expression in adult and developing retinae: evidence of two
 RT novel CNS laminins.",
 RL J. Neurosci. 20:6517-6528(2000).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin-5 complex is an heterotrimer composed of three
 CC chains (alpha-5/beta-2/gamma-3) which are bound to each other by
 CC disulfide bonds into a cross-shaped molecule comprising one long
 CC and three short arms with globules at each end.
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -1- TISSUE SPECIFICITY: Expressed in heart, lung, kidney, skeletal
 CC muscle, pancreas, retina and placenta. Little or no expression in
 CC brain and liver.

CC -1- DOMAIN: Domain G is globular and is part of the major cell-binding
 CC site located in the long arm of the laminin heterotrimer.
 CC -1- SIMILARITY: Contains 22 laminin EGF-like domains.
 CC -1- SIMILARITY: Contains 5 laminin G-like domains.
 CC -1- SIMILARITY: Contains 1 laminin IV domains.
 CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, AL354836; CAC22309.1; AL7_SEQ.
 DR EMBL, AL354836; CAC2230.1; -.
 DR EMBL, AB067494; BAB67800.1; -.
 DR EMBL, AB011105; BAA25459.1; -.
 DR HSSP, Z95636; CAB09137.1; -.
 DR HSSP, P02468; INPE.
 DR Genew; HGNC:6485; LAMV5.
 DR MIM; 601033; -.
 DR InterPro; IPR008985; ConA_like_jec_g1.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR000034; Laminin_B.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR009254; Laminin_I.
 DR InterPro; IPR010307; Laminin_II.
 DR InterPro; IPR008211; Laminin_N.
 DR InterPro; IPR008212; Lam_N2.
 DR InterPro; IPR003129; TSP_N.
 DR Pfam; PF000052; Laminin_B_1.
 DR Pfam; PF000053; Laminin_EGF_18.
 DR Pfam; PF000054; Laminin_EGF_2.
 DR Pfam; PF06008; Laminin_I_1.
 DR Pfam; PF06009; Laminin_I_2.
 DR Pfam; PF06009; Laminin_II_1.
 DR Pfam; PF00055; Laminin_N_1.
 DR PRINTS; PRO0011; EGF_LAMININ.
 DR ProDom; PD003031; Laminin_B_1.
 DR PROSITE; PS00022; EGF_1; 19.
 DR PROSITE; PS01248; EGF_2; 3.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
 DR PROSITE; PS50025; LAM_G_DOMAIN_5.
 KW Basement membrane; Cell adhesion; Coiled coil; Extracellular matrix;
 KW Glycoprotein; Laminin EGF-like domain; Repeat; Signal.
 FT SIGNAL 1 35
 FT CHAIN 36 3695
 FT DOMAIN 36 299 Laminin N-terminal (domain VI).
 FT DOMAIN 300 358 Laminin EGF-like 1.
 FT DOMAIN 359 428 Laminin EGF-like 2.
 FT DOMAIN 429 474 Laminin EGF-like 3.
 FT DOMAIN 494 540 Laminin EGF-like 4.
 FT DOMAIN 541 586 Laminin EGF-like 5.
 FT DOMAIN 587 631 Laminin EGF-like 6.
 FT DOMAIN 632 676 Laminin EGF-like 7.
 FT DOMAIN 677 722 Laminin EGF-like 8.
 FT DOMAIN 723 775 Laminin EGF-like 9.
 FT DOMAIN 776 828 Laminin EGF-like 10.
 FT DOMAIN 829 850 Laminin EGF-like 11 (incomplete).
 FT DOMAIN 851 1437 Laminin domain IV 1 (domain IV B).
 FT DOMAIN 1438 1483 Laminin EGF-like 12.
 FT DOMAIN 1484 1527 Laminin EGF-like 13.
 FT DOMAIN 1528 1576 Laminin EGF-like 14.
 FT DOMAIN 1577 1627 Laminin EGF-like 15.
 FT DOMAIN 1628 1637 Laminin EGF-like 16 (N-terminal).
 FT DOMAIN 1638 1830 Laminin domain IV 2 (domain IV A).
 FT DOMAIN 1831 1863 Laminin EGF-like 16 (C-terminal).
 FT DOMAIN 1864 1912 Laminin EGF-like 17.
 FT DOMAIN 1913 1968 Laminin EGF-like 18.

FT DOMAIN 1969 2022 Laminin EGF-like 19.
FT DOMAIN 2023 2069 Laminin EGF-like 20.
FT DOMAIN 2070 2116 Laminin EGF-like 21.
FT DOMAIN 2117 2166 Laminin EGF-like 22.
FT DOMAIN 2167 2735 Laminin I and I.
FT DOMAIN 2167 2735 Laminin G-like 1.
FT DOMAIN 2292 2941 Laminin G-like 2.
FT DOMAIN 2941 3115 Laminin G-like 3.
FT DOMAIN 3124 3292 Laminin G-like 4.
FT DOMAIN 3340 3513 Laminin G-like 5.
FT DOMAIN 3520 3692 Laminin G-like 5.
FT DOMAIN 2203 2221 Coiled coil (Potential).
FT DOMAIN 2335 2466 Coiled coil (Potential).
FT DOMAIN 2510 2670 Coiled coil (Potential).
FT DOMAIN 1722 1724 Cell attachment site (Potential).
FT SITE 1838 1840 Cell attachment site (Potential).
FT DISULFID 300 309 By similarity.
FT DISULFID 302 322 By similarity.
FT DISULFID 324 333 By similarity.
FT DISULFID 336 356 By similarity.
FT DISULFID 359 368 By similarity.
FT DISULFID 361 393 By similarity.
FT DISULFID 396 405 By similarity.
FT DISULFID 408 426 By similarity.
FT DISULFID 429 440 By similarity.
FT DISULFID 431 447 By similarity.
FT DISULFID 449 458 By similarity.
FT DISULFID 461 471 By similarity.
FT DISULFID 494 506 By similarity.
FT DISULFID 517 526 By similarity.
FT DISULFID 529 538 By similarity.
FT DISULFID 541 553 By similarity.
FT DISULFID 543 560 By similarity.
FT DISULFID 562 571 By similarity.
FT DISULFID 574 584 By similarity.
FT DISULFID 587 599 By similarity.

Query Match 24.2%; Score 712; DB 1; Length 3695;

Best Local Similarity 33.1%; Pred. No. 6.4e-35; Matches 194; Conservative 96; Mismatches 214; Indels 82; Gaps 21;

1 MRFGKSGVEVRLDNDLEDKGYTSLFLQRPDLRENGGTEDEFWYVYLNKNGKSKOYIG 60
2737 MKRGRSGVQRTPRDLADLAATYALKFYLOGPPEGQTEDEFWYVYVMTSGKATGYMG 2796
61 MAVVDGQLTCVYNGDR-EAEVQIDQVLTSESGEAVMDRVKQRIYQPAKANTYKE--- 116
2797 VSLRDKKVMHYVQGEAGPAVLSTIDEDIGEO-----FAAVSLDRITLQFGHMSVTVRKM 2850
117 --ATSKPKAPAYVDLEGGSSNTLANTDPEDAVYVGGYPPDFELPSRLRPPYKGCIEL 174
2851 IORFKGDTVAPGA---EG-----LANTRPDPFVYVGGYSTFPPLLPFGYRGCIEM 2902
175 DDLNENVLSTYNTKTEFNLTTEVBPGRREK-----SDKNYEGTGVARIPTQPN-AP 228
2903 DTLNBEVAVSLYNTFRITQLDANDRPAKRSKSTGDPMLTDSYIDGFAKISDSQIST 2962
229 FPNFIQTLQTTVDKGLLFAENQDNFTSLNIEDGNLWVRYKANS-----EPP----- 275
2963 TKRPEGLRLVSVSGVFLPKQSQOFLCLAVQBSLVLLVDFGAKKAVPLQPPPLTS 3022
276 KKKIRITINDGKDHSLITITGKQKGMVNVN---SVRISEITDFSTYYIGI--- 329
3023 ASKAIQ-----VFLGSGRKRVLVREBATAVYVSEQDNDLEADAYVYGGVPPD 3071
330 --PFAIRERFNISTPAFGCKMKNL--KTSGVRLNDYTVYTKKSGDMVLVTASFSR 384
3072 QLPSPSLMWRP-TGGSVRGCKYKALKAGKYVDLRLN-TTGVASGCTRADLLVGAMTFHG 3129
385 GG--QMSFTNLDVSTDRPOLSPFGQTFQPSGTLNQTRTSLVLTLEDGHIELSTRDS 442
3130 HGFLRLALSNV-ADLTGVVYSGFGFHSADQSALLYTRASPDGLQGVSLQGRVSLQTLRT 3188

443 NIPFSGPGTYMDGLAHNVSVISDTSGRLRLIDDV--LRNRQLPSPFNAQOS---LR 496
3189 EV---KTQAGFADGAPHYVAFYSNATGCVWLTVYDDQLQGMCPHSGPPELQPPGPPRL 3245
497 LGG-----GHFEGCISNVLVQPSQSPFVLDLASKSTYKCDASLG 535
3246 LGGLPESGRTYNSFGCSISNVFQRLLCQKRVFPLQOQMGVNVSTG 3291
RESULT 11
Q8TDF8
ID O8TDF8 PRELIMINARY; PRT; 3695 AA.
AC O8TDF8
DT 01-JUN-2002 (TREMURel. 21, Created)
DT 01-JUN-2002 (TREMURel. 21, Last sequence update)
DT 01-MAR-2004 (TREMURel. 26, Last annotation update)
DE Laminin alpha5 chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21935381; Pubmed=11821406; DOI=10.1074/jbc.M11228200;
RA Doi M., Thyboll J., Kortsema J., Jansson K., Iivanainen A.,
RA Parvardeh M., Timpl R., Hedin U., Swedenborg J., Trygsvason K.,
RT "Recombinant human laminin-10 (alpha5beta3gamma1). Production,
RT purification, and migration-promoting activity on vascular endothelial
RT cells.";
RT J. Biol. Chem. 277:12741-12748 (2002).
DR EMBL; AF443072; AAM12527.1; -.
DR HSSP; P02468; INPB.
DR GO; GO:0005605; C:basal lamina; NAS.
DR GO; GO:0005178; F:structural molecule activity; IC.
DR GO; GO:0001525; P:angiogenesis; NAS.
DR GO; GO:0016477; P:cell migration; IDA.
DR GO; GO:0008283; P:cell proliferation; NAS.
DR GO; GO:0008037; P:cell recognition; NAS.
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; NAS.
DR GO; GO:00049790; P:embryonic development; NAS.
DR GO; GO:0045446; P:endothelial cell differentiation; NAS.
DR GO; GO:0048041; P:focal adhesion formation; NAS.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IMP.
DR InterPro; IPR008985; ConA-like_1ec_91.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR009030; Grow fac_recept.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR008211; Laminin_N.
DR InterPro; IPR001638; SBP_bac_3.
DR InterPro; IPR001368; TNFR_c6.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00052; Laminin_EGF_1.
DR Pfam; PF00053; Laminin_EGF_20.
DR Pfam; PF02210; Laminin_G_2; 4.
DR Pfam; PF06008; Laminin_I_1.
DR Pfam; PF06009; Laminin_II_1.
DR Pfam; PF06010; Laminin_III_1.
DR Pfam; PF00055; Laminin_N_1.
DR PRINTS; PR00011; EGF_LAMININ.
DR ProDom; PD003031; Laminin_B_1.
DR SMART; SM00180; EGF_Lam; 20.
DR SMART; SM00281; LamG_1.
DR SMART; SM00282; LamG_5.
DR SMART; SM00136; LamG_1.
DR PROSITE; PS00022; EGF_1; 19.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01248; LAMININ TYPE EGF; 19.
DR PROSITE; PSS0025; LAM_G_DOMAIN; 5.

DR PROSITE; PS01039; SBP_BACTERIAL_3; UNKNOWN_1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 1.
 KM Laminin EGF-like domain; Signal.
 FT SIGNAL 1 35 Potential.
 FT CHAIN 36 3695 Laminin alpha5 chain.
 SQ SEQUENCE 3695 AA; 399645 MW; 69703852536E0A3 CRC64;

Query Match 24.2%; Score 712; DB 2; Length 3695;
 Best Local Similarity 33.1%; Pred. No. 6,4e-39;
 Matches 194; Conservative 96; Mismatches 214; Indels 82; Gaps 21;

QY 1 MRNNGSGVFRRLNDLEIKGTSLSLFLQRPDLNENGTEDMPVYLGAKDASDYIG 60
 DB 2737 MKENGSGVQLRTFRPDLADLAAYTALKFYLQGEPEPEPGQTEDEFVYMGSQATGDYNG 2796
 QY 61 MAVVDQGLTCVNLGDR-EAEVQIDQVLTSESGEAMDRVKQRILYQPAKNTYGE--- 116
 DB 2797 VSLDKKVMWVYQLGEGPAVLSIDEDIGQ-----FAAVSLDKTLQFGHMSVTVEROM 2850
 QY 117 --ATSNKPKAPAVYDLGGSSNTLNLNDPDAVFYVGGYPPDELPRLFPYKGCIEL 174
 DB 2851 IQETKGDVYAPGA---EG-----LNLNRPDPVYFYGGYSTTPPRLRFPGRGCIEM 2902
 QY 175 DDLNENVLSLYNKTFTNLTTEVEPCRRKEE---SDKNYFEETGYARIPQEN-AP 228
 DB 2903 DTLNEEVSLYNFERFTQDLTAVDPRCAKSTGTDPWLTGSGYLDGTGFARISFDSQISR 2962
 QY 229 FPHPIQITVTYRGILFPAENDNPISLNIEDGNLMVRKLS-----EPP----- 275
 DB 2963 TKRFEGLRLVSYSGVLFKQSQFLCAVQSGSLVLDFAGLKRAVLPQPPPLTS 3022
 QY 276 KKKGIDTINDKDHSLITIGLKQKMWNVNER---SVRIKEIFDFSTYIIGI--- 329
 DB 3023 ASKALQ-----VELLGSRRKRVLYVERATYVSQBNDLEADAYILGGVPP 3071
 QY 330 --DLAIRERNISTPAFQCGMKLK---KTSGVRLNDVGVTKKSEDMKLVRTASFSR 384
 DB 3072 QLPPSLRFLFP-TGSGVRGCVKGIKALGKYVDLKLRL-TTGVSAAGTADLLVERAMTFHG 3129
 QY 385 CG--QMSFTMLDVPSIDRPLSGFQFQPSGTLNMQTSSLLVTLBEGHLELSTRS 442
 DB 3130 HGLRLALSNV-APLTGNVSYSGVFSHAQDSALLYYRASPDGLQVELQGRVSLQLRT 3188
 QY 443 NIPIFKSPGYMDGLLHVSVISDTSGRLILDDV--LRRNRLPSFSNAQOS---LR 496
 DB 3189 EV---KTQAGFADGAPHYVAFYSNATCWMLYVDDQLQGMKPHGPPHELQPGEGPRL 3245
 QY 497 LGG-----GHFEGCISNVLVQFSSQSPVLDLASKTYKQASLG 535
 DB 3246 LGGILPESGTYNFSGCISNVFVQRLGLGPRVFDLQQWLAGSVNVSTG 3291

RESULT 12
 LMA4_HUMAN STANDARD; PRT; 1816 AA.
 ID LMA4_HUMAN Q16363; Q14735; Q15335; Q9UE18; Q9UJN9;
 AC Q16363; Q14735; Q15335; Q9UE18; Q9UJN9;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Laminin alpha-4 chain precursor.
 DS Name=LMA4;
 OS Homo sapiens (Human).
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteleostomi; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Petal lung;
 MEDLINE=95300971; Pubmed=7781776; DOI=10.1016/0014-5793(95)00462-1;
 RA Iivanainen A., Sainio K., Satiola H., Tryggvason K.;
 RT "Primary structure and expression of a novel human laminin alpha 4 chain.";

RL FEBS Lett. 365:183-188(1995).
 (2)
 RP SEQUENCE FROM N.A.
 RP TISSUE=Heart;
 RX MEDLINE=97454279; Pubmed=9310354;
 RA Richard A.J., Lucocart C., Pope F.M.;
 RT "The structural organisation of LMA4, the gene encoding laminin alpha4.";
 RL Eur. J. Biochem. 248:15-23(1997).
 (3)
 RP SEQUENCE OF 236-1816 FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=95048381; Pubmed=7959779;
 RA Richard A.J., Al-Imara L., Carter N.P., Lloyd J.C., Leversha M.A., Pope F.M.;
 RT "Localisation of the gene (LMA4) to chromosome 6q21 and isolation of a partial cDNA encoding a variant laminin A chain.";
 RL Genomics 22:237-239(1994).
 (4)
 RP SEQUENCE OF 66-1816 FROM N.A.
 RP Tubby B.;
 RA Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end.
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement membranes (major component).
 CC -1- TISSUE SPECIFICITY: In adult, strong expression in heart, lung, ovary small and large intestines, placenta, liver; weak or no expression in skeletal muscle, kidney, pancreas, testis, prostate, brain. High expression in fetal lung and kidney. Expression in fetal and newborn tissues is observed in certain mesenchymal cells in tissues such as smooth muscle and dermis.
 CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact with other laminin chains to form a coiled coil structure.
 CC -1- DOMAIN: Domain G is globular.
 CC -1- SIMILARITY: Contains 4 laminin G-like domains.
 CC -1- SIMILARITY: Contains 5 laminin G-like domains.
 CC -1- CAUTION: Gene LMA4 was formerly called LMA3.
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 CC
 CC EMBL; S78569; AAB34635.1; -
 CC EMBL; X91171; CAAC2596.1; -
 CC EMBL; Y14240; CAAT4636.1; -
 CC EMBL; X76939; CAAS4258.1; -
 CC EMBL; Z59289; -; NOT_ANNOTATED_CDS.
 CC PIR; S68960; S68960.
 CC HSSP; P02468; INPE.
 CC DR Genew; HGNC:6484; LAMA4.
 CC MIM; 600133; -
 CC DR GO; GO:0005605; Cibaal lamina; TAS.
 CC GO; GO:0005201; Fextracellular matrix structural constituent; TAS.
 CC DR InterPro; IPR008985; Cona_1like_1ec_g1.
 CC DR InterPro; IPR006209; EGF_1like.
 CC DR InterPro; IPR002049; Laminin_EGF.
 CC DR InterPro; IPR001791; Laminin_G.
 CC DR InterPro; IPR009254; Laminin_I.
 CC DR InterPro; IPR010307; Laminin_II.
 CC DR InterPro; IPR003129; TSP_N.
 CC Pfam; PF00053; Laminin_EGF; 3.

DR Pfam; PF00054; Laminin G; 3.
 DR Pfam; PF06008; Laminin I; 1.
 DR Pfam; PF06009; Laminin II; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN 1.
 DR PROSITE; PS00025; LAM G DOMAIN; 5.
 DR PROSITE; PS01248; LAMININ TYPE EGF; 3.
 KM Basement membrane; Cell adhesion; Coiled coil; Extracellular matrix;
 KM Glycoprotein; Laminin EGF-like domain; Repeat; Signal.
 PT SIGNAL 1
 PT CHAIN 24
 PT 25 1816 Laminin alpha-4 chain.
 PT 82 131 Laminin EGF-like 1.
 PT 132 186 Laminin EGF-like 2.
 PT 187 240 Laminin EGF-like 3.
 PT 241 255 Laminin EGF-like 4 (incomplete).
 PT 256 825 Domain I and I.
 PT 826 1028 Laminin G-like 1.
 PT 1040 1220 Laminin G-like 2.
 PT 1227 1395 Laminin G-like 3.
 PT 1462 1633 Laminin G-like 4.
 PT 1640 1813 Laminin G-like 5.
 PT 313 396 Coiled coil (potential).
 PT 466 521 Coiled coil (potential).
 PT 574 607 Coiled coil (potential).
 PT 655 717 Coiled coil (potential).
 PT 770 799 Coiled coil (potential).
 PT SITE 717 719 Cell attachment site (potential).
 PT 82 91 By similarity.
 PT 84 98 By similarity.
 PT 101 110 By similarity.
 PT 113 129 By similarity.
 PT 132 146 By similarity.
 PT 134 155 By similarity.
 PT 157 166 By similarity.
 PT 169 184 By similarity.
 PT 187 202 By similarity.
 PT 189 209 By similarity.
 PT 212 221 By similarity.
 PT 224 238 By similarity.
 PT 266 266 Interchain (Probable).
 PT 269 269 Interchain (Probable).
 PT 104 104 N-linked (GlcNAc). (Potential).
 PT 215 215 N-linked (GlcNAc). (Potential).
 PT 308 308 N-linked (GlcNAc). (Potential).
 PT 458 458 N-linked (GlcNAc). (Potential).
 PT 524 524 N-linked (GlcNAc). (Potential).
 PT 550 550 N-linked (GlcNAc). (Potential).
 PT 571 571 N-linked (GlcNAc). (Potential).
 PT 574 574 N-linked (GlcNAc). (Potential).
 PT 631 631 N-linked (GlcNAc). (Potential).
 PT 639 639 N-linked (GlcNAc). (Potential).
 PT 735 735 N-linked (GlcNAc). (Potential).
 PT 751 751 N-linked (GlcNAc). (Potential).
 PT 754 754 N-linked (GlcNAc). (Potential).
 PT 780 780 N-linked (GlcNAc). (Potential).
 PT 803 803 N-linked (GlcNAc). (Potential).
 PT 1086 1086 N-linked (GlcNAc). (Potential).
 PT 1281 1281 N-linked (GlcNAc). (Potential).
 PT 1359 1359 N-linked (GlcNAc). (Potential).
 PT 1411 1411 N-linked (GlcNAc). (Potential).
 PT 143 143 A -> P (in Ref. 1).
 PT 178 178 L -> P (in Ref. 1).
 PT 265 265 G -> GNDCTPIS (in Ref. 4).
 PT 276 276 D -> A (in Ref. 4).
 PT 491 491 Y -> H (in Ref. 2 and 3).
 PT 1057 1057 T -> P (in Ref. 1).
 PT CONFLICT 1110 1112 SGR -> GGP (in Ref. 4).
 PT CONFLICT 1816 1816 AA; 201908 MM; 04B9A379A0FAAD CRC64;
 SQ SEQUENCE

Query Match 23.3%; Score 686; DB 1; Length 1816;
 Best Local Similarity 32.2%; Pred. No. 1.4e-37;
 Matches 194; Conservative 101; Mismatches 245; Indels 62; Gaps 21;

QY 1 MRNKGSGVEVRLPNDEJDKGYTSLFLP-----QRDLAENGSTEDMFMVIGNKAASK 56

DB 829 MFEDGSAVEVHERSTMDLAKFTSLYKKEPVKPELLE---TDQFLVLGSKNAK 885
 QY 57 DYIGAAVVDGQLTCVYNLGDREAEVQIDVLTSESOEAVMDVKFQRIYQAKANTYKE 116
 DB 886 EYVGLAIKIDNLLVYVYNLGTQKVEIPLDS--KEVSSWPAFYSIVKIERVKGHGVFLTP 943
 QY 117 ATENKRAKAVYDLBEGSSVTLNLPEDAVFVGVGVPDPPELPSRLRFPFYGCLELD 176
 DB 944 SLSTLBEKFKIKKGEESGDSLLDLPEDVFFVGVGVPSPFKPPTSLNLGFPVGCLELAT 1003
 QY 177 LNEVNLVNFKTPFNLTTEVEPCRRK-----EESDKNFGTGYA--RIYQPN--A 227
 DB 1004 LNDVSLVNFKTIYMDSTVPCARDKLAFTQSPAASFFPDGSGAVVADTRKCKFG 1063
 QY 228 PEPNFIQTITQTVDRGLLPAENQDNFISINEDNLMVRY-----KLNSEPPKKEGI 280
 DB 1064 QVTRFDIEVTRPADNGLILMVNGSMFPLEMANGVLIHVYDGFSGRVHLDTLKKA- 1122
 QY 281 RDTINDKDHSLITTGKLOKRWIVNERSVAI---EGEIPFSTYLGIP-----I 331
 DB 1123 --QINDAKTHEISI--YHNDKMKILVDRHVKSMONKKKLPFTDIYIGAPPEILQSR 1179
 QY 332 AIRERFNISPPAFQGMKUL---KKTSGVVRLLDVTGVTCKGSEMDKLVRTASFRGQM 388
 DB 1180 ALPAHHPPLDI-NFRGCKGQFOQKQPNLEQTEYLGVGCEPDSILSRATFN--GQS 1236
 QY 389 SPTNLD-VSTDRFQLSFGQFPQPSGTLNMQRTSLVLTLEDGHIELSTDSNIPF 447
 DB 1237 FASIQKISFPDFEGFPNRTIQPNGLLFYASGSDVFSISDNGVIMDVK--GIKVQ 1294
 QY 448 KSPGTTMDGLHVSIVISDTSGLR--LLID-DQVLRNQRLEPSFNAQSLR--LGG-- 499
 DB 1295 SVDKQVNDGISHP--YISSVSPRYELIVDKSVGSKNPKFKIEQTOSEKFFYFGSP 1352
 QY 500 -----GHPGCTSNVLVQRPSSQPEVLDLASKSTKQDASIGGSLNKPPLMFKSPKR 554
 DB 1353 ISAQVNFPGTCSNAYFTRVDVEBDFQRYEKVHTSLYBCPISSPLFLHKKGK 1412
 QY 555 NK 556
 DB 1413 SK 1414
 DB 1413 SK 1414

RESULT 13
 Q91VVO PRELIMINARY; PRT; 1254 AA.
 AC Q91VVO;
 DT 01-DRG-2001 (T-EMBLrel. 19, Created)
 DT 01-DRG-2001 (T-EMBLrel. 19, Last sequence update)
 DE 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 LN Llama4 protein (Fragment).
 GN Name=Lama4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=mx FVB/N; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen R.D., Schuler G.D.,
 RA Altschuler S.F., Zeeberg B., Buote R.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Datchenko L., Marsina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzinski M.I., Skaleja U., Smalins D.E., Schnerch A., Schein J.B.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=mlx FVB/N; TISSUE=Mammary tumor;
 RA Strausberg R.,
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC008533; AA008533.1; -.
 DR HSSP; Q60675; 1QD0.
 DR MGD; MG1:109321; Lama4.
 DR GO; GO:0005605; C:basal lamina; IDA.
 DR GO; GO:0005615; C:extracellular space; TMS.
 DR GO; GO:0001568; P:blood vessel development; IMP.
 DR Pfam; PF02210; Laminin_G_2; 5.
 DR Pfam; PF06009; Laminin_II; 1.
 DR SMART; SM00282; LamG; 5.
 DR PROSITE; PSS0025; LAM_G_DOMAIN; 5.
 DR NON TER 1
 SQ SEQUENCE 1254 AA; 139723 MW; 54D49EF763D37CD9 CRC64;
 Query Match 23.3%; Score 685; DB 2; Length 1254;
 Best Local Similarity 32.2%; Pred. No. 9,7e-38;
 Matches 193; Conservative 100; Mismatches 251; Indels 56; Gaps 20;
 QY 1 MRNGSGVAVRLPNDLEDKGTSLSLQ--RPDLBNGSTEDMFMVYLGAKQASD 57
 DB 267 MMEFGGSAVEHVKVAVVDLKKATSLSLYKPPKAEPTGVAVAQFVLVLGSKNAKKE 326
 QY 58 YIGMAVVDGQLTCVNLGDBEAQVOIDQVLTESQEAQVMDRFGQRIQFAKLANTKXA 117
 DB 327 YMGALAKNDLVVYVNLGMKQVLELDS--KPVSSPAFYSIKIRVGKGVFLVPS 384
 QY 118 TSNKPRAPAVYDLEGGSSNTLLNLDPEDAVFYGVYPPFELPSRLRPPYKGCIELDL 177
 DB 385 LSTAEKFKIKGEFAGDDSLDLTLEDYFYGVGPANPKLPASLNLBSYSCLELATL 444
 QY 178 NENVSLVNFKTFNLTTEVEPCRRK---EESDKVFEGTGYA--RIPTQPN--AP 228
 DB 445 NNDVLSLVNFKXLYNMDPSKSVPCARDKLAFTQSRASVYFDDSSYAVVADITRGKFGQ 504
 QY 229 FPFETIGTQTVNRGLLFFAENDNFIINIEDGNLMVRYKLN--SRPKKGIKRD----- 283
 DB 505 VTRFDIEIRTPADNGVLVLLMVNGSMFSLMRNGYLHVFDFGFSNGPVH--LEDTLKKA 562
 QY 284 -INDGDHSHLITIGKLQKRMWVNVBSVRI---EGELPFDFTYILGIPAIIRRFNI 339
 DB 563 QINDAKYHEISI-IYNDKKMLLVDRRHVKSINDKKKIPFDIYITGAPQGVLOSRTL 621
 QY 340 STPA-----FQGGMKNL---KKTSGVRLNDVYVTKKCEMDKLVRTASFSHGQMSFT 391
 DB 622 RAHLPLDINFRGCMKMFQFQKQFNLLEQTELTGVCGEDESLISRRAVFN--GGSFLA 679
 QY 392 NLD-VSTDRFQSLSPGFQFQPSGTLNHNQTRSSSLVLTLEDHIELSTRDSNIPFKSP 450
 DB 680 STICKISFPFGFEGGFNRLQPNGLFYTSGSDVFSISLNDNTVMDVK--GIKWSMD 737
 QY 451 GTYMDGLLHH-VSVISDTSGRLILDDQVLRRQRRLPSFSAQOS-----LRLGG----- 499
 DB 738 KQYHDLGPHFVVISIDTR-YELVVDKSRIRGKN--PTKKAQQTQTEKKKFFGGSPTS 794
 QY 500 ---GHFEGCISNVLVORFSGSPVLDLASKSTKQDASLGCSLNKPPMLLFPKSPRPNK 556
 DB 795 PQYANFTGCISNAYFTRLDRAVEDVDFQRYSEKVAHTSLVCEPIESSPLFLHKKGNSSK 854

ID LMA4_MOUSE STANDARD; PRT; 1816 AA.
 AC P97927; 088785; P70409;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Laminin alpha-4 chain precursor.
 GN Name=Lama4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 462-469, 478-483, 776-782 AND
 RP 940-945.
 RC STRAIN=BALB/c; TISSUE=Endothelial cells;
 RX MEDLINE=9736307; PubMed=9219532;
 RA Friessner M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,
 RA Sorokin L.M.,
 RT "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of
 RT endothelium.";
 RL Eur. J. Biochem. 246:727-735(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=97202462; PubMed=9049981; DOI=10.1016/S0945-053X(96)90162-6;
 RA Liu J., Mayne R.,
 RT "The complete cDNA coding sequence and tissue-specific expression of
 RT the mouse laminin alpha 4 chain.";
 RL Matrix Biol. 15:433-437(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=98010627; PubMed=9346933; DOI=10.1074/jbc.272.44.27862;
 RA Iivanainen A., Kortemaa J., Sahberg C., Morita T., Bergmann U.,
 RA Theisfeldt J., Tryggvason K.,
 RT "Primary structure, developmental expression, and immunolocalization
 RT of the murine laminin alpha4 chain.";
 RL J. Biol. Chem. 272:27862-27868(1997).
 RN [4]
 RP SEQUENCE OF 836-1106 FROM N.A.
 RC STRAIN=ICR; TISSUE=Placenta;
 RX MEDLINE=97296337; PubMed=9151674; DOI=10.1083/jcb.137.3.685;
 RA Miner J.H., Patton B.L., Lentz S.I., Gilbert D.J., Snider W.D.,
 RA Jenkins N.A., Copeland N.G., Sane J.R.,
 RT "The laminin alpha chains: expression, developmental transitions, and
 RT chromosomal locations of alpha-5, identification of heterotrimeric
 RT laminin 8-11, and cloning of a novel alpha3 isoform.";
 RL J. Cell Biol. 137:685-702(1997).
 RN [5]
 RP SEQUENCE OF 1467-1691 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97187457; PubMed=9034910;
 RX DOI=10.1002/(SICI)1096-9861(19970224)378:4<547::AID-CMB93>3.0.CO;2-2;
 RA Lentz S.I., Miner J.H., Sane J.R., Snider W.D.,
 RT "Distribution of the ten known laminin chains in the pathways and
 RT targets of developing sensory axons.";
 RL J. Comp. Neurol. 378:547-561(1997).
 CC -I- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -I- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end.
 CC -I- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -I- TISSUE SPECIFICITY: Strongly expressed in peripheral nerves,
 CC cardiac muscle, fat, dermis, lung stroma, aortic endothelium,
 CC endocardium and endothelium of blood vessels in skin and brain.
 CC -I- DOMAIN: The alpha-helical domains I and II are thought to interact
 CC with other laminin chains to form a coiled coil structure.

RESULT 14
 LMA4_MOUSE

DB 1300 KQYHDELPHEVVISIDTR-YELVVKSRIRGN--PTKGAKQOTTEKKYFGSSPIS 1356
QY 500 ---GHEEGCISNVLVQRFQSPSEVLDLASKSTRKDALGCGSILNKPPFLMLFKSPRRFNK 556
DB 1357 PQVANTPGCISNAYFRLDRDVEVEDFQRYSEKVHTSLVECPLESSPLFLHKKGNSSK 1416
RESULT 15
Q6ZQAI
ID Q6ZQAI PRELIMINARY; PRT, 1524 AA.
AC Q6ZQAI;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MKIA0533 protein (Fragment).
GN Name=MKIA0533;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic tail;
RX PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Iamamoto S., Koseki H., Hiraoka S.,
RA Saza Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIA gene:
RT II. the complete nucleotide sequences of 500 mouse KIA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.",
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129157; BAC97967.2; -
DR GO; GO:0005604; C:basement membrane; IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005178; P:integrin binding; IDA.
DR GO; GO:000515; P:protein binding; IPT.
DR GO; GO:0001763; P:branching morphogenesis; IDA.
DR GO; GO:0030324; P:lung development; IMP.
DR GO; GO:0007517; P:muscle development; IMP.
DR InterPro; IPR008985; Cona like_1ec_g1.
DR InterPro; IPR006209; EGF like_IDA.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR001368; TNFR_c6.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00053; Laminin_EGF; 2.
DR Pfam; PF02210; Laminin_G_2; 4.
DR Pfam; PF06008; Laminin_I; 1.
DR Pfam; PF06009; Laminin_II; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR SMART; SM00180; EGF_Lam; 2.
DR SMART; SM00282; LamG; 5.
DR PROSITE; PS00022; EGF_1; UNKNOWN_3.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
KW Laminin EGF-like domain.
FT NON_TER 1
FT NON_TER 1524
SQ SEQUENCE 1524 AA; 166516 MW; F43411828FFB691 CRC64;

Query Match 23.2%; Score 683; DB 2; Length 1524;
Best Local Similarity 31.8%; Pred. No. 1.8e-37;
Matches 186; Conservative 111; Mismatches 210; Indels 78; Gaps 22;

QY 1 MRENGSGVEVRLPNLDELKGYTSLPLQRPDLRENGG--TEDMPVWYLGKDKASKDY 58
DB 572 MKRNGSGVRLKPRDLADLAAYTALKFHIQSFVPAPBEGKNTGDHFLVLMGSSRQATGDY 631

QY 59 IGMNAVVGQLTGVNULGDR-EAEVQIDVLTSSSQEAVMDRYKQRYIQPAKNTYKEA 117
DB 632 MGVSLRNQKVMWVYRLGKAGPTTLISIDENIGQ-----PAVVSIDRTLQFHNMSVYVE- 684
QY 118 TSNKPKAPAVYDLBEGS-----SNTLNLDPEDAVFYGGYPPDPFLPSRLRPPYKGCIE 173
DB 685 -----KQVHEIKADTYAPSGSEGLNLHPDDFVYVVGYSNFTPPBPLRPPGLGCTE 738
QY 174 LIDLINENVLSTVNFKTTFNLTTEVEPCRRKKE-----SDKNYEGTGAYRIPQPNAP 228
DB 739 METLINEBVSLYNFQGTMLDTAVDKPCARSKATGDPMLTDGSLYDGSGLPARIPEKQ-- 796
QY 228 FPN---PIQITQTYVDRGLLPPAENQDNFISLINDGMLMRYKLS-----EPK- 276
DB 797 FENTKRFPQDELVLVSNGIIFPLKQESQFLCIAVQEGTLVLYFDGSGLKKADPLQPPQA 856
QY 277 ----EKGIKDTINDKQHSILITIGKLDKRMKMINVNSRSVRBGIIPPSTYYLGGI--- 329
DB 857 LTAASKALQVFLLAGNRKRLV--KVERATVFSVDQDNML--EMAD--AYLLGAVPPE 908
QY 330 --PIAIRERFNISTPFAFGCMKNLK--KTSGVVNLNDTVGVTKKSEDMWKLVRTASFSR 384
DB 909 QLPPLSLRQLFP-SGGSVAGCIKIGIKALGKYVDLKRNL--TTGISFGCTADLVLGRMTFHG 966
QY 385 GGQMSFTNLDV-PTSDRFQLSGFQTFQPSGTLNLHQTRTSLVLTLEDGHIELSTRSN 443
DB 967 HGFLLPALPDAVPIITEVYSGFGFRGTQDNMLLYRTSPDGPYQVSLREGHVTLAFPMQ 1026
QY 444 IIFSPGTYMDGLLHVSVISDTSGLRLTIDD--QVLRNRQRLPSFNAQ-----QSLRL 497
DB 1027 V--ETQRYFADGAPHYVAFYSNVTGVMVLYDDQLQVLKSHRTTPMLQLQPEBSRLLL 1083
QY 498 GG-----GHEEGCISNVLVQRFQSPSEVLDLASKSTRKDALG 535
DB 1084 GGLPVSCTPHNNSGCISNVFYQRLAGPQRYFPLHQNMGSVAVSVG 1128

Search completed: February 22, 2005, 08:24:23
Job time : 98.5943 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:04:10 : Search time 104.16 Seconds
(without alignments)
2097.921 Million cell updates/sec

Title: US-10-817-423-4
Perfect score: 2940
Sequence: 1 MRNKGSGVVRLPNDLEDI.....MLFKSPRFRNKRIFVNVQL 565

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2940	100.0	1694	3 AAB48461	Aab48461 Rat lamin
2	2940	100.0	1725	3 AAB48460	Aab48460 Rat lamin
3	2439	83.0	1693	3 AAB48459	Aab48459 Human lam
4	2439	83.0	1693	3 AAB48457	Aab48457 Human lam
5	2439	83.0	1713	3 AAB48458	Aab48458 Human lam
6	2439	83.0	1713	6 ABR92102	ABR92102 Human cer
7	2439	83.0	1713	7 ADD29904	Add29904 Human lam
8	2439	83.0	1713	7 ADG37225	Adg37225 Human lam
9	2439	83.0	1713	8 ABM81957	Adm81957 Tumour-as
10	2439	83.0	1724	3 AAB48456	Aab48456 Human lam
11	2439	83.0	1724	3 AAB48456	Aab48456 Human lam
12	2439	83.0	3332	7 ADE08094	Ade08094 Novel pro
13	2431	82.7	1713	2 AAR70148	Aar70148 Deduced s
14	1310	44.6	770	2 AAW26584	Aaw26584 Rat hemid
15	717.5	24.4	3597	5 ABB09503	Abb09503 Human lam
16	717.5	24.4	3600	5 ABB09501	Abb09501 Human lam
17	717.5	24.4	3690	8 ADM87254	Adm87254 Human pro
18	715	24.3	1677	8 ADM87708	Adm87708 Human EST
19	715	24.3	3695	8 ADI28030	Adi28030 ECKCAD pr
20	715	24.3	3695	8 ADN04478	Adn04478 Antipso
21	715	24.3	3696	5 AAE17310	Aae17310 Human lam
22	715	24.3	3705	5 AAE17309	Aae17309 Human lam
23	712	24.2	1601	4 AAM39009	Aam39009 Human pol
24	712	24.2	1640	5 ABB09504	Abb09504 Human lam
25	712	24.2	1640	8 ADO10049	Ado10049 Novel hum

ALIGNMENTS

RESULT 1
AAB48461 standard; protein; 1694 AA.
ID AAB48461; (first entry)
AC AAB48461;
XX
XX
DT 02-MAR-2001
DE Rat lamin 5 polypeptide, SEQ ID NO: 12.
XX
XX Rat; laminin 5; vulnary; antitumor; antidiabetic;
XX cell adhesion promoter; wound healing; ulcers; burn; skin graft;
XX periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
XX Rattus norvegicus.
OS
XX
XX WO200066731-A2.
PN
XX
PD 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US011459.
PP
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
XX (BIOS-) BIOSYSTEMS INC.
PA
XX
XX Boutaud A;
PI
XX WPI, 2000-687538/67.
DR N-PSDB; AAC83722.
XX
XX Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burns, acute wounds and skin grafts.
XX
XX Claim 3; Page 117-122; 232pp; English.
PS
XX
XX The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotrimeric laminin, whereas

26	712	24.2	1645	7	ADL15098	Adl15098 Human mal
27	712	24.2	1645	7	ADN95658	Adn95658 Human BEC
28	712	24.2	3695	5	ABB81588	Abb81588 Human lam
29	694	23.6	1792	3	AAB48443	Aab48443 Human lam
30	694	23.6	1800	3	AAB48445	Aab48445 Human lam
31	694	23.6	1816	3	AAB48442	Aab48442 Human lam
32	694	23.6	1816	8	ADR87600	Adr87600 Human lam
33	694	23.6	1824	3	AAB48444	Aab48444 Human lam
34	688	23.4	1823	3	ABP63020	Abp63020 Human pol
35	686.5	23.4	3597	8	ADO10047	Ado10047 Novel hum
36	686	23.3	1581	7	ADJ68348	Adj68348 Human hea
37	685	23.3	1816	8	ADP08401	Adp08401 Human lam
38	685	23.3	953	5	AAM50358	Aam50358 Human lam
39	683	23.2	984	5	ABB80819	Abb80819 Heparin b
40	683	23.2	1792	3	AAB48447	Aab48447 Mouse lam
41	683	23.2	1816	3	AAB48446	Aab48446 Mouse lam
42	683	23.2	1816	7	ADC01877	Adc01877 Human lam
43	681	23.2	1816	7	ADC01879	Adc01879 Human lam
44	681	23.2	3635	5	ABB81589	Abb81589 Mouse lam
45	681	23.2	3635	5	AAM50357	Aam50357 Mouse lam

CC prior art cell lines have been created that produce but do not secrete
 CC only one or two chain laminins
 XX
 XX
 SQ Sequence 1694 AA;

Query Match 100.0%; Score 2940; DB 3; Length 1694;
 Best Local Similarity 100.0%; Pred. No. 1.5e-261;
 Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFNGSGVEVRLPNDLBDKGYTSLFLQRPDLRENGTEPMFMYLGNDKADSKDYIG 60
 DB 751 MRFNGSGVEVRLPNDLBDKGYTSLFLQRPDLRENGTEPMFMYLGNDKADSKDYIG 810
 QY 61 MAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAVMDRYKFORIYQPAKLNTYKATSN 120
 DB 811 MAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAVMDRYKFORIYQPAKLNTYKATSN 870
 QY 121 KKPAAVYDLEGGSSNTLLNLPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLLEN 180
 DB 871 KKPAAVYDLEGGSSNTLLNLPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLLEN 930
 QY 181 VLSLYNFKTTFNLNTTEVEPCRRKESDKNYFEGYARIPQPNAPFPNFIOITQTV 240
 DB 931 VLSLYNFKTTFNLNTTEVEPCRRKESDKNYFEGYARIPQPNAPFPNFIOITQTV 990
 QY 241 DRGLFPAENQDNFISLNIEDGNLWRYKLNSEPPKKGIRDTINDGKHSILITIGKQ 300
 DB 991 DRGLFPAENQDNFISLNIEDGNLWRYKLNSEPPKKGIRDTINDGKHSILITIGKQ 1050
 QY 301 KKMWINVRSVRIRIEGIFDFSTYYLGGIPAIRERFNISTPAFGCKMKLKTSGVRL 360
 DB 1051 KKMWINVRSVRIRIEGIFDFSTYYLGGIPAIRERFNISTPAFGCKMKLKTSGVRL 1110
 QY 361 NDTVGYTKKCSBDMKLVRTASFRGGQMSFTNLDPVSTDRFQLSFGFQTFOPSGTLLNHQ 420
 DB 1111 NDTVGYTKKCSBDMKLVRTASFRGGQMSFTNLDPVSTDRFQLSFGFQTFOPSGTLLNHQ 1170
 QY 421 TRTSSLVLTLEDEGHIELSTRDSNIPIFKSPGYMDGLLHVSVISDTSGLRLIIDQVLR 480
 DB 1171 TRTSSLVLTLEDEGHIELSTRDSNIPIFKSPGYMDGLLHVSVISDTSGLRLIIDQVLR 1230
 QY 481 RNQRLPSPSNAQOSLRLGGHFEBCISNVLVQRFQSPRYLDLASKSTKQASLGCCSLN 540
 DB 1231 RNQRLPSPSNAQOSLRLGGHFEBCISNVLVQRFQSPRYLDLASKSTKQASLGCCSLN 1290
 QY 541 KPPFLMLFKSPKRFNKGRIFNNQL 565
 DB 1291 KPPFLMLFKSPKRFNKGRIFNNQL 1315

RESULT 2
 AAB48460
 ID AAB48460 standard; protein; 1725 AA.

XX AAB48460;
 AC
 DT 02-MAR-2001 (first entry)
 XX

DE Rat laminin 5 polypeptide, SEQ ID NO: 10.

XX Rat; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;
 KW cell adhesion promoter; wound healing; burn; skin graft;
 XX periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.

OS Rattus norvegicus.

XX WO200066731-A2.

XX 09-NOV-2000.

PF 28-APR-2000; 2000MO-US011459.

XX 30-APR-1999; 99US-0131720P.

PR 21-AUG-1999; 99US-0149738P.
 PR 24-SEP-1999; 99US-0155945P.
 XX
 XX
 PA (BIOS-) BIOSTATUM INC.

PI Bouteaud A;
 PT WPI; 2000-687538/67.
 DR N-PSDB; AAC3721.

PT Laminin 5-expressing cells, used to accelerate wound healing associated
 with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
 PT burns, acute wounds and skin grafts.

PS Claim 3; Page 104-109; 232pp; English.

CC The present sequence is a laminin 5 chain polypeptide. Recombinant
 CC laminin 5-expressing cells are used to accelerate wound healing,
 CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
 CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
 CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
 CC improve the biocompatibility of medical devices, and to promote cell
 CC adhesion to a surface. They can be used for the ex vivo treatment of type
 CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
 CC line produces and secretes recombinant heterotimeric laminin, whereas
 CC prior art cell lines have been created that produce but do not secrete
 CC only one or two chain laminins

XX Sequence 1725 AA;

Query Match 100.0%; Score 2940; DB 3; Length 1725;
 Best Local Similarity 100.0%; Pred. No. 1.5e-261;
 Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFNGSGVEVRLPNDLBDKGYTSLFLQRPDLRENGTEPMFMYLGNDKADSKDYIG 60
 DB 782 MRFNGSGVEVRLPNDLBDKGYTSLFLQRPDLRENGTEPMFMYLGNDKADSKDYIG 841
 QY 61 MAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAVMDRYKFORIYQPAKLNTYKATSN 120
 DB 842 MAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAVMDRYKFORIYQPAKLNTYKATSN 901
 QY 121 KKPAAVYDLEGGSSNTLLNLPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLLEN 180
 DB 902 KKPAAVYDLEGGSSNTLLNLPEDAVFYVGGYPPDFELPSRLRPPYKGCIELDLLEN 961
 QY 181 VLSLYNFKTTFNLNTTEVEPCRRKESDKNYFEGYARIPQPNAPFPNFIOITQTV 240
 DB 962 VLSLYNFKTTFNLNTTEVEPCRRKESDKNYFEGYARIPQPNAPFPNFIOITQTV 1021
 QY 241 DRGLFPAENQDNFISLNIEDGNLWRYKLNSEPPKKGIRDTINDGKHSILITIGKQ 300
 DB 1022 DRGLFPAENQDNFISLNIEDGNLWRYKLNSEPPKKGIRDTINDGKHSILITIGKQ 1081
 QY 301 KKMWINVRSVRIRIEGIFDFSTYYLGGIPAIRERFNISTPAFGCKMKLKTSGVRL 360
 DB 1082 KKMWINVRSVRIRIEGIFDFSTYYLGGIPAIRERFNISTPAFGCKMKLKTSGVRL 1141
 QY 361 NDTVGYTKKCSBDMKLVRTASFRGGQMSFTNLDPVSTDRFQLSFGFQTFOPSGTLLNHQ 420
 DB 1142 NDTVGYTKKCSBDMKLVRTASFRGGQMSFTNLDPVSTDRFQLSFGFQTFOPSGTLLNHQ 1201
 QY 421 TRTSSLVLTLEDEGHIELSTRDSNIPIFKSPGYMDGLLHVSVISDTSGLRLIIDQVLR 480
 DB 1202 TRTSSLVLTLEDEGHIELSTRDSNIPIFKSPGYMDGLLHVSVISDTSGLRLIIDQVLR 1261
 QY 481 RNQRLPSPSNAQOSLRLGGHFEBCISNVLVQRFQSPRYLDLASKSTKQASLGCCSLN 540
 DB 1262 RNQRLPSPSNAQOSLRLGGHFEBCISNVLVQRFQSPRYLDLASKSTKQASLGCCSLN 1321
 QY 541 KPPFLMLFKSPKRFNKGRIFNNQL 565
 DB 1322 KPPFLMLFKSPKRFNKGRIFNNQL 1346

```
RESULT 3
AAB48457
ID AAB48457 standard; protein; 1693 AA.
XX
AC AAB48457;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human laminin 5 polypeptide, SEQ ID NO: 8.
XX
KW Human; laminin 5; vulnery; antiulcer; antiinflammatory; antidiabetic;
KW cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS Homo sapiens.
XX
PN MO20006731-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000MO-US011459.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (BIOS-) BIOSTATUM INC.
XX
PI Boutaud A;
XX
DR WPI; 2000-687538/67.
DR N-PSDB; AAC83720.
XX
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burn, acute wounds and skin grafts.
XX
PS Claim 3; Page 91-97; 232pp; English.
XX
XX The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
CC line produces and secretes recombinant heterotrimeric laminin, whereas
CC prior art cell lines have been created that produce but do not secrete
CC only one or two chain laminins
XX
SQ Sequence 1693 AA;
XX
Query Match 83.0%; Score 2439; DB 3; Length 1693;
Best Local Similarity 81.9%; Pred. No. 3e-215;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;
QY 1 MRFNGSGVEVRIPNDLEDIKGYTSLFQRPDLRENGGHEMFVYVLGNKXSKXYIG 60
DB 751 MRFNGSGVEVRIPNDLEDIKGYTSLFQRPDLRENGGHEMFVYVLGNKXSKXYIG 810
QY 61 MAVVDGQLTCVYVNGDBREAEVDQVLTESSEGEAVNDVRYKFORIYOPAKLNTYKATSN 120
DB 811 MAVVDGQLTCVYVNGDBREAEVDQVLTESSEGEAVNDVRYKFORIYOPAKLNTYKATSN 870
QY 121 KPRAPAYVDLEGGSSNTLINDPDANFYVGGYPPDELRSLRFPFYKGCIBLDDINEN 180
DB 871 KPRAPAYVDLEGGSSNTLINDPDANFYVGGYPPDELRSLRFPFYKGCIBLDDINEN 930
QY 181 VLSLYNFKTFNLTTEVEPCRRKESDKNYFEGTGVARIPTPNAPFPNFIQTITV 240
DB 181 VLSLYNFKTFNLTTEVEPCRRKESDKNYFEGTGVARIPTPNAPFPNFIQTITV 240
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18b 931 VLSLYNFKTFNLTTEVEPCRRKESDKNYFEGTGVARIPTPNAPFPNFIQTITV 990
QY 241 DRGLFPAERQONPFIANTEDGTLNRYKLNSEPPREKGRDITNGKHSILITGKQ 300
DB 991 DRGLFPAERQONPFIANTEDGTLNRYKLNSEPPREKGRDITNGKHSILITGKQ 1050
QY 301 KRMWVNVRSVRIEIEIFDFTYYLGGIPIAIRERFNISTPAFGCKMILKXTSGVRL 360
DB 1051 KRMWVNVRSVRIEIEIFDFTYYLGGIPIAIRERFNISTPAFGCKMILKXTSGVRL 1110
QY 361 NDTVGVTKCSSEWKLVRGASFGSGOMSFNLDVSTDRFQUSFGQTFQPSGTLINQ 420
DB 1111 NDTVGVTKCSSEWKLVRGASFGSGOMSFNLDVSTDRFQUSFGQTFQPSGTLINQ 1170
QY 421 TRTSLSLVTEDEHILSTRDSNIPFKSPGTMDGLHVVYSITSGRLIIDQVLR 480
DB 1171 TWTRNLQVTLDEYIYLSSTSDSGPIFKSPGTMDGLHVVYSITSGRLIIDQVLR 1230
QY 481 NRQLPSPSNAOQSLRGGHFGCISNVLVORFSPQSEVYLDASKSTKDAIAGGCSLN 540
DB 1231 NRQLPSPSNAOQSLRGGHFGCISNVLVORFSPQSEVYLDASKSTKDAIAGGCSLN 1290
QY 541 KPPEFLMLFKSPKRNKRIENVNL 565
DB 1291 KPPEFLMLFKSPKRNKRIENVNL 1315
XX
RESULT 4
AAB48457
ID AAB48457 standard; protein; 1693 AA.
XX
AC AAB48457;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human laminin 5 polypeptide, SEQ ID NO: 4.
XX
KW Human; laminin 5; vulnery; antiulcer; antiinflammatory; antidiabetic;
KW cell adhesion promoter; wound healing; ulcers; burn; skin graft;
KW periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
OS Homo sapiens.
XX
PN MO20006731-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000MO-US011459.
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
XX
PA (BIOS-) BIOSTATUM INC.
XX
PI Boutaud A;
XX
DR WPI; 2000-687538/67.
DR N-PSDB; AAC83718.
XX
PT Laminin 5-expressing cells, used to accelerate wound healing associated
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
PT burn, acute wounds and skin grafts.
XX
PS Claim 3; Page 66-71; 232pp; English.
XX
XX The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type
```

CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
 CC line produces and secretes recombinant heterotrimeric laminin, whereas
 CC prior art cell lines have been created that produce but do not secrete
 CC only one or two chain laminins
 XX

SO Sequence 1693 AA;

Query Match 83.0%; Score 2439; DB 3; Length 1693;
 Best Local Similarity 81.9%; Pred. No. 3e-215;
 Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRNNGSGVEVRLPNDLEDKGYTSLSLFQRPDLRENGTDMFVMTLGNKDAKDYIG 60
 DB 751 MRNNGSGVEVRLPNDLEDKGYTSLSLFQRPDLRENGTDMFVMTLGNKDAKDYIG 810
 QY 61 MAVVDGQLTCVNLGDRBAEVOIDVLTSESOEAVMDRKPFRITQPMANTKATSN 120
 DB 811 MAVVDGQLTCVNLGDRBAEVOIDVLTSESOEAVMDRKPFRITQPMANTKATSN 870
 QY 121 KPRAPAVYDLGGSSNTLLNLDPEDAVFYGGYPPDFELPSRLRPPYKGCIELDLNN 180
 DB 871 KPRAPAVYDMGNSNTLLNLDPEDAVFYGGYPPDFELPSRLRPPYKGCIELDLNN 930
 QY 181 VLSLNFKTTFNLTTEVEPCRRKESDKNYFEGTGARIPQPNAPFPNFQITQTV 240
 DB 931 VLSLNFKTTFNLTTEVEPCRRKESDKNYFEGTGARIPQPNAPFPNFQITQTV 990
 QY 241 DRGLLFFAENODNFIISLINEDGNLMRYKLNSEPPKEKIRDTINDGKHSLITIGKQ 300
 DB 991 DRGLLFFAENODNFIISLINEDGNLMRYKLNSEPPKEKIRDTINDGKHSLITIGKQ 1050
 QY 301 KRMWNNVRSVRIEGBIPDSTYYLGGIPAIIRERFNISTPAFGCKMKLKKTSGVRL 360
 DB 1051 KRMWNNVQNTIIDGVDFDSTYYLGGIPAIIRERFNISTPAFGCKMKLKKTSGVRL 1110
 QY 361 NDVGVTKKCSBWKVKTATSESRGGMSFTNLDPVSTDRFQLSFGPQTFQPSGTLNMQ 420
 DB 1111 NDVGVTKKCSBWKVKTATSESRGGMSFTNLDPVSTDRFQLSFGPQTFQPSGTLNMQ 1170
 QY 421 TRTSLLVLTLEDEGHILSTSDSNIPFKSPGTMDGLHHVSIYSTGSRLLIIDVOYR 480
 DB 1171 TRTSLLVLTLEDEGHILSTSDSNIPFKSPGTMDGLHHVSIYSTGSRLLIIDVOYR 1230
 QY 481 RNQRLPSFNAQOSRLRGGHFEGCISNVLVQRFQSPPEVLDASKSTKDAKSLGGCSLN 540
 DB 1231 NSKRLKHISRSRQSLRGGHFEGCISNVLVQRFQSPPEVLDASKSTKDAKSLGGCSLN 1290
 QY 541 KPFLMLFKSPKRFNKGRIFFNVNQL 565
 DB 1291 KPFLMLFKSGTRFNKTRFRIINQL 1315

RESULT 5
 AAB48458
 ID AAB48458 standard; protein; 1713 AA.

XX AC AAB48458;
 XX DT 02-MAR-2001 (first entry)
 XX DE Human laminin 5 polypeptide, SEQ ID NO: 6.
 XX KM Human; laminin 5; vulnary; antiulcer; antiinflammatory; antidiabetic;
 XX KM cell adhesion promoter; wound healing; ulcers; burn; skin graft;
 XX KM periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
 XX OS Homo sapiens.
 XX PN MO200066731-A2.
 XX PD 09-NOV-2000.
 XX PF 28-APR-2000; 2000MO-US011459.

XX 30-APR-1999; 99US-0131720P.
 PR 21-AUG-1999; 99US-0149738P.
 PR 24-SEP-1999; 99US-0155945P.
 XX

PA (BIOS-) BIOSSTATUM INC.

PI Boulaud A;

DR WPI; 2000-687538/67.

DR N-PSDB; AAC83719.

PT Laminin 5-expressing cells, used to accelerate wound healing associated
 with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
 burns, acute wounds and skin grafts.

PS Claim 3; Page 79-84; 232pp; English.

CC The present sequence is a laminin 5 chain polypeptide. Recombinant
 CC laminin 5-expressing cells are used to accelerate wound healing,
 CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
 CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
 CC intestinal ulcers, periodontitis, and gingivitis. They are also used to
 CC improve the biocompatibility of medical devices, and to promote cell
 CC adhesion to a surface. They can be used for the ex vivo treatment of
 CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
 CC line produces and secretes recombinant heterotrimeric laminin, whereas
 CC prior art cell lines have been created that produce but do not secrete
 CC only one or two chain laminins
 XX

SO Sequence 1713 AA;

Query Match 83.0%; Score 2439; DB 3; Length 1713;
 Best Local Similarity 81.9%; Pred. No. 3.1e-215;
 Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRNNGSGVEVRLPNDLEDKGYTSLSLFQRPDLRENGTDMFVMTLGNKDAKDYIG 60
 DB 771 MRNNGSGVEVRLPNDLEDKGYTSLSLFQRPDLRENGTDMFVMTLGNKDAKDYIG 830
 QY 61 MAVVDGQLTCVNLGDRBAEVOIDVLTSESOEAVMDRKPFRITQPMANTKATSN 120
 DB 831 MAVVDGQLTCVNLGDRBAEVOIDVLTSESOEAVMDRKPFRITQPMANTKATSN 890
 QY 121 KPRAPAVYDLGGSSNTLLNLDPEDAVFYGGYPPDFELPSRLRPPYKGCIELDLNN 180
 DB 891 KPRAPAVYDMGNSNTLLNLDPEDAVFYGGYPPDFELPSRLRPPYKGCIELDLNN 950
 QY 181 VLSLNFKTTFNLTTEVEPCRRKESDKNYFEGTGARIPQPNAPFPNFQITQTV 240
 DB 951 VLSLNFKTTFNLTTEVEPCRRKESDKNYFEGTGARIPQPNAPFPNFQITQTV 1010
 QY 241 DRGLLFFAENODNFIISLINEDGNLMRYKLNSEPPKEKIRDTINDGKHSLITIGKQ 300
 DB 1011 DRGLLFFAENODNFIISLINEDGNLMRYKLNSEPPKEKIRDTINDGKHSLITIGKQ 1070
 QY 301 KRMWNNVRSVRIEGBIPDSTYYLGGIPAIIRERFNISTPAFGCKMKLKKTSGVRL 360
 DB 1071 KRMWNNVQNTIIDGVDFDSTYYLGGIPAIIRERFNISTPAFGCKMKLKKTSGVRL 1130
 QY 361 NDVGVTKKCSBWKVKTATSESRGGMSFTNLDPVSTDRFQLSFGPQTFQPSGTLNMQ 420
 DB 1131 NDVGVTKKCSBWKVKTATSESRGGMSFTNLDPVSTDRFQLSFGPQTFQPSGTLNMQ 1190
 QY 421 TRTSLLVLTLEDEGHILSTSDSNIPFKSPGTMDGLHHVSIYSTGSRLLIIDVOYR 480
 DB 1191 TRTSLLVLTLEDEGHILSTSDSNIPFKSPGTMDGLHHVSIYSTGSRLLIIDVOYR 1250
 QY 481 RNQRLPSFNAQOSRLRGGHFEGCISNVLVQRFQSPPEVLDASKSTKDAKSLGGCSLN 540
 DB 1251 NSKRLKHISRSRQSLRGGHFEGCISNVLVQRFQSPPEVLDASKSTKDAKSLGGCSLN 1310
 QY 541 KPFLMLFKSPKRFNKGRIFFNVNQL 565

Db 1311 KPPEFLMLKSGSTRFNKTKTFRINQL 1335

RESULT 6
ABR92102
ID ABR92102 standard; protein; 1713 AA.

XX ABR92102;

DT 10-SEP-2003 (first entry)

DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:113.

XX Human; cervical cancer; cervical cancer marker; cancer therapy;

KW detection; gene therapy; vaccine.

OS Homo sapiens.

XX WO2002101075-A2.

PD 19-DEC-2002.

PF 12-JUN-2002; 2002WO-US018638.

PR 13-JUN-2001; 2001US-0298155P.

PR 13-JUN-2001; 2001US-0298155P.

PR 14-NOV-2001; 2001US-0335936P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Schlögel R, Chen Y, Zhao X, Monahan JB, Kamatkar S;

PI Gannavarapu M, Glatt K, Hoersch S;

XX WPI; 2003-156967/15.

XX N-PSDB; ACF12884.

XX New isolated nucleic acid molecule useful for detecting, characterizing,

PT preventing and treating human cervical cancers, in various prognostic and

PT diagnostic assays, in pharmacogenomics and in monitoring clinical trials.

XX Claim 4; Page 269-273; 386pp; English.

XX ACF12828 to ACF12947 encode the human cervical cancer marker proteins (1)

CC given in ABR92047 to ABR92164. A higher level of expression of (1) than

CC normal indicates the presence of cervical cancer. Also described: (1) a

CC vector (II) containing (1); (2) a host cell (III) containing (1); and (3)

CC assessing (MI) whether a patient is afflicted with cervical cancer,

CC comprising comparing the level of expression of a marker in a patient's

CC sample, and the normal level of expression of the marker in a control non

CC -cervical cancer sample, where a significant increase in the level of

CC expression of the marker in the patient's sample relative to that in the

CC control sample is an indication that the patient is afflicted with

CC cervical cancer. (1) has cytostatic activity, and can be used in gene

CC therapy and in vaccines. (II) is useful in detecting, characterizing,

CC preventing and treating human cervical cancers. (I) may also be used in

CC various prognostic and diagnostic assays, pharmacogenomics and in

CC monitoring clinical trials

XX Sequence 1713 AA;

XX Query Match 83.04; Score 2439; DB 6; Length 1713;

XX Best Local Similarity 81.94; Pred. No. 3.1e-215;

XX Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

XX Db 1 MRFGKSGVEVRLEPNLEDEKGYTSLPTLPORPLRNGGTEDMVFVYLGAKDASKXYIG 60

XX 771 MRFGKSGVEVRLEPNLEDEKGYTSLPTLPORPLRNGGTEDMVFVYLGAKDASKXYIG 830

XX 61 MAVVDGQLTCVYNIGDREAEVQIDVLTSESQDAVNDRYKFORIYOPAKLNTYKATSN 120

XX 831 MAVVDGQLTCVYNIGDREAEVQIDVLTSESQDAVNDRYKFORIYOPAKLNTYKATSN 890

QY 121 KPRAPAVYDLEGGSSNTLNLDPEDAVFYVGYPDPFELPSRLRPPRYKGCIELDLNEN 180

Db 891 KPRTPEVYMDGNSMTNLNDPENNVFYVGYPDPFELPSRLRPPRYKGCIELDLNEN 950

QY 181 VLSVNFKTTFNINTEVEPCRRRKEESDKNTFEGTGIARIPQPNAPFPNFIQTITV 240

Db 951 VLSVNFKTTFNINTEVEPCRRRKEESDKNTFEGTGIARIPQPNAPFPNFIQTITV 1010

QY 241 DRGLTFEAPNQNPFISLNTEDGLMRYKLNSPPEKGRDITNGKHSIIITGKQ 300

Db 1011 DRGLTFEAPNQNPFISLNTEDGLMRYKLNSPPEKGRDITNGKHSIIITGKQ 1070

QY 301 KRMWIVNERSVAREGEIDPFSTYVGGIPAIAREFNISTPAFGCKMKLTKTSGVRL 360

Db 1071 KRMWIVNQNITIDSEVDFSTYVGGIPAIAREFNISTPAFGCKMKLTKTSGVRL 1130

QY 361 NDTVGVTKCSBEDMKLVRSAPSRGQMSFTMLDVPSTDRFOLSPFGQTPOPSGTLINQ 420

Db 1131 NDTVGVTKCSBEDMKLVRSAPSRGQMSFTMLDVPSTDRFOLSPFGQTPOPSGTLINQ 1190

QY 421 TRTSSLLVTLDEGHIELSTRDSNIPFKSPGTYMDGLHVSYSITSGRLIIDQVLR 480

Db 1191 TRTSSLLVTLDEGHIELSTRDSNIPFKSPGTYMDGLHVSYSITSGRLIIDQVLR 1250

QY 481 RNORLPSFNAQOSLRLGGGHPGCTSNVLVORFSQSPVYLDASRTKKDASLGGCSLN 540

Db 1251 RNORLPSFNAQOSLRLGGGHPGCTSNVLVORFSQSPVYLDASRTKKDASLGGCSLN 1310

QY 541 KPPEFLMLFKSPKRNKRIENVQL 565

Db 1311 KPPEFLMLFKSGSTRFNKTKTFRINQL 1335

RESULT 7

ADD29904

ID ADD29904 standard; protein; 1713 AA.

XX ADD29904;

XX 15-JAN-2004 (first entry)

XX Human laminin alpha 3 seq id 2.

XX ophthalmological; dermatological; laminin alpha 3; G3 domain;

XX cell adhesion function; cell movement effect; epithelial tissue function;

XX retinal detachment; cosmetic surgery; skin graft; human.

XX Homo sapiens.

XX JP2003093064-A.

XX 02-APR-2003.

XX 20-SEP-2001; 2001JP-00287519.

XX 20-SEP-2001; 2001JP-00287519.

XX (KAGA-) KAGAKU GIYUTSU SHINKO JIGYODAN.

XX (KIH-) ZH KIHARA KINEN YOKOHAMA SHIMEI KAGAKU.

XX WPI; 2003-817304/77.

XX N-PSDB; ADD29903.

XX Novel modified G3 domain of laminin alpha 3 chain useful for controlling

XX cell adhesion and cell movement.

XX Claim 1; SEQ ID NO 2; 49pp; Japanese.

XX The invention describes a modified laminin alpha3 chain comprising one or

XX more amino acid deletions, substitutions or additions at region

XX corresponding to a region of G3 domain having amino acids 1214-1324 of

XX laminin alpha3 chain having a fully defined sequence of 1713 amino acids

XX as given in the specification. (II) can control cell adhesion function and

CC cell movement effect. A composition comprising laminin is useful for
CC maintaining or treating the function of epithelial tissue and for
CC treatment or prevention of retinal detachment and in cosmetic surgery and
CC skin graft. The modified region of laminin alpha3 chain can control cell
CC adhesion function and cell movement effect. This is the amino acid
CC sequence of human laminin alpha 3.

XX Sequence 1713 AA;

Query Match 83.0%; Score 2439; DB 7; Length 1713;

Best Local Similarity 81.9%; Pred. No. 3,1e-215;

Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

```
QY 1 MRFNGSGVEVRLPNDLEDLKGYSLSLFLQRPDLRENGSTEDMFVWYLGKNDASRDYIG 60
DB 771 MRFNGSGVEVRLPNDLEDLKGYSLSLFLQRPDSRENGSTEDMFVWYLGKNDASRDYIG 830
QY 61 MAVVNGQLTCVYNLGDREARLQVDQILTSSESGQAMDRVKQRIYQPAKNTYKATSN 120
DB 831 MAVVNGQLTCVYNLGDREARLQVDQILTSSESGQAMDRVKQRIYQPAKNTYKATSN 890
QY 121 KKPAPAVYDLEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPPYKGCIELDLLEN 180
DB 891 KKPAPAVYDLEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPPYKGCIELDLLEN 950
QY 181 VLSLVNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGARIPQPNAPPPNFQTIQTTV 240
DB 951 VLSLVNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGARIPQPNAPPPNFQTIQTTV 1010
QY 241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEGIRDTINGKHSILITIGKQ 300
DB 1011 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEGIRDTINGKHSILITIGKQ 1070
QY 301 KMMINNVRSVRIEIGEIFDFSTYYLGGIPAIAREFNISTPAFOGCKMLKKTSGVRL 360
DB 1071 KMMINNVRSVRIEIGEIFDFSTYYLGGIPAIAREFNISTPAFOGCKMLKKTSGVRL 1130
QY 361 NDVTGVTKKCSBDMKLVRTASFSRGGQMSFTNLDPVSTDRFQLSFGQTFQPSGTLNHQ 420
DB 1131 NDVTGVTKKCSBDMKLVRTASFSRGGQMSFTNLDPVSTDRFQLSFGQTFQPSGTLNHQ 1190
QY 421 TRTSSLVTLBEDGHIELSTRDSNIPFKSPGTMYDGLAHVSVISDTSGALLIDDOYLR 480
DB 1191 TRTSSLVTLBEDGHIELSTRDSNIPFKSPGTMYDGLAHVSVISDTSGALLIDDOYLR 1250
QY 481 RNQRLPSFSNAQOSRLGSGHPEGICSNLVORFSGSPFVLDASKSTKKDASLGCCSLN 540
DB 1251 RNQRLPSFSNAQOSRLGSGHPEGICSNLVORFSGSPFVLDASKSTKKDASLGCCSLN 1310
QY 541 KPPFLMLFKSPKRGKRIFFVNOQL 565
DB 1311 KPPFLMLFKSGTRFKTKTFRINQL 1335
```

RESULT 8

ADG37225 ID ADG37225 standard; protein; 1713 AA.

XX ADG37225;

XX 26-FEB-2004 (first entry)

XX Human laminin-6 alpha 3 subunit.

XX human; laminin-6; alpha 3; B1 subunit; B2 subunit; cell-movement;

XX cell-adhesion; dermatological; neuroprotective; muscular;

XX epithelial tissue; nervous tissue; varicella disease.

XX Homo sapiens.

XX JP2003212791-A.

XX 30-JUL-2003.

XX 17-JAN-2002; 2002JP-00009227.
XX 17-JAN-2002; 2002JP-00009227.
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX WPI; 2003-819867/77.
XX N-PsDB; ADG37224.

PT Composition comprising laminin-6 for regulation of cell-movement activity
PT and/or cell-adhesion activity, useful for treating or maintaining
PT function of epithelial tissue, nervous tissue and muscles.

PS Claim 2; SEQ ID NO 2; 55pp; Japanese.

CC This invention describes a novel composition comprising the human laminin
CC -6 alpha 3, B1 or B2 subunits for regulation of cell-movement activity
CC and/or cell-adhesion activity. The products of the invention have
CC dermatological, neuroprotective and muscular activity. The composition of
CC the invention is useful for treating or maintaining the function of the
CC epithelial tissue, the nervous tissue and muscles and is also useful for
CC treatment or prevention of varicella disease.

XX Sequence 1713 AA;

Query Match 83.0%; Score 2439; DB 7; Length 1713;

Best Local Similarity 81.9%; Pred. No. 3,1e-215;

Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

```
QY 1 MRFNGSGVEVRLPNDLEDLKGYSLSLFLQRPDLRENGSTEDMFVWYLGKNDASRDYIG 60
DB 771 MRFNGSGVEVRLPNDLEDLKGYSLSLFLQRPDSRENGSTEDMFVWYLGKNDASRDYIG 830
QY 61 MAVVNGQLTCVYNLGDREARLQVDQILTSSESGQAMDRVKQRIYQPAKNTYKATSN 120
DB 831 MAVVNGQLTCVYNLGDREARLQVDQILTSSESGQAMDRVKQRIYQPAKNTYKATSN 890
QY 121 KKPAPAVYDLEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPPYKGCIELDLLEN 180
DB 891 KKPAPAVYDLEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPPYKGCIELDLLEN 950
QY 181 VLSLVNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGARIPQPNAPPPNFQTIQTTV 240
DB 951 VLSLVNFKTTFNLNTTEVEPCRRRKEESDKNYFEGTGARIPQPNAPPPNFQTIQTTV 1010
QY 241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEGIRDTINGKHSILITIGKQ 300
DB 1011 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEGIRDTINGKHSILITIGKQ 1070
QY 301 KMMINNVRSVRIEIGEIFDFSTYYLGGIPAIAREFNISTPAFOGCKMLKKTSGVRL 360
DB 1071 KMMINNVRSVRIEIGEIFDFSTYYLGGIPAIAREFNISTPAFOGCKMLKKTSGVRL 1130
QY 361 NDVTGVTKKCSBDMKLVRTASFSRGGQMSFTNLDPVSTDRFQLSFGQTFQPSGTLNHQ 420
DB 1131 NDVTGVTKKCSBDMKLVRTASFSRGGQMSFTNLDPVSTDRFQLSFGQTFQPSGTLNHQ 1190
QY 421 TRTSSLVTLBEDGHIELSTRDSNIPFKSPGTMYDGLAHVSVISDTSGALLIDDOYLR 480
DB 1191 TRTSSLVTLBEDGHIELSTRDSNIPFKSPGTMYDGLAHVSVISDTSGALLIDDOYLR 1250
QY 481 RNQRLPSFSNAQOSRLGSGHPEGICSNLVORFSGSPFVLDASKSTKKDASLGCCSLN 540
DB 1251 RNQRLPSFSNAQOSRLGSGHPEGICSNLVORFSGSPFVLDASKSTKKDASLGCCSLN 1310
QY 541 KPPFLMLFKSPKRGKRIFFVNOQL 565
DB 1311 KPPFLMLFKSGTRFKTKTFRINQL 1335
```

RESULT 9

ABM81957

ID ABM81957 standard; protein; 1713 AA.
 XX
 AC ABM81957;
 XX
 DT 18-NOV-2004. (first entry)
 XX
 DE Tumour-associated antigenic target (TAT) polypeptide PRO2799, SEQ:5041.
 XX
 KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN MO2004030615-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 29-SEP-2003; 2003MO-US028547.
 XX
 PR 02-OCT-2002; 2002US-0414971P.
 XX
 (GENTH) GENENTECH INC.
 XX
 PI Wu TD, Zhang Z, Zhou Y;
 XX
 DR MPI; 2004-347921/32.
 DR N-PSDB; ACN40327.
 XX
 PT New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 PS Claim 12; SEQ ID NO 5041; 7273bp; English.
 XX
 CC The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT polypeptide of the invention
 XX
 SQ Sequence 1713 AA;
 Query Match 83.0%; Score 2439; DB 8; Length 1713;
 Best Local Similarity 81.9%; Pred. No. 3, le-215;
 Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;
 QY 1 MRNGSGVAVRPNLEDEIKGTTSLFLQRPDLRNGTDMFWYLGKXASADYIG 60
 DB 771 MRNGSGVAVRPNLEDEIKGTTSLFLQRPDLRNGTDMFWYLGKXASADYIG 830
 QY 61 MAVVDGQLTCVYMLGDBEAELQVDQILTKSETKBAVMDRVKFORIYQPARLNTYKATSS 120

DB 831 MAVVDGQLTCVYMLGDBEAELQVDQILTKSETKBAVMDRVKFORIYQPARLNTYKATSS 890
 QY 121 KPKAPAVYDLEGSSSTLTLNLPEDAVFYVGGFPDPPELPSRLRFPYKGCIELDLNEN 180
 DB 891 KPEPVGVMYMDGNSNTLTLNLPEDAVFYVGGFPDPPELPSRLRFPYKGCIELDLNEN 950
 QY 181 VLSLVNFKTTPNLTTEVEPCRRKKEESDKNYEGGVARIPTQPNAPFPNFIQTIQTV 240
 DB 951 VLSLVNFKTTPNLTTEVEPCRRKKEESDKNYEGGVARIPTQPNAPFPNFIQTIQTV 1010
 QY 241 DRGLLFAENQDNFISLNTEDGMLNRYKLSNPPKRGIRDTINDKHSILITGKIQ 300
 DB 1011 DRGLLFAENQDNFISLNTEDGMLNRYKLSNPPKRGIRDTINDKHSILITGKIQ 1070
 QY 301 KRMWIVNRSVRIEELIDFSTYYIGIPIAIRERFNISTPAFQCMNKLKTSSEVNL 360
 DB 1071 KRMWIVNRSVRIEELIDFSTYYIGIPIAIRERFNISTPAFQCMNKLKTSSEVNL 1130
 QY 361 NDTVGVTKKCSSEDMKLVRTASFSRGQMSFTNLDVSTDPFOLSPFGQTFQSGTLLNHQ 420
 DB 1131 NDTVGVTKKCSSEDMKLVRTASFSRGQMSFTNLDVSTDPFOLSPFGQTFQSGTLLNHQ 1190
 QY 421 TRTSLLVTLBDGHEILSTRDSNIPFKSPGYMDGLNHRVYSIDTSGRLRLIDQVLR 480
 DB 1191 TWTRNLQVTLDEGYIELSTDSGGLPKSPQYMDGLNHRVYSIDTSGRLRLIDQVLR 1250
 QY 481 RNQRLPFSNAQSLRLGGGHEGCLSNLVQRFQSPRYLTLASSTKDKSLGGCSLN 540
 DB 1251 NSKRLKHISRSRSLTLDGSGNFEGLSINVFQGLSLSPVLDLTSLNKLKDVSLGGCSLN 1310
 QY 541 KPPEFLMLFKSPKRNKRIENVQL 565
 DB 1311 KPPEFLMLFKSPKRNKRIENVQL 1335
 RESULT 10
 ADR87606
 ID ADR87606 standard; protein; 1713 AA.
 XX
 AC ADR87606;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human laminin alpha 3 (nicein), SEQ ID 10.
 XX
 KW Cytostatic; Gene Therapy; renal cell carcinoma; Wilms tumour; human;
 KW laminin alpha 3; nicein.
 XX
 OS Homo sapiens.
 XX
 PN WO2004075835-A2.
 XX
 PD 10-SEP-2004.
 XX
 PF 20-FEB-2004; 2004MO-US005042.
 XX
 PR 21-FEB-2003; 2003US-00372683.
 XX
 (GENTH) GENENTECH INC.
 XX
 PI Gerritsen ME, Peale FV, Wu TD;
 XX
 DR MPI; 2004-676901/66.
 DR N-PSDB; ADR87605.
 XX
 PT New anti-EDNRA antibody, useful in preparing a composition for diagnosing
 PT or inhibiting the growth of renal cell carcinoma or Wilms tumor.
 XX
 PS Example 1; SEQ ID NO 10; 257bp; English.
 XX
 CC The present invention relates to novel antibodies which bind to proteins
 CC which are overexpressed in renal cell carcinomas or Wilms tumour. The
 CC antibody can bind to a protein comprising CXCR4 (ADR87598), Laminin alpha

CC 4 (ADR87600), TIMP1 (ADR87602), Type IV collagen alpha 1 (ADR87604),
CC laminin alpha 3 (nicotin) (ADR87606), Adrenomedullin (ADR87608), Type IV
CC collagen alpha 2 (ADR87610), Thrombospondin 1 (ADR87612), Type I collagen
CC alpha 2 (ADR87614), Type VI collagen alpha 3 (ADR87616), Latent TGF-beta
CC binding protein 2 (LMBP2) (ADR87618), Serine or cysteine protease
CC inhibitor heat shock protein 47 (HSP47) (ADR87620), Procollagen-lysine, 2
CC -oxoglutarate 5-dioxygenase (ADR87622), connexin 43 (ADR87624), Type IV
CC collagen alpha 2 (ADR87626), Connexin 37 (ADR87628), Ephrin A1
CC (ADR87630), laminin beta 2 (ADR87632), Integrin alpha 1, hevin
CC (ADR87635), Stanniocalcin 1 (ADR87637), Thrombospondin 4 (ADR87639), CD36
CC polypeptide (ADR87641), Endothelin receptor A (EDNRA, ADR87643) or
CC Endothelin receptor B (EDNRB, ADR87645). The proteins of ADR87598-ADR87641
CC and ADR87645 are all overexpressed in renal cell carcinoma, and ADR87643
CC (EDNRA) is overexpressed in Wilms tumour. The antibodies are useful in
CC preparing a composition for diagnosing or inhibiting the growth of renal
CC cell carcinoma or Wilms tumour. The present sequence is one such protein
CC of the invention.

XX XX Sequence 1713 AA;

Query Match 83.0%; Score 2439; DB 8; Length 1713;

Best Local Similarity 81.9%; Pred. No. 3.1e-215;

Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRFNKGSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMTLGNKDAKDYIG 60
DB 771 MRFNKGSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRNGGTENMFVMTLGNKDAKDYIG 830
QY 61 MAVVDGQLTCVYNLGDREAEVQIDVLTSESGEAMVDRPKPRITQPAKLANTKCATSN 120
DB 831 MAVVDGQLTCVYNLGDREAEVQIDVLTSESGEAMVDRPKPRITQPAKLANTKCATSN 890
QY 121 KPRKAPAVYDLBEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPFPYKGCIELDLNEN 180
DB 891 KPRTPGVYDMDGNSNTLNLDPEDAVFYVGGYPPDFELPSRLRPFPYKGCIELDLNEN 950
QY 181 VLSLVNFKTFFNLNTTEVEPCRRRKEESDKNYFEGGYARIPQPNAPFPNFIQTITTV 240
DB 951 VLSLVNFKTFFNLNTTEVEPCRRRKEESDKNYFEGGYARIPQPNAPFPNFIQTITTV 1010
QY 241 DRGLLFFPANGDNFISLNIEDGNLMRYKLNSEPRKEKGRDITNGKSHLITIGKIQ 300
DB 1011 DRGLLFFPANGDNFISLNIEDGNLMRYKLNSEPRKEKGRDITNGKSHLITIGKIQ 1070
QY 301 KRMWNNVRSVRIEIGEIPDFSTYYLGIPAIIRERFNISTPAFOGCMKLNKKTSGVRL 360
DB 1071 KRMWNNVQNTIIDEVDFSTYYLGIPAIIRERFNISTPAFOGCMKLNKKTSGVRL 1130
QY 361 NDTVGVTKKCSSEDMKLVRTASFSRGGQMSFTNLDPVSTDRFQLSPGFQTFQPSGTLNHQ 420
DB 1131 NDTVGVTKKCSSEDMKLVRSASFRRGQLSTFDLGLPTDHLQASFGQTFQPSGTLNHQ 1190
QY 421 TRTSLLVLTLEDGHIESTRDSNIPFKSPGTMDGLHHVSYISTSGRLIIDOVLR 480
DB 1191 TRTRNLQVLTLEDGHIESTRDSNIPFKSPGTMDGLHHVSYISTSGRLIIDOVLR 1250
QY 481 RNQRLPSFSAQOGLRIGGHPFEGCISNVLVQRFSSPEVLDLASKTKDASLGCCSIN 540
DB 1251 NSRRLKHISRSRSLGSGNFGCISNVVQGLSLSPVLDLTSNSLRDVSGLGCCSIN 1310
QY 541 KPPFLMLFKSPKFNKGRIFNVNQL 565
DB 1311 KPPFLMLFKSGSTRFNKTFRINQL 1335

RESULT 11

AAB48456 standard; protein; 1724 AA.

XX AAB48456;

XX 02-MAR-2001 (first entry)

XX

DE Human laminin 5 polypeptide, SEQ ID NO: 2.

XX Human; laminin 5; vulnery; antilulcer; antiinflammatory; antidiabetic;

XX cell adhesion promoter; wound healing; ulcers; burn; skin graft;

XX periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.

XX Homo sapiens.

OS WO20006731-A2.

XX 09-NOV-2000.

XX 28-APR-2000; 2000MO-US011459.

XX 30-APR-1999; 99US-0131720P.

XX 21-AUG-1999; 99US-0149738P.

XX 24-SEP-1999; 99US-0155945P.

XX (BIOS-) BIOSTATUM INC.

XX Boutaud A;

XX MPI: 2000-687538/67.

XX N-PSDB; AAC83717.

XX laminin 5-expressing cells, used to accelerate wound healing associated

XX with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,

XX burns, acute wounds and skin grafts.

XX Claim 3; Page 53-59; 232pp; English.

XX The present sequence is a laminin 5 chain polypeptide. Recombinant

XX laminin 5-expressing cells are used to accelerate wound healing,

XX especially diabetic foot ulcers, venous ulcers, pressure sores, skin

XX surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-

XX intestinal ulcers, periodontitis, and gingivitis. They are also used to

XX improve the biocompatibility of medical devices, and to promote cell

XX adhesion to a surface. They can be used for the ex vivo treatment of Type

XX I diabetes. Laminin can also be used to regulate angiogenesis. The cell

XX line produces and secretes recombinant heterotrimeric laminin, whereas

XX prior art cell lines have been created that produce but do not secreted

XX only one or two chain laminins

XX Sequence 1724 AA;

SQ Query Match 83.0%; Score 2439; DB 3; Length 1724;

Best Local Similarity 81.9%; Pred. No. 3.1e-215;

Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRFNKGSGVEVRLPNDLEDLKGYTSLSLFLQRPDLRENGGTEDMFVMTLGNKDAKDYIG 60
DB 782 MRFNKGSGVEVRLPNDLEDLKGYTSLSLFLQRPNSRNGGTENMFVMTLGNKDAKDYIG 841
QY 61 MAVVDGQLTCVYNLGDREAEVQIDVLTSESGEAMVDRPKPRITQPAKLANTKCATSN 120
DB 842 MAVVDGQLTCVYNLGDREAEVQIDVLTSESGEAMVDRPKPRITQPAKLANTKCATSN 901
QY 121 KPRKAPAVYDLBEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPFPYKGCIELDLNEN 180
DB 902 KPRTPGVYDMDGNSNTLNLDPEDAVFYVGGYPPDFELPSRLRPFPYKGCIELDLNEN 961
QY 181 VLSLVNFKTFFNLNTTEVEPCRRRKEESDKNYFEGGYARIPQPNAPFPNFIQTITTV 240
DB 962 VLSLVNFKTFFNLNTTEVEPCRRRKEESDKNYFEGGYARIPQPNAPFPNFIQTITTV 1021
QY 241 DRGLLFFPANGDNFISLNIEDGNLMRYKLNSEPRKEKGRDITNGKSHLITIGKIQ 300
DB 1022 DRGLLFFPANGDNFISLNIEDGNLMRYKLNSEPRKEKGRDITNGKSHLITIGKIQ 1081
QY 301 KRMWNNVRSVRIEIGEIPDFSTYYLGIPAIIRERFNISTPAFOGCMKLNKKTSGVRL 360
DB 1082 KRMWNNVQNTIIDEVDFSTYYLGIPAIIRERFNISTPAFOGCMKLNKKTSGVRL 1141

QY 361 NDTVGVTKKCSBDMKLVRTASFSRGGOMSFPTNLDVPTDRFOLSFQGFQTPSGTLLAHQ 420
 DB 1142 NDTVGVTKKCSBDMKLVRTASFSRGGOLSTDLGLPTDHLQASFGQTQPSGILLDHQ 1201
 QY 421 TRTSSLVLTLEDGHIELSTDSNIPFKSPGYMDGLLHVSVISDTSGRLIIDQVLR 480
 DB 1202 TWTRNLQVLTLEDGYIELSTDSGSPFKSPQTYMDGLLHVSVISDNGSLRLIIDQLLR 1261
 QY 481 RNQRLPSFNAOOSLRLGGHFECCISNVLYORFSQSPRYLDLASKTKDASIGGCSLN 540
 DB 1262 NSRRLKHIISSRSOSLRLGGSNFECISNVFQRLSLSPRYLDLTSNLSLKDVSLGGCSLN 1321
 QY 541 KPPEFLMLFKSPKPKRPFNKGRIFNVNQL 565
 DB 1322 KPPEFLMLKSGTFRPKTKTRINQL 1346
 RESULT 12
 ADE08094
 ID ADE08094 standard; protein; 3332 AA.
 AC ADE08094;
 XX
 DT 29-JAN-2004 (first entry)
 DE Novel protein (useful for identifying genetic disorders) #249.
 XX
 KW novel gene; novel protein; tissue marker; molecular weight marker;
 KM chromosome marker; genetic disorder.
 XX
 OS Unidentified.
 XX
 PN WO2003054152-A2.
 PD 03-JUL-2003.
 PF 10-DEC-2002; 2002WO-US039555.
 PR 10-DEC-2001; 2001US-0339739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-0365091P.
 PR 14-MAR-2002; 2002US-0365384P.
 PR 12-APR-2002; 2002US-0372381P.
 PR 12-APR-2002; 2002US-0372615P.
 PR 22-APR-2002; 2002US-00128558.
 PR 24-APR-2002; 2002US-0376045P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Auand V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
 PI Ghosh M, Xue AJ, Wehman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
 XX
 DR WPI: 2003-569235/53.
 DR N-PSDB; ADE07183.
 XX
 PT New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.
 XX
 PS Claim 20; SEQ ID NO 1160; 1177pp; English.
 CC The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present amino acid sequence represents a protein
 CC of the invention.
 XX
 SQ Sequence 3332 AA;

Query Match 83.0%; Score 2439; DB 7; Length 3332;
 Best Local Similarity 81.9%; Pred. No. 8,9e-215;
 Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;
 QY 1 MRFNGSGVVRLLPNLDELKGYTSLSLFQRPDLBENGTEDMFVNTGNKASKDYIG 60
 DB 2390 MRFNGSGVVRLLPNLDELKGYTSLSLFQRPDLBENGTEDMFVNTGNKASKDYIG 2449
 QY 61 MAVYDQGLTCVYMLGPREAVQIDQVLTRESQEAWMDRKYRQRIQFALNTKATSN 120
 DB 2450 MAVYDQGLTCVYMLGPREAVQIDQVLTRESQEAWMDRKYRQRIQFALNTKATSN 2509
 QY 121 KPRAPAVYDLEGSSNTLNLADPEDAVFYVGGYPPDFELPSRLRFPYKCIELDLNEN 180
 DB 2510 KPRTPGVYDMDGNSTLNLADPENAVFYVGGYPPDFELPSRLSFPYKCIELDLNEN 2569
 QY 181 VLSLYNFKTTFNLNTEVEPCRRKESDKNYFEGTYARIPQPNAPFNFQTIQTV 240
 DB 2570 VLSLYNFKTTFNLNTEVEPCRRKESDKNYFEGTYARIPQPNAPFNFQTIQTV 2629
 QY 241 DRGLLPPAENQDNFISLNTEDGMLNRYKLNSEPPKRGIRDTINDGKHSILITGKQ 300
 DB 2630 DRGLLPPAENQDNFISLNTEDGMLNRYKLNSEPPKRGIRDTINDGKHSILITGKQ 2689
 QY 301 KRMVINVNRSVRIEGRIPDFTYVGGYPIAIRERFNISTPAFOGCMKULKXTSGVRL 360
 DB 2690 KRMVINVNRSVRIEGRIPDFTYVGGYPIAIRERFNISTPAFOGCMKULKXTSGVRL 2749
 QY 361 NDTVGVTKKCSBDMKLVRTASFSRGGOMSFPTNLDVPTDRFOLSFQGFQTPSGTLLAHQ 420
 DB 2750 NDTVGVTKKCSBDMKLVRTASFSRGGOLSTDLGLPTDHLQASFGQTQPSGILLDHQ 2809
 QY 421 TRTSSLVLTLEDGHIELSTDSNIPFKSPGYMDGLLHVSVISDTSGRLIIDQVLR 480
 DB 2810 TWTRNLQVLTLEDGYIELSTDSGSPFKSPQTYMDGLLHVSVISDNGSLRLIIDQLLR 2869
 QY 481 RNQRLPSFNAOOSLRLGGHFECCISNVLYORFSQSPRYLDLASKTKDASIGGCSLN 540
 DB 2870 NSRRLKHIISSRSOSLRLGGSNFECISNVFQRLSLSPRYLDLTSNLSLKDVSLGGCSLN 2929
 QY 541 KPPEFLMLFKSPKPKRPFNKGRIFNVNQL 565
 DB 2930 KPPEFLMLKSGTFRPKTKTRINQL 2954
 RESULT 13
 AAR70148
 ID AAR70148 standard; protein; 1713 AA.
 AC AAR70148;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-OCT-1995 (first entry)
 DE Deduced sequence of cDNA corresp. to the alpha-3BPA transcript.
 XX
 KW E170; epithelial ligand glycoprotein; epiligrin complex;
 KM epithelial cell binding.
 XX
 OS Homo sapiens.
 XX
 PN WO9506660-A1.
 PD 09-MAR-1995.
 PF 02-SEP-1994; 94WO-US010261.
 PR 02-SEP-1993; 93US-00115918.
 XX
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 XX
 PI Carter WC, Gil SG, Ryan MC;

DR WPI, 1995-115398/15.
 DR N-PSDB; AA083236.
 XX
 PT New nucleic acid encoding epigargin, an epithelial ligand complex - also
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT therapeutically, and diagnostically, e.g., in cases of inflammation and to
 PT induce cancer cell differentiation.
 XX
 XX Claim 12; Fig 15A-F; 187pp; English.
 XX
 CC AA083235 depicts the nt. sequence compiled from sequencing cDNA clones
 CC corresp. to the alpha-3 Bpa transcript. The invention includes nt
 CC sequences in the gp. comprising the nt sequence shown in AA083235, the
 CC cDNA clone Bp-1 (ATCC No. 75540) shown in AA083234, the cDNA clone 1-1
 CC (ATCC No. 75539), and the cDNA clone 8-6 (ATCC No. 75538), or the nt.
 CC sequences shown in AA083236. The entire nt region encoding E170 is
 CC depicted in AA083236, and corresp. to the SO of alpha-3. AA083236
 CC consists of a composite sequence derived from several overlapping clones.
 CC A synthetic polypeptide of at least 5 AAs that corresp. to part or all of
 CC the nt. sequence shown in AA083236 is claimed. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 XX Sequence 1713 AA;
 SQ
 Query Match 82.7%; Score 2431; DB 2; Length 1713;
 Best Local Similarity 81.8%; Pred. No. 1.7e-214;
 Matches 462; Conservative 47; Mismatches 56; Indels 0; Gaps 0;
 QY 1 MRPNKSGVEVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMFWYLGNDKASDXYG 60
 DB 771 MRPNKSGVEVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMFWYLGNDKASDXYG 830
 QY 61 MAVVDQQLTCVYNLGDREAEVQIDQVLTSESQEAAMDVRYKFORIYQFALNTKATSN 120
 DB 831 MAVVDQQLTCVYNLGDREAEVQIDQVLTSESQEAAMDVRYKFORIYQFALNTKATSN 890
 QY 121 KKPAPAVYDLEGSSNTLNLDPEDAVFYGYGYPPELPSRLRFPYKCIELDDLNN 180
 DB 891 KKPAPAVYDLEGSSNTLNLDPEDAVFYGYGYPPELPSRLRFPYKCIELDDLNN 950
 QY 181 VLSLVNFKTTFNLTTEVEPCRRRKESDKNYFEGGYARIPQPNAPFPNFQITQTV 240
 DB 951 VLSLVNFKTTFNLTTEVEPCRRRKESDKNYFEGGYARIPQPNAPFPNFQITQTV 1010
 QY 241 DRGLLFAENODNFISLNTEDGMLNRYKLNSEPPKEKGRDITNGKHSILITGKIQ 300
 DB 1011 DRGLLFAENODNFISLNTEDGMLNRYKLNSEPPKEKGRDITNGKHSILITGKIQ 1070
 QY 301 KRWMIIVNERSVRIEGEIPFSTYYTGGIPAIIRERNISTPAPQGMKNLKTSGVRL 360
 DB 1071 KRWMIIVNERSVRIEGEIPFSTYYTGGIPAIIRERNISTPAPQGMKNLKTSGVRL 1130
 QY 361 NDTVGVTKKCSSEDMKLVRTASFSRGGOMFTNLDVSTSRFQSLSPRQFQPSGTLNMQ 420
 DB 1131 NDTVGVTKKCSSEDMKLVRTASFSRGGOMFTNLDVSTSRFQSLSPRQFQPSGTLNMQ 1190
 QY 421 TRTSLSLVLTLEDGHIESTRDSNIPFKSPGYMDGLLHHVYSISPTSGRLIIDQVLR 480
 DB 1191 TWTRNLQVLTLEDGHIESTRDSNIPFKSPGYMDGLLHHVYSISPTSGRLIIDQVLR 1250
 QY 481 RNORLPSFSNAQSLRGGHFEGCISNVLVQFSGSPYVLDLASKSTKQDASLGCCSIN 540
 DB 1251 NSKRLKHISSRSQSLRGGHFEGCISNVLVQFSGSPYVLDLASKSTKQDASLGCCSIN 1310
 QY 541 KPEFLMLFKSPKRFNKGRIFFNVOL 565
 DB 1311 KPEFLMLFKSPKRFNKGRIFFNVOL 1335

RESULT 14
 AAM26584
 ID AAM26584 standard; protein; 770 AA.
 XX

AC AAM26584;
 XX
 XX 25-MAR-2003 (revised)
 DT 21-JAN-1998 (first entry)
 XX
 DE Rat hemidesmosome formation inducing protein 154 kDa subunit.
 XX
 KW Hemidesmosome; laminin; epithelial cell; cell attachment; adhesion;
 KW bladder carcinoma; 804G; NBT-II; rat; dental implant.
 XX
 OS Rattus sp.
 XX
 PN US5658789-A.
 XX
 PD 19-AUG-1997.
 XX
 PF 19-MAY-1995; 95US-00445135.
 XX
 PR 12-NOV-1993; 93US-00151134.
 XX
 PA (DESM-) DESMOS INC.
 XX
 PI Hormia M, Quaranta V;
 XX
 DR WPI, 1997-424242/39.
 XX
 PT Soluble protein that induces hemidesmosome formation in epithelial cells
 PT - useful for stimulating epithelial cell attachment, e.g. to dental
 PT implants or teeth.
 XX
 PS Claim 2; Col 21-26; 20pp; English.
 XX
 CC This polypeptide comprises the 154 kDa alpha chain of an isolated soluble
 CC protein that induces hemidesmosome formation in epithelial cells normally
 CC unable to form hemidesmosomes. The 146 kD gamma chain (see AAM26584) and
 CC the N-terminal portion (see AAM26585) of the 139 kDa beta chain sequence
 CC were also determined. The protein has properties including: (a)
 CC solubility in aqueous media; (b) binding by antibodies present in the
 CC serum of rabbits inoculated with an extracellular matrix deposited by
 CC 804G rat bladder carcinoma cells or NBT-II rat bladder carcinoma cells;
 CC (c) being bound by monoclonal antibodies generated against extracellular
 CC matrix; (d) promoting rapid epithelial cell adhesion to substrates coated
 CC with at least one of the three protein chains; and (e) being obtainable
 CC from 804G rat bladder carcinoma cells or NBT-II rat bladder carcinoma
 CC cells. The protein (secreted laminin) is used to induce hemidesmosome
 CC formation in epithelial cells and to facilitate their growth (claimed).
 CC It may be used to promote cell attachment to solid surfaces, e.g. to
 CC dental implants, and may also be of use in studies concerning
 CC hemidesmosome morphogenesis and alpha 6 beta 4 integrin interactions with
 CC the epithelial extracellular matrix. (Updated on 25-MAR-2003 to correct
 CC PF field.)
 XX
 SQ Sequence 770 AA;
 Query Match 44.6%; Score 1310; DB 2; Length 770;
 Best Local Similarity 90.9%; Pred. No. 2.1e-111;
 Matches 259; Conservative 3; Mismatches 13; Indels 10; Gaps 4;
 QY 1 MRPNKSGVEVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMFWYLGNDKASDXYG 60
 DB 491 MRPNKSGVEVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMFWYLGNDKASDXYG 550
 QY 61 MA----VVDQQLTCVYNLGDREAEVQIDQVLTSESQEAAMDVRYKFORIYQFALNTYK 115
 DB 551 IGGCRMPAD---VCLQPGGPR--SVSDSGITSESQEAAMDVRYKFORIYQFALNTYK 605
 QY 116 EATSNKPRAPAVYDLEGSSNTLNLDPEDAVFYGYGYPPELPSRLRFPYKCIELD 175
 DB 606 EATSNKPRAPAVYDLEGSSNTLNLDPEDAVFYGYGYPPELPSRLRFPYKCIELD 665
 QY 176 DLTENVLSLYNFKTTFNLTTEVEPCRRRKESDKNYFEGGYARIPQPNAPFPNFQIT 235
 DB 666 DLTENVLSLYNFKTTFNLTTEVEPCRRRKESDKNYFEGGYARIPQPNAPFPNFQIT 725

QY 236 IOTTVDRLGLFFPAENQDNFISLNIEDGNLWRYKLNSEPPKXGI 280
 DB 726 IOTTVDRLGLFFPAENQDNFISLNIEDGNLWRYKLNSEPPKXGI 770

RESULT 15

ABB09503
 ID ABB09503 standard; protein; 3597 AA.

AC ABB09503;

DT 01-NOV-2002 (first entry)

DE Human laminin alpha-5-like NOVIC protein, SEQ ID NO:6.

XX Human; NOVIC; neurological disorder; Alzheimer's disease;
 XX Huntington's disease; Parkinson's disease; pain; behavioural disorder;
 XX addiction; tuberos sclerosis; cancer; immune disorder; allergy;
 XX autoimmune disease; myasthenia gravis; aschma; arthritis; diabetes;
 XX thyroiditis; cardiovascular disease; hypertension; reproductive disorder;
 XX endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;
 XX pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;
 XX polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;
 XX atherosclerosis; cell signal processing-related disorder;
 XX metabolic pathway regulation disorder; cytostatic; neuroprotective;
 XX antiinflammatory; immunosuppressive; anaesthetic; antithrombotic;
 XX dermatological; antidiabetic; antitarrhetic; hepatotropic; neurogenesis;
 XX differentiation; proliferation; motility; haematopoiesis; wound healing;
 XX angiogenesis; forensic biology; transgenic animal; drug screening;
 XX gene therapy; NOVIC; laminin alpha-5-like; chromosome 20.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..14

FT Protein /label=Signal_peptide

FT Protein /note="Mature NOVIC protein"

XX MO200253742-A2.

XX 11-JUL-2002.

XX 07-JAN-2002; 2002MO-US000375.

XX 05-JAN-2001; 2001US-0260018P.

XX 08-JAN-2001; 2001US-0260360P.

XX 28-FEB-2001; 2001US-0272411P.

XX 02-MAR-2001; 2001US-0272817P.

XX 05-JUL-2001; 2001US-0303231P.

XX 12-JUL-2001; 2001US-0305060P.

XX 10-SEP-2001; 2001US-0318405P.

XX 12-SEP-2001; 2001US-0318700P.

XX 04-JAN-2002; 2002US-00037417.

XX (CURA-) CURAGEN CORP.

XX WPI; 2002-583619/62.

XX N-PSDB; ABQ3881.

XX Novel polypeptides and nucleic acids homologous to transmembrane

XX receptor, thymosin, neuromodulin-like family of proteins for diagnosing,

XX treating cancer, atherosclerosis, neurological, skin and autoimmune

XX disorder.

XX Claim 1c; Page 20-21; 323pp; English.

XX The invention relates to 24 novel human proteins designated NOVI-NOV14
 CC (ABB09501-ABB09524), collectively referred to as NOVIC proteins, and
 CC nucleic acids encoding them (ABQ3879-ABQ3902). NOVIC proteins and
 CC nucleotides are useful in the treatment, diagnosis or prevention of NOVIC-
 CC associated disorders or in the manufacture of a medicament for treating
 CC such disorders, with specific applications described for each of the 24
 CC NOVIC proteins, based on their homology to known proteins. Various
 CC disorders are associated with NOVIC proteins including neurological
 CC disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),
 CC pain, behavioural disorders, addiction, tuberos sclerosis, cancers
 CC (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders
 CC (e.g., allergies and autoimmune diseases), myasthenia gravis, aschma,
 CC various forms of arthritis, diabetes, thyroiditis, cardiovascular disease
 CC (e.g., hypertension), reproductive disorders, endometriosis,
 CC incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis,
 CC cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine
 CC disorders, obesity, bacterial infections and particularly cardiomyopathy,
 CC atherosclerosis, cell signal processing-related disorders and disorders
 CC of metabolic pathway regulation. NOVIC nucleic acids and polypeptides may
 CC be used to identify cellular receptors or downstream effectors which
 CC bind to a NOVIC protein, and are also useful as targets for the
 CC identification of small molecules that modulate or inhibit processes such
 CC as neurogenesis, cell differentiation, cell motility, cellular
 CC proliferation, haematopoiesis, wound healing and angiogenesis. NOVIC
 CC nucleic acid sequences can be used to identify a cell or tissue type and
 CC are useful as a source of primers or probes for forensic biology and for
 CC identifying and cloning NOVIC homologues in other cell types. Cells
 CC comprising NOVIC nucleic acids are useful for producing non-human
 CC transgenic animals which are useful for studying the function and
 CC activity of NOVIC proteins and for identifying and evaluating modulators
 CC of NOVIC activity. The present sequence represents the laminin alpha-5-
 CC like protein NOVIC. The gene encoding NOVIC is located on chromosome 20
 CC XX

XX Sequence 3597 AA;

XX Query Match 24.4%; Score 717.5; DB 5; Length 3597;

XX Best Local Similarity 31.7%; Pred. No. 1.4e-85;

XX Matches 200; Conservative 100; Mismatches 222; Indels 109; Gaps 22;

QY 1 MRFNGKSGVEVRLPNDLBDLKGYSLSLFLQRPDLRENGTDEDMFYLGKNDASNDYIG 60
 DB 2712 MKEFNRSQVQLRFRPLADLAAYTALKFYLQGRPEPGQTEBDFVWYMSRQATGDMYG 2771
 QY 61 MAVVDQLTCVYVNLGR-EAEVQIDVLTRESQEAEMVRKQRIYQPKLNTYK--- 116
 DB 2772 VSLRDKKVMVYQLGSGAPAVLSIDEDIGSQ-----FAVSLDKRTLQFGHMSVTEROM 2825
 QY 117 --ATSNKPRAPAYYDLGGSSNTLNLDPEDAVFYVGYPPDELSRLRFPYKGCIEL 174
 DB 2826 IQETKADTYAPGA---EG-----LNLRPDDVFYVGGIPSTTPPLRFPGRGCIEM 2877
 QY 175 DDLNENVLSLYNEKTFNNTTEVEPCRRKKEB-----SDKNYFEGTGYARIPQNP-AP 228
 DB 2878 DTLNEEVSLSYNERFOLDIANDRCARSKSGDPMWDGSLDGTGFRISFDQISIT 2937
 QY 229 FPNFIQTTIOTVDRLGLFFPAENQDNFISLNIEDGNLWRYKLNSEPPKXGI 275
 DB 2938 TKRFEQELRLVSYSGVLFPLKQSQPLCLAVQSGSLVLYDFAGAKKAVLPPLPPLTS 2997
 QY 276 KKKGIADTINDGDHSLITIGLQKRMWNVNVR---SVRIEGEIFDFSTYVLGGIP- 330
 DB 2998 ASRAIQ-----VPLGSSRRVLRERATVYSVEQNDLEADAYTLGGVPPD 3046
 QY 331 -IAIRFPISTPAFOGCKMNLK---KTSQVVALNDTVGTYKCSSEDMKLVRTASPSRG 386
 DB 3047 QLPSLRLRPTGSGVAGCVKIGALKYVDLKRKLN--TTGVSACQADLVLRAMTFRHG 3105
 QY 387 --QMSFTNLDPSTDRFQUSFGQTQPSGTLNMQTRSSSLVLTEDGHSISTDSNT 444
 DB 3106 FLRLASNV-APLTGNVYSGFPHSAQDSALTYRASPVPRPHQVSLQGGVSLQLLRTEV 3164
 QY 445 PIRKSGTYMDGLLHVSVISDTSGRLRLIDDV--LRNRQRLPSFSNAQGS---LRLG 498

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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:19:00 ; Search time 75.7216 Seconds
(without alignments)
2441.722 Million cell updates/sec

Title: US-10-817-423-4

Perfect score: 2940
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Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	2940	100.0	1694	US-10-603-725-12 Sequence 12, App1
2	2940	100.0	1725	US-10-603-725-10 Sequence 10, App1
3	2439	83.0	1693	US-10-603-725-4 Sequence 4, App1
4	2439	83.0	1693	US-10-603-725-8 Sequence 8, App1
5	2439	83.0	1713	US-10-171-311-113 Sequence 113, App1
6	2439	83.0	1713	US-10-372-683-10 Sequence 10, App1
7	2439	83.0	1713	US-10-603-725-6 Sequence 6, App1
8	2439	83.0	1724	US-10-603-725-5 Sequence 2, App1
9	2439	83.0	1724	US-10-603-725-6 Sequence 2, App1
10	2439	83.0	1724	US-10-603-725-6 Sequence 2, App1
11	2439	83.0	1724	US-10-603-725-6 Sequence 2, App1
12	2439	83.0	1724	US-10-603-725-6 Sequence 2, App1
13	2439	83.0	1724	US-10-603-725-6 Sequence 2, App1

14	715	24.3	3695	15	US-10-312-352-22	Sequence 22, App1
15	715	24.3	3696	15	US-10-312-088-31	Sequence 31, App1
16	715	24.3	3705	15	US-10-312-088-30	Sequence 30, App1
17	712	24.2	1640	15	US-10-037-417-8	Sequence 8, App1
18	712	24.2	3695	14	US-10-037-182-2	Sequence 2, App1
19	694	23.6	1816	15	US-10-372-683-4	Sequence 457, App
20	688	23.4	1823	15	US-10-363-616-457	Sequence 154, App
21	686	23.3	1581	16	US-10-408-765A-154	Sequence 4, App1
22	685	23.3	953	9	US-09-845-583-4	Sequence 50, App1
23	685	23.3	953	15	US-10-037-417-50	Sequence 2, App1
24	683	23.2	1816	14	US-10-299-058-2	Sequence 2, App1
25	681	23.2	1816	14	US-10-299-058-4	Sequence 2, App1
26	681	23.2	3635	9	US-09-845-583-2	Sequence 4, App1
27	681	23.2	3635	14	US-10-037-417-47	Sequence 47, App1
28	681	23.2	3635	15	US-10-106-698-5877	Sequence 5877, App
29	680	23.1	469	14	US-10-106-698-5877	Sequence 4, App1
30	578	19.7	908	15	US-10-037-417-4	Sequence 103, App
31	395	13.4	3712	13	US-10-108-605-103	Sequence 48, App1
32	395	13.4	3712	15	US-10-037-417-48	Sequence 51, App1
33	395	13.4	3712	15	US-10-037-417-51	Sequence 5, App1
34	322.5	11.0	286	14	US-10-299-058-5	Sequence 6, App1
35	322.5	11.0	286	14	US-10-299-058-6	Sequence 13, App1
36	321	10.9	289	14	US-10-299-058-13	Sequence 6146, App
37	298.5	10.2	3672	15	US-10-369-493-6146	Sequence 4, App1
38	280	9.5	3084	9	US-09-938-275-4	Sequence 2, App1
39	280	9.5	3084	14	US-10-262-670-2	Sequence 5, App1
40	270	9.2	3075	9	US-09-938-275-5	Sequence 7, App1
41	252	8.6	3070	10	US-09-961-403-7	Sequence 5220, App
42	222.5	7.6	2823	15	US-10-369-493-5220	Sequence 26, App1
43	222.5	7.6	2823	15	US-10-369-493-5221	Sequence 22, App1
44	213.5	7.3	1399	15	US-10-187-975-26	
45	213.5	7.3	1438	15	US-10-187-975-22	

ALIGNMENTS

RESULT 1	US-10-603-725-12	Application US/10603725
Sequence 12, App1	US-10-603-725-12	Application No. US20040014655A1
GENERAL INFORMATION:		
APPLICANT:	Boutand, Ariel	
TITLE OF INVENTION:	Recombinant Laminin 5	
FILE REFERENCES:	99-274-C	
CURRENT APPLICATION NUMBER:	US/10/603,725	
CURRENT FILING DATE:	2003-06-25	
NUMBER OF SEQ ID NOS:	36	
SOFTWARE:	Patentin Ver. 2.0	
SEQ ID NO 12		
LENGTH:	1694	
TYPE:	PRT	
ORGANISM:	Rattus norvegicus	
US-10-603-725-12		
Query Match	100.0%; Score 2940; DB 15; Length 1694;	
Best Local Similarity	100.0%; Pred. No. 7.6e-240;	
Matches	565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MRNKGSGVVRLPNDLEDLKGYSLSLFLORDLRNGSTGMFWYILGNKASKQYIG 60
DB	751	MRNKGSGVVRLPNDLEDLKGYSLSLFLORDLRNGSTGMFWYILGNKASKQYIG 810
QY	61	MAVVDGQLTCVNIAGREAEVQIDQVLTESGSEAVMDRVKFORIQPAKANTYKATSN 120
DB	811	MAVVDGQLTCVNIAGREAEVQIDQVLTESGSEAVMDRVKFORIQPAKANTYKATSN 870
QY	121	KPRAPVYDLEGGSSNTLNLDEDAVFYGGVPPPELPSRLRFPYKCIETLDNEN 180
DB	871	KPRAPVYDLEGGSSNTLNLDEDAVFYGGVPPPELPSRLRFPYKCIETLDNEN 930
QY	181	VLSTNYKTFNNATTEVEPCRRRKESDNGVEGTCYARIPTQNPAPFNFIQTQTV 240

Db 931 VLSLNVFKTTFNLTNTTEVEBCRRRKEESDKNVEGTGYARIPTQPNAPFPNFIQTITQTV 990
Qy 241 DRGLLFFAENQDNFISLNIEDGNLWRYKLNSEPPKEKGRDITINDGKHSILITIGKQ 300
Db 991 DRGLLFFAENQDNFISLNIEDGNLWRYKLNSEPPKEKGRDITINDGKHSILITIGKQ 1050
Qy 301 KKMWINNERSVARIIEGIFDFSTYYLGGIPAIARRFNISTPAPQCMKMLKKTSGVRL 360
Db 1051 KKMWINNERSVARIIEGIFDFSTYYLGGIPAIARRFNISTPAPQCMKMLKKTSGVRL 1110
Qy 361 NDTVGATKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGPOTFQPSGTLNMQ 420
Db 1111 NDTVGATKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGPOTFQPSGTLNMQ 1170
Qy 421 TRTSSLVLTLEBDEHIELSTRDSNIPIFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 480
Db 1171 TRTSSLVLTLEBDEHIELSTRDSNIPIFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 1230
Qy 481 RNQRLPFSNMQOSLRLGGHFEGCISNVLVORFQSPPEVLDLASKSTKQDASLGCCSLN 540
Db 1231 RNQRLPFSNMQOSLRLGGHFEGCISNVLVORFQSPPEVLDLASKSTKQDASLGCCSLN 1290
Qy 541 KPPFLMLFKSPKRFNKGRIFFVNL 565
Db 1291 KPPFLMLFKSPKRFNKGRIFFVNL 1315

RESULT 2
US-10-603-725-10
/ Sequence 10, Application US/10603725
/ Publication No. US20040014665A1
/ GENERAL INFORMATION:
/ APPLICANT: Bouland, Ariel
/ TITLE OF INVENTION: Recombinant Laminin 5
/ FILE REFERENCE: 99-274-C
/ CURRENT APPLICATION NUMBER: US/10/603,725
/ CURRENT FILING DATE: 2003-06-25
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 10
/ LENGTH: 1725
/ TYPE: PRP
/ ORGANISM: Rattus norvegicus
US-10-603-725-10

Query Match 100.0%; Score 2940; DB 15; Length 1725;
Best Local Similarity 100.0%; Pred. No. 7.8e-240;
Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMFVYLGNDKASRDYTG 60
Db 782 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMFVYLGNDKASRDYTG 841
Qy 61 MAVVDGQLTCVYNLGDREAVQIDQVLTSESQEAAMDVRVKFORIYQPAKLNTYKATSN 120
Db 842 MAVVDGQLTCVYNLGDREAVQIDQVLTSESQEAAMDVRVKFORIYQPAKLNTYKATSN 901
Qy 121 KKPAPAVYDLEGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKGCIELDDLNN 180
Db 902 KKPAPAVYDLEGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKGCIELDDLNN 961
Qy 181 VLSLNVFKTTFNLTNTTEVEBCRRRKEESDKNVEGTGYARIPTQPNAPFPNFIQTITQTV 240
Db 962 VLSLNVFKTTFNLTNTTEVEBCRRRKEESDKNVEGTGYARIPTQPNAPFPNFIQTITQTV 1021
Qy 241 DRGLLFFAENQDNFISLNIEDGNLWRYKLNSEPPKEKGRDITINDGKHSILITIGKQ 300
Db 1022 DRGLLFFAENQDNFISLNIEDGNLWRYKLNSEPPKEKGRDITINDGKHSILITIGKQ 1081
Qy 301 KKMWINNERSVARIIEGIFDFSTYYLGGIPAIARRFNISTPAPQCMKMLKKTSGVRL 360
Db 1082 KKMWINNERSVARIIEGIFDFSTYYLGGIPAIARRFNISTPAPQCMKMLKKTSGVRL 1141

Qy 361 NDTVGATKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGPOTFQPSGTLNMQ 420
Db 1142 NDTVGATKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGPOTFQPSGTLNMQ 1201
Qy 421 TRTSSLVLTLEBDEHIELSTRDSNIPIFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 480
Db 1202 TRTSSLVLTLEBDEHIELSTRDSNIPIFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 1261
Qy 481 RNQRLPFSNMQOSLRLGGHFEGCISNVLVORFQSPPEVLDLASKSTKQDASLGCCSLN 540
Db 1261 RNQRLPFSNMQOSLRLGGHFEGCISNVLVORFQSPPEVLDLASKSTKQDASLGCCSLN 1321
Qy 541 KPPFLMLFKSPKRFNKGRIFFVNL 565
Db 1322 KPPFLMLFKSPKRFNKGRIFFVNL 1346

RESULT 3
US-10-603-725-4
/ Sequence 4, Application US/10603725
/ Publication No. US20040014665A1
/ GENERAL INFORMATION:
/ APPLICANT: Bouland, Ariel
/ TITLE OF INVENTION: Recombinant Laminin 5
/ FILE REFERENCE: 99-274-C
/ CURRENT APPLICATION NUMBER: US/10/603,725
/ CURRENT FILING DATE: 2003-06-25
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 1693
/ TYPE: PRP
/ ORGANISM: Homo sapiens
US-10-603-725-4

Query Match 83.0%; Score 2439; DB 15; Length 1693;
Best Local Similarity 81.9%; Pred. No. 2.6e-197;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

Qy 1 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMFVYLGNDKASRDYTG 60
Db 751 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRENGGTEDMFVYLGNDKASRDYTG 810
Qy 61 MAVVDGQLTCVYNLGDREAVQIDQVLTSESQEAAMDVRVKFORIYQPAKLNTYKATSN 120
Db 811 MAVVDGQLTCVYNLGDREAVQIDQVLTSESQEAAMDVRVKFORIYQPAKLNTYKATSN 870
Qy 121 KKPAPAVYDLEGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKGCIELDDLNN 180
Db 871 KKPAPAVYDLEGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKGCIELDDLNN 930
Qy 181 VLSLNVFKTTFNLTNTTEVEBCRRRKEESDKNVEGTGYARIPTQPNAPFPNFIQTITQTV 240
Db 931 VLSLNVFKTTFNLTNTTEVEBCRRRKEESDKNVEGTGYARIPTQPNAPFPNFIQTITQTV 990
Qy 241 DRGLLFFAENQDNFISLNIEDGNLWRYKLNSEPPKEKGRDITINDGKHSILITIGKQ 300
Db 991 DRGLLFFAENQDNFISLNIEDGNLWRYKLNSEPPKEKGRDITINDGKHSILITIGKQ 1050
Qy 301 KKMWINNERSVARIIEGIFDFSTYYLGGIPAIARRFNISTPAPQCMKMLKKTSGVRL 360
Db 1051 KKMWINNERSVARIIEGIFDFSTYYLGGIPAIARRFNISTPAPQCMKMLKKTSGVRL 1110
Qy 361 NDTVGATKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGPOTFQPSGTLNMQ 420
Db 1111 NDTVGATKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGPOTFQPSGTLNMQ 1170
Qy 421 TRTSSLVLTLEBDEHIELSTRDSNIPIFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 480
Db 1171 TRTSSLVLTLEBDEHIELSTRDSNIPIFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 1230
Qy 481 RNQRLPFSNMQOSLRLGGHFEGCISNVLVORFQSPPEVLDLASKSTKQDASLGCCSLN 540
Db 1230 RNQRLPFSNMQOSLRLGGHFEGCISNVLVORFQSPPEVLDLASKSTKQDASLGCCSLN 1290

Db 1231 NSKRLKHSSRSOSRLRGSNFECCISNVFQRLSLSPVLDLITNSLAKDVSIGGCSLN 1290
 QY 541 KPPELMLFKSPKRFNKRIFVNO 565
 Db 1291 KPPELMLKSGSTRFNKTRINOL 1315

RESULT 4

US-10-603-725-8
 ; Sequence 8, Application US/10603725
 ; Publication No. US20040014665A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bouland, Ariel
 ; TITLE OF INVENTION: Recombinant Laminin 5
 ; FILE REFERENCE: 99-274-C
 ; CURRENT APPLICATION NUMBER: US/10/603,725
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 1693
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-603-725-8

Query Match 83.0%; Score 2439; DB 15; Length 1693;
 Best Local Similarity 81.9%; Pred. No. 2.6e-197;
 Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRENGSGVEVRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYVLGNKQASXDYG 60
 Db 751 MRENGSGVEVRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYVLGNKQASRYIG 810
 QY 61 MAVVDQQLTCVYNLGDREAEVQIDQVLTSESOEAVMDRYKFORIYOPAKLNTKATSN 120
 Db 811 MAVVDQQLTCVYNLGDREAEVQIDQVLTSESKAEAVMDRYKFORIYOPAKLNTKATSS 870
 QY 121 KPAKPAVYDLGGSSNTLNLMDPEDAVFYGGYPPDELSRLRFPYKGCIELDNLNEN 180
 Db 871 KPETPGYDDMDGRNSNTLNLMDPENVVFYGGYPPDKLPSRLSPPYKGCIELDNLNEN 930
 QY 181 VLSLYNFKTFNNTTEVEPCRRKESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTV 240
 Db 931 VLSLYNFKTFNNTTEVEPCRRKESDKNYFEGTGYARVPTQPHAPITPFGQTIQTV 990
 QY 241 DRGLPFAENQDNFISLNIEDGNLMVRYKLNSEBPYKGIADTINDKHSILITIGKLQ 300
 Db 991 DRGLPFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDALINNGRHSIQIKIGKLQ 1050
 QY 301 KRWMINVNSRVAREGIPDPSTYYLGGIPIAIRERNISTPAFQCGMKLKTSGVRL 360
 Db 1051 KRWMINVQNTIIDEVDFPSTYYLGGIPIAIRERNISTPAFQCGMKLKTSGVRL 1110
 QY 361 NDVYGVTKKCSBPMKLVRTASFSRQGMSPFTNLDVSTDRFQLSFGFOTQPSGTLINHQ 420
 Db 1111 NDVYGVTKKCSBPMKLVRTASFSRQGLSFTDGLPFTDHLQASFGQOTQPSGTLINHQ 1170
 QY 421 TRTSLLVLTLEDGHIELSTDSNIPFKSPGYTMDGLLHVSVISDTSGLRLIIDQVLR 480
 Db 1171 TWTRNLQVLTLEDGYIELSTDSGGRIFKSPQTYMDGLLHVSVISDMSGRLIIDQDLR 1230
 QY 481 RNQRLPSFSAQOSLRLGGGHFEGCISNVLVQRFOSQPEVLDLASKTKQDASIGGCSLN 540
 Db 1231 NSKRLKHSSRSOSRLRGSNFECCISNVFQRLSLSPVLDLITNSLAKDVSIGGCSLN 1290
 QY 541 KPPELMLFKSPKRFNKRIFVNO 565
 Db 1291 KPPELMLKSGSTRFNKTRINOL 1315

RESULT 5
 US-10-171-311-113
 ; Sequence 113, Application US/10171311

; Publication No. US20030087270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Chen, Yan
 ; APPLICANT: Zhao, Xumei
 ; APPLICANT: Monahan, John
 ; APPLICANT: Kamackar, Shubhangi
 ; APPLICANT: Glat, Karen
 ; APPLICANT: Ganavaram, Manjula
 ; APPLICANT: Hoerish, Sebastian
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
 ; TITLE OF INVENTION: OF CERVICAL CANCER
 ; FILE REFERENCE: MRI-035
 ; CURRENT APPLICATION NUMBER: US/10/171,311
 ; CURRENT FILING DATE: 2002-06-12
 ; PRIOR APPLICATION NUMBER: US 60/298,159
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/298,155
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/335,936
 ; PRIOR FILING DATE: 2001-11-14
 ; NUMBER OF SEQ ID NOS: 238
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 113
 ; LENGTH: 1713
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-171-311-113

Query Match 83.0%; Score 2439; DB 14; Length 1713;
 Best Local Similarity 81.9%; Pred. No. 2.6e-197;
 Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRENGSGVEVRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYVLGNKQASXDYG 60
 Db 771 MRENGSGVEVRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYVLGNKQASRYIG 830
 QY 61 MAVVDQQLTCVYNLGDREAEVQIDQVLTSESOEAVMDRYKFORIYOPAKLNTKATSN 120
 Db 831 MAVVDQQLTCVYNLGDREAEVQIDQVLTSESKAEAVMDRYKFORIYOPAKLNTKATSS 890
 QY 121 KPAKPAVYDLGGSSNTLNLMDPEDAVFYGGYPPDELSRLRFPYKGCIELDNLNEN 180
 Db 891 KPETPGYDDMDGRNSNTLNLMDPENVVFYGGYPPDKLPSRLSPPYKGCIELDNLNEN 950
 QY 181 VLSLYNFKTFNNTTEVEPCRRKESDKNYFEGTGYARIPTQPNAPFPNFIQTIQTV 240
 Db 951 VLSLYNFKTFNNTTEVEPCRRKESDKNYFEGTGYARVPTQPHAPITPFGQTIQTV 1010
 QY 241 DRGLPFAENQDNFISLNIEDGNLMVRYKLNSEBPYKGIADTINDKHSILITIGKLQ 300
 Db 1011 DRGLPFAENGDRFISLNIEDGKLMVRYKLNSELPKERGVGDALINNGRHSIQIKIGKLQ 1070
 QY 301 KRWMINVNSRVAREGIPDPSTYYLGGIPIAIRERNISTPAFQCGMKLKTSGVRL 360
 Db 1071 KRWMINVQNTIIDEVDFPSTYYLGGIPIAIRERNISTPAFQCGMKLKTSGVRL 1130
 QY 361 NDVYGVTKKCSBPMKLVRTASFSRQGMSPFTNLDVSTDRFQLSFGFOTQPSGTLINHQ 420
 Db 1131 NDVYGVTKKCSBPMKLVRTASFSRQGLSFTDGLPFTDHLQASFGQOTQPSGTLINHQ 1190
 QY 421 TRTSLLVLTLEDGHIELSTDSNIPFKSPGYTMDGLLHVSVISDTSGLRLIIDQVLR 480
 Db 1191 TWTRNLQVLTLEDGYIELSTDSGGRIFKSPQTYMDGLLHVSVISDMSGRLIIDQDLR 1250
 QY 481 RNQRLPSFSAQOSLRLGGGHFEGCISNVLVQRFOSQPEVLDLASKTKQDASIGGCSLN 540
 Db 1251 NSKRLKHSSRSOSRLRGSNFECCISNVFQRLSLSPVLDLITNSLAKDVSIGGCSLN 1310
 QY 541 KPPELMLFKSPKRFNKRIFVNO 565
 Db 1311 KPPELMLKSGSTRFNKTRINOL 1335

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RESULT 6
US-10-372-683-10
; Sequence 10, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: BEALE JR., FRANKLIN V.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 10
; LENGTH: 1713
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-372-683-10
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Query Match      83.0%; Score 2439; DB 15; Length 1713;
Best Local Similarity 81.9%; Pred. No. 2.6e-197;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;
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```
QY 1 MRPNKSGVEVRLPNLDLKGYSLSLFLQRPDLRENGTEEMFVMTLGNDAASKDYIG 60
DB 771 MRPNKSGVEVRLPNLDLKGYSLSLFLQRPNSRENGTEEMFVMTLGNDAASHDYIG 830
QY 61 MAVVDGQLTCVYNLDREAEVQIDQVLTBESQBAVMDRVKFORIYQPAKLNTYKATSN 120
DB 831 MAVVDGQLTCVYNLDREAEVQIDQVLTBESQBAVMDRVKFORIYQPAKLNTYKATSN 890
QY 121 KPRAPAVYDLGEGSSNTLNLNDBDAVYVGGYPPDFELPSRLRPPYKGCIELDLNEN 180
DB 891 KPRPQVYDMGDRNSNTLNLNDBENVVYVGGYPPDFELPSRLRPPYKGCIELDLNEN 950
QY 181 VLSVNFKTFPLNTTEVEPCRRRKEESDKNYFEGTGARLPTQPNAPFPNFQTIQTIV 240
DB 951 VLSVNFKTFPLNTTEVEPCRRRKEESDKNYFEGTGARLPTQPNAPFPNFQTIQTIV 1010
QY 241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIKRTINDGKHSILITIGKQ 300
DB 1011 DRGLLFFAENQDRFISLNIEDGKLMVRYKLNSELPEKRGVGDALNNGRHSIQIKIGKQ 1070
QY 301 KKMWINVNERSVRIEGEIPDPSTYYLGGIPIAIRERFNISTPAFQCGMKNLKKTSGVRL 360
DB 1071 KKMWINVQNTIIDGEVFDSTYYLGGIPIAIRERFNISTPAFQCGMKNLKKTSGVRL 1130
QY 361 NDVTVGTYKCSBDMKLVTRTASFSRGGQMSFTNLDVSTDRFQLSFGQTFQPSGTLNMQ 420
DB 1131 NDVTVGTYKCSBDMKLVTRTASFSRGGQMSFTNLDVSTDRFQLSFGQTFQPSGTLNMQ 1190
QY 421 TRTSSLVTLDEGHIETLSTSDSNIPFKSPGTMDGLLHVVSISDTSGRLIIDQVLR 480
DB 1191 TWTRNLQVTLDEGYIELSTSDSGGPIFKSPQTYMDGLLHVVSISDTSGRLIIDQVLR 1250
QY 481 RNQRLPSFNAQOSRLRGHPEGICISNVLVQRFQSPSEVLDLASKTKKASLGCCSLN 540
DB 1251 NSKRLKHITSSRSQSLRGHPEGICISNVVQRLSPSEVLDLTSNLSLRDVS LGCCSLN 1310
QY 541 KPPFLMLFKSPKRFNKGRIFFNVNQL 565
DB 1311 KPPFLMLKSGTRFNKTKTFRINQL 1335
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```
RESULT 7
US-10-603-725-6
; Sequence 6, Application US/10603725
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```
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boutand, Arlet
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1713
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-725-6
```

```
Query Match      83.0%; Score 2439; DB 15; Length 1713;
Best Local Similarity 81.9%; Pred. No. 2.6e-197;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;
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```
QY 1 MRPNKSGVEVRLPNLDLKGYSLSLFLQRPDLRENGTEEMFVMTLGNDAASKDYIG 60
DB 771 MRPNKSGVEVRLPNLDLKGYSLSLFLQRPNSRENGTEEMFVMTLGNDAASHDYIG 830
QY 61 MAVVDGQLTCVYNLDREAEVQIDQVLTBESQBAVMDRVKFORIYQPAKLNTYKATSN 120
DB 831 MAVVDGQLTCVYNLDREAEVQIDQVLTBESQBAVMDRVKFORIYQPAKLNTYKATSN 890
QY 121 KPRAPAVYDLGEGSSNTLNLNDBDAVYVGGYPPDFELPSRLRPPYKGCIELDLNEN 180
DB 891 KPRPQVYDMGDRNSNTLNLNDBENVVYVGGYPPDFELPSRLRPPYKGCIELDLNEN 950
QY 181 VLSVNFKTFPLNTTEVEPCRRRKEESDKNYFEGTGARLPTQPNAPFPNFQTIQTIV 240
DB 951 VLSVNFKTFPLNTTEVEPCRRRKEESDKNYFEGTGARLPTQPNAPFPNFQTIQTIV 1010
QY 241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIKRTINDGKHSILITIGKQ 300
DB 1011 DRGLLFFAENQDRFISLNIEDGKLMVRYKLNSELPEKRGVGDALNNGRHSIQIKIGKQ 1070
QY 301 KKMWINVNERSVRIEGEIPDPSTYYLGGIPIAIRERFNISTPAFQCGMKNLKKTSGVRL 360
DB 1071 KKMWINVQNTIIDGEVFDSTYYLGGIPIAIRERFNISTPAFQCGMKNLKKTSGVRL 1130
QY 361 NDVTVGTYKCSBDMKLVTRTASFSRGGQMSFTNLDVSTDRFQLSFGQTFQPSGTLNMQ 420
DB 1131 NDVTVGTYKCSBDMKLVTRTASFSRGGQMSFTNLDVSTDRFQLSFGQTFQPSGTLNMQ 1190
QY 421 TRTSSLVTLDEGHIETLSTSDSNIPFKSPGTMDGLLHVVSISDTSGRLIIDQVLR 480
DB 1191 TWTRNLQVTLDEGYIELSTSDSGGPIFKSPQTYMDGLLHVVSISDTSGRLIIDQVLR 1250
QY 481 RNQRLPSFNAQOSRLRGHPEGICISNVLVQRFQSPSEVLDLASKTKKASLGCCSLN 540
DB 1251 NSKRLKHITSSRSQSLRGHPEGICISNVVQRLSPSEVLDLTSNLSLRDVS LGCCSLN 1310
QY 541 KPPFLMLFKSPKRFNKGRIFFNVNQL 565
DB 1311 KPPFLMLKSGTRFNKTKTFRINQL 1335
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RESULT 8
US-10-603-725-2
; Sequence 2, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boutand, Arlet
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
```



```

; LENGTH: 1724
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-725-2

Query Match      83.0%; Score 2439; DB 15; Length 1724;
Best Local Similarity 81.9%; Pred. No. 2.6e-197;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRRNGSGVVRRLPNLEDEIKGYSLSLFLQRPDLRNGTDMFVNYLGNKASKYIG 60
DB 782 MRRNGSGVVRRLPNLEDEIKGYSLSLFLQRPDLRNGTDMFVNYLGNKASKYIG 841
QY 61 MAVVDGQLTCVNYLGDREAEVQIDVLTSESSQAVNDVRYFORIYQPAKLTAKTSN 120
DB 842 MAVVDGQLTCVNYLGDREAEVQIDVLTSESSQAVNDVRYFORIYQPAKLTAKTSN 901
QY 121 KPRAPAVYDLGGSSNTLLNLDPEDAVYVGYGPPDFELPSRLFPFYKGCIBLDLNN 180
DB 902 KPETPGYDMDGNSNTLLNLDPENNVFYVGYGPPDFELPSRLFPFYKGCIBLDLNN 961
QY 181 VLSLYNFKTFNLTTEVEPCRRKESDXYFEGTGYARIPTQPNAPFNFITQITTV 240
DB 962 VLSLYNFKTFNLTTEVEPCRRKESDXYFEGTGYARPTQPHAPIPTFGQITQTV 1021
QY 241 DRGLLFAENQDPIFINIDGNLMRYKLNSEPRKGIKRTINDKDSILITGKIQ 300
DB 1022 DRGLLFAENGDRPISINIDGKLMRYKLNSELPKRERGVGDALNNRDSIQIKIGKIQ 1081
QY 301 KRWMINNERSVRLEGIPDFSTYYLGGIPLAIRERFNIPTAPQGGKMLKTSGVVRL 360
DB 1082 KRWMINVDVQNTIIDGVFPSTYYLGGIPLAIRERFNIPTAPQGGKMLKTSGVVRL 1141
QY 361 NDTVGVTKKCSBDMKLVRTASFSRQGMSTNLDPSTDRFQLSFGFTQPSGTLNMQ 420
DB 1142 NDTVGVTKKCSBDMKLVRTASFSRQGLSTFDLGLPTDHLQASFGFTQPSGTLNMQ 1201
QY 421 TRTSLLVLTEDGHEISTDSNIPFKSPGTVDGILHVSVDSPSGRLITIDQVR 480
DB 1202 TWRNLDVLTEDGHEISTDSGSPFKSPGTVDGILHVSVDSPSGRLITIDQVR 1261
QY 481 RNORLSPFSAQOGLRIGGHEGECISNVLPQSPGPEVLDLASKSTKQDASLGCSLN 540
DB 1262 NSKRKLHISSSRGLRIGGHEGECISNVLPQSPGPEVLDLASKSTKQDASLGCSLN 1321
QY 541 KPPLMLFKSPKRFNKRIFNVQL 565
DB 1322 KPPLMLFKSTRTNKTFRINQL 1346

RESULT 9
US-10-037-417-6
; Sequence 6, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Rameesh
; APPLICANT: Alsbrook II, John P
; APPLICANT: Tcherev, Vellizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Paturajan, Meera
; APPLICANT: Groese, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine B
; APPLICANT: Vermet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
```

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; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Sheno, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles B
; APPLICANT: Bisen, Andrew J
; TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3597
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-037-417-6

Query Match      24.4%; Score 717.5; DB 15; Length 3597;
Best Local Similarity 31.7%; Pred. No. 1.1e-50;
Matches 200; Conservative 100; Mismatches 222; Indels 109; Gaps 22;

QY 1 MRRNGSGVVRRLPNLEDEIKGYSLSLFLQRPDLRNGTDMFVNYLGNKASKYIG 60
DB 2712 MRRNGSGVVRRLPNLEDEIKGYSLSLFLQRPDLRNGTDMFVNYLGNKASKYIG 2771
QY 61 MAVVDGQLTCVNYLGDREAEVQIDVLTSESSQAVNDVRYFORIYQPAKLTAKTSN 116
DB 2772 VSLRDKKXHVYDLGEGRAVLSDIDBIDGQ-----FAVSLDRITLQFGHMSVTVRQM 2825
QY 2772 VSLRDKKXHVYDLGEGRAVLSDIDBIDGQ-----FAVSLDRITLQFGHMSVTVRQM 2825
QY 117 -ATSNKPRAPAVYDLGGSSNTLLNLDPEDAVYVGYGPPDFELPSRLFPFYKGCIBL 174
DB 2826 IQETKCDTPVAPGA---EG-----LNMIRPDDFVYVGYGPPDFELPSRLFPFYKGCIBL 2877
QY 175 DDLNENVALSYNFKTFNLTTEVEPCRRKESDXYFEGTGYARIPTQPNAPFNFITQITTV 228
DB 2878 DTLNEEVSLSYNFKTFNLTTEVEPCRRKESDXYFEGTGYARIPTQPNAPFNFITQITTV 2937
QY 229 PFNFITQITTVDRGLLFAENQDPIFINIDGNLMRYKLNSEPRKGIKRTINDKDSILITGKIQ 275
DB 2938 TKRFBQELRIVSYGVFLFKQSQFLCLAVGSGSLVLDPAAGLKKAVPLQPPPLTYS 2997
QY 276 KKGIRDTINDGKHSILITGKIQKRWMINVNER--SVRIGEIFDFSTYYLGGIP-- 330
DB 2998 ASRAIQ-----VFLLGSRKXKVLVRVERATVYSVEQNDLADAYLGGVPPD 3046
QY 331 -IAIRERFNIPTAPQGGKMLKTSGVNLPNDVGVTKKCSBDMKLVRTASFSRQGM 386
DB 3047 QLPGLRLFLPTGGSVRCVKGIALGKYVDLKLIN--TTGVSAGCTADLVGRAMTFRGHG 3105
QY 387 --QMSPTNLDPSTDRFQLSFGFTQPSGTLNHNQRTSSLLVLTEDGHEISTDSNIT 444
DB 3106 FLRLALSNV-APLTGNVYSGFGFHSAGDSALLVYRASPVAPPHQVSLQGGVAVSLQLLRETV 3164
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OY 445 PIFKSPGYMGLLHVSVISPTGLRLIDPV--LRNRORLPSFSNAQS----LRLG 498
Db 3165 ---KTQAGFADGAEHYVAFYSNATVWLVDYDQLQDMKPHRPPPELQPPQEGPRLILG 32221
OY 499 G-----GHEFGCISNLYVORFQSPPEVLDL----- 523
Db 3222 GLPESGRTIYFNSGCSINFFVQGLLGPQRVFLDQNLGSVNVSITGCAPALQACTPELGPRQ 3281
OY 524 ASKSTKQDASLGCGCLNKPPLMLFKSRPR 554
Db 3282 ASRNSRQPARHPACML--PPLHRTTRDSYQF 3310

RESULT 10
US-10-037-417-2
; Sequence 2, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alachbrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spylek, Kimberly A
; APPLICANT: PatluraJan, Meera
; APPLICANT: Groesse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vermet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rotenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eissen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3600
; TYPE: PRT
; ORGANISM: Homo sapiens

```

```

US-10-037-417-2
Query Match 24.4%; Score 717.5; DB 15; Length 3600;
Best Local Similarity 31.7%; Pred. No. 1,1e-50;
Matches 200; Conservative 100; Mismatches 222; Indels 109; Gaps 22.

OY 1 MRPNKGSGVEVRLLPNDELDELDKGYTSLSLFQRPDLREKGGTEDMFVMYLGAKNDKADKYIG 60
Db 2715 MKFNGRSGVQRTRELDLADLAAYTALKFYLQGPPEPQGGTEDFVMYMSGKQATGDMG 2774
OY 61 MAVVDGQLTCYNTIGDR EAEVQIDQVLTBESQDAVMDRYKFORIYQFALKNTYKE-- 116
Db 2775 VSLDDKQHWNYQLGEAGPAVLSIDBIDIGD-----FAAVSLDRTLQFGHMSVYVERQM 2828
OY 117 --ATSNKPAAVAVVDLEGSSNTLLNDPEBAVAVYGGYPPDFELPSRLRPPYKCIEL 174
Db 2829 IQETKGDITVABGA--EG-----LNLNRPDVFYVGGYESTFPPLRLRPPKRGCIEM 2886
OY 175 DDLNENYLSLYNFKTFENLNTTEVEPCRRKKE-----SDKNYEGETGABAPIQPN-AP 228
Db 2881 DTLNEBAYVSLYNFERTFQDLTAVDNRPCARSKSTGDPMLTDSYLDGTGFALISFDSQIST 2944
OY 229 FPNFIQTITQTVBGLLFPBANQNFSLNIEDGNLMRYKLN-----EPP----- 275
Db 2941 TKREGEQLRLVYSYSGVLFELKQSQFCLAVQESLVLXDPFGALKKAVPLQPPPLTS 3000
OY 276 KEKEIRDTINDKQHSILITTKGLQKTMIMVNR--SVRIEGRIDPFSTYYLGGIP-- 330
Db 3001 ASKAIQ-----VFLLGSRKVLVVERBATYYSVEGDNDLDELADAYILGGVPPD 3049
OY 331 -IAIRERNISTPAPFGCMKMK--KTSGVYRLNDVYGVTKKCSSEDMKLVRTASFSRGG 386
Db 3050 QLPRLRLFPFGGSGVRGCVKQIKALGXVYDLKRLN-TTGVASGCTADLLVGRAMTFHGG 3108
OY 387 --QMSFTNLVPSIDRFQLSFQTFOPSPGTLNHOVRTSSLVTLIEDGHIELSTRDSNI 444
Db 3109 FLRLALSNV-APLTGNVYSGGFGHSADSLLYTRASVYRHHQVSLQOGRVSLQILREIV 3166
OY 445 PIFKSPGTWMDGLLHHVSVISDTSGLRLLLDDQV-LRRNQRLPSFSAQOS---LRLG 498
Db 3168 ---KTQAGFADGAPHYVAFYSNAGWMLYVDQIQQMKPHRGPPPELQPPQEGPRLILG 3224
OY 499 G-----GHEEGCISNVLNORFSQSPRYDL----- 523
Db 3225 GLPESGTTYNSSGCTISNVFQVRLRGPPQRFVFLQONLGSVNVSTGCAPALQATPGLGRQ 3284
OY 524 ASKSTKQDASLGCSLNPFLMLFKSPKRP 554
Db 3285 ASRSRQPAHRHPACML--PPLRLRTTRDSYQF 3313

RESULT 11
US-10-112-944-347
Sequence 347, Application US/10112944
Publicatation No. US20040048249A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Gezhi
APPLICANT: Zhang, Jie
APPLICANT: Ren, Peiyan
APPLICANT: Xue, Aiding J.
APPLICANT: Wang, Jilan-Rui
APPLICANT: Weinman, Tom
APPLICANT: Ghosh, Malabika
APPLICANT: Wang, Dunrui
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Zhiwei
TITLE OR INVENTION: No. US20040048249A1el Nucleic Acids and
FILE REFERENCE: 805A
CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28

```

	Query Match	24.4%	Score 717;	DB 15	Length 3690;
	Best Local Similarity	31.7%	Pred. No. 1,3e-50		
	Matches	201;	Conservative 101;	Mismatches 219;	Indels 114;
					Gaps 23;
QY	1	MRFNKSGSEVRLPNDELDKGYTSLSLFQRPDLRENGEDTDFMYLGNKNDASKDYIG	60		
Db	2737	MKFNGRSGVQARTPRDLADLAAAYLAKFYLLQGPPEPQGTEDRFRVMWMSGRQATGDYWG	2796		
QY	61	MAVVDGQLTGVYNIGDR-EAEVQIDQVLTSEBSQAAVMDRYKFGQIYQFALNTYKE---	116		
Db	2797	VSLDKCKWHMYQLQSEAGPAVALSIDEDIGEQ-----FAAVALSDTLTQGHMSVTEKQM	2850		
QY	117	--ATSNKKAAYVDLEGGSSNTLLNPDEDAVFYGVGYPDPFELPSRLRPPPYKGTIEL	174		
Db	2651	IQETKAGDVAAGA---EG-----LLNLNRPDDPVFVGVGYPSTFTPEPLRLRFGYRGCIEM	2902		
QY	175	DDLAEVNLSTLNYFKTTFWLNTTEVBPCKRRKE-----SDKNYFEGTGAAPITQPN-AP	228		
Db	2903	DTLNEEVSLSLNYFETFPQDITDAVDRPCRSKSTGDPMLTDSYLDGTGFARISPDQIST	2962		
QY	229	PFNFQITQTVVDRCLLFFEAENODPISLANTEDGNLWRYKLS-----EPP-----	275		
Db	2963	TKREGEIRLAYSYSGLVLPFLKQOSQFLCLAVQESGLVLLIDFGAELKKAAPLOPPRLTS	3022		
QY	276	KEKGIRDTINDKCHSILITTKLQKRMWINNER---SVRIGEIPFSTYYLIGI---	329		
Db	3023	ASKAIQ-----VFLGSGSRKVLVVERATVYSVEQNDLIELADAVYLGAVPPD	3071		
QY	330	--PLAIRERENISTPAFGQCKMNK---KTSGVRLNLTQVYTKKCSDMKLVLRASGR	384		
Db	3072	QLPSRLRLFP-TGGSVVRGCVKGIKALKKYVDLKLIN-TTGSACCTADLVLRGMTPHG	3129		
QY	385	GG--QMSFTNLIDVESTDRFQLSFGFQTPQPSGTLNTHQTRTSSLLVLTEDGHIELSTRDS	442		
Db	3130	HGFLRLALSNV-APLTGNVYSGFGRHSAQDSALLVYRASPDGLCQVSLQQGRVSLQLLRT	3188		
QY	443	NIPFLKSGTGYMDGLLHVSVISDTSGRLRLIDQV--LRNRQRLPSSNAQGS---LR	496		
Db	3189	EV---KTQAGPADGAPHYVAAPSNATGYWLVYDDQLQMKRHPGRPPBLQPOPEGPRLTL	3245		
QY	497	LGG-----GHFEQGISNVLVQRFSGSPBEVLDL-----	523		
Db	3246	LGGIPESGTYVNFSGCISNVFQRLRLGQRVYDQLQNGSVNVSTGCAPALQAGTPGIGP	3309		
QY	524	-----ASKSTKQDASLGSGSLNKPPPLMLPKSKRP	554		
Db	3306	RGLOASRSRSRQPARHPACML--PPLRLKTRTSYQF	3338		

```

RESULT 12
US-10-037-417-49
Sequence 49, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
  APPLICANT: Kekuda, Ramesh
  APPLICANT: Alcobrook II, John P
  APPLICANT: Tchernev, Vellizar T
  APPLICANT: Liu, Xiaohong
  APPLICANT: Spytek, Kimberly A
  APPLICANT: Patturajan, Meera
  APPLICANT: Grose, William M
  APPLICANT: Iepley, Denise M
  APPLICANT: Burgess, Catherine B
  APPLICANT: Vermet, Corine A.M.
  APPLICANT: Li, Li
  APPLICANT: Gorman, Linda
  APPLICANT: Edinger, Shlomit R
  APPLICANT: Sciore, Paul
  APPLICANT: Killerman, Karen
  APPLICANT: Malynkar, Uriel M
  APPLICANT: Rothenberg, Mark
  APPLICANT: Stone, David J
  APPLICANT: Boldog, Ferenc L
  APPLICANT: Guo, Xiaojia
  APPLICANT: Shenoy, Suresh G
  APPLICANT: Anderson, David W
  APPLICANT: Padigaru, Muralidhara
  APPLICANT: Taupier Jr, Raymond J
  APPLICANT: Miller, Charles B
  APPLICANT: Bisen, Andrew J
  TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
  FILE REFERENCE: 21402-235
  CURRENT APPLICATION NUMBER: US/10/037,417
  CURRENT FILING DATE: 2002-09-20
  PRIOR APPLICATION NUMBER: 60/260,018
  PRIOR FILING DATE: 2001-01-05
  PRIOR APPLICATION NUMBER: 60/260,360
  PRIOR FILING DATE: 2001-01-08
  PRIOR APPLICATION NUMBER: 60/272,411
  PRIOR FILING DATE: 2001-02-28
  PRIOR APPLICATION NUMBER: 60/272,817
  PRIOR FILING DATE: 2001-03-02
  PRIOR APPLICATION NUMBER: 60/291,186
  PRIOR FILING DATE: 2001-05-15
  PRIOR APPLICATION NUMBER: 60/303,231
  PRIOR FILING DATE: 2001-07-05
  PRIOR APPLICATION NUMBER: 60/305,060
  PRIOR FILING DATE: 2001-07-12
  PRIOR APPLICATION NUMBER: 60/318,405
  PRIOR FILING DATE: 2001-09-10
  PRIOR APPLICATION NUMBER: 60/318,700
  PRIOR FILING DATE: 2001-09-12
  NUMBER OF SEQ ID NOS: 227
  SOFTWARE: PatentIn Ver. 2.1
  SEQ ID NO 49
  LENGTH: 1634
  TYPE: PRT
  ORGANISM: Homo sapiens
US-10-037-417-49

Query Match      24.3%; Score 715; DB 15; Length 1634;
Best Local Similarity 33.1%; Pred. No. 5.5e-51;
Matches 194; Conservative 96; Mismatches 214; Indels 82; Gaps 21

      1  MRFGKSGVGEVRLNPNDELDLKGYSLSLFLQRPDLRENGGTEDMEFVMTLGNKDKSKYIG 60
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 676  MKFNGRSGVQRTFRDLADLAALYALKRYLQGPBBPQGGTFEDRFVMTMGSRQATGDMG 735

      61  MAVVDQGLTCYNTNGDR-EAEVQIDQVLTSESQEAWMDRKFRQRIYPALANTYKE--- 116
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 736  VSLDDKKVHWYQLEGKGPATLSIDEDIGEQ-----FAAVSLDRITLQFGHNSVTVSRQM 789
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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QY 117 --ATSNKPKAPAVYDLBEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPYKCIETL 174
DB 790 IORTKDDTVAPGA---EG-----LNLNRPDDVFVYGGYSTFTPLLRFPYRGCIEM 841
QY 175 DDLNENVALSYNFKTTFNLTTEVEPCRRKEE-----SDKNYFEGTGARIPTQPN-AP 228
DB 842 DTLNEEVALSYNFKTTFOLDTAVDRPCARSKSTGDPWLTDGSLYLDGTGFARISFDSQIST 901
QY 229 FPNFIQTITQTVDRGLLPPAENODNFIISLNIEDGNLMVRYKLS-----EPP----- 275
DB 902 TRFEBELRLVSYSGVLFLLKQSQFLCLAVOGSLVLYLDFGALKKAVPLQPPPLTS 961
QY 276 KEGGIDTINDGDHSLITITGLQKRMWINVER---SVRIEGRIPFSTYLLGI--- 329
DB 962 ASKAIQ-----VFLLGSRKRVLYVERATVYSVEQNDLELADAYLGGVPPD 1010
QY 330 --PIAIRERFNISTPAFGCMKLNK---KTSGVRLNDTVGYTKKSEDMKLVRTASFSR 384
DB 1011 QLPPLRLRFP--TGSSVRCGVKGIKALGKYVDLKRNL--TTGVSAGCTADLLVGRAMTFHG 1068
QY 385 GG--QMSFTNLDPVSTRFQLSFGFOTFQPSGTLNLHQRRTSSLLVTEDEGHIELSTRDS 442
DB 1069 HGFRLALASNV-APLITGVNYSFGFHSADBSALLYRASPDGLCOVSLQOGVSVSLQLRT 1127
QY 443 NIPFSPGTYMDGLLHVSVISDTSGLRLIIDQV--LRNQRPLSPSMAQOS---LR 496
DB 1128 EV---KTOAGFADGAPHYAFYSNATGWMLYVDDQLQMKPHRGPPPLQPPBEPRL 1184
QY 497 LGG-----GHFEGCISNVLVGRFSQSPREVLDLASKSTKQDASLG 535
DB 1185 LGGLPESGTYVNFSGCISNVFQRLGPRVFDLQONLGSVNVSTG 1230

```

RESULT 13

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US-10-112-944-801
; Sequence 801, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1 Nucleic Acids and
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_fl_genes Version 5.0

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; SEQ ID NO 801
; LENGTH: 1677
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-112-944-801

```

Query Match 24.3%; Score 715; DB 15; Length 1677;
 Best Local Similarity 33.1%; Pred. No. 5,7e-51;
 Matches 194; Conservative 96; Mismatches 214; Indels 82; Gaps 21;

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QY 1 MAFNKGSGVRYVLPNDLELTKYTSLSLFLQRPDLRENGCTEDMVMYLGAKDASKDYIG 60
DB 687 MKNFNRSGVQLTTPPDLADLAAYTALKFYLGQBEPEPGGTEDRRVMTMGSHQATGDVWG 746
QY 61 MAVVQGLTCVYNLQDR--EAEVQIDQVLTSSSQAVMDRVKFORIYOPAKLNYRKE--- 116
DB 747 VSLRDKKAMVYQLSGAGPAVSLIDEDIGEQ-----FAVSLDTLQFGHSVTEROM 800
QY 117 --ATSNKPKAPAVYDLBEGSSNTLNLDPEDAVFYVGGYPPDFELPSRLRPPYKCIETL 174
DB 801 IORTKDDTVAPGA---EG-----LNLNRPDDVFVYGGYSTFTPLLRFPYRGCIEM 852
QY 175 DDLNENVALSYNFKTTFNLTTEVEPCRRKEE-----SDKNYFEGTGARIPTQPN-AP 228
DB 853 DTLNEEVALSYNFKTTFOLDTAVDRPCARSKSTGDPWLTDGSLYLDGTGFARISFDSQIST 912
QY 229 FPNFIQTITQTVDRGLLPPAENODNFIISLNIEDGNLMVRYKLS-----EPP----- 275
DB 913 TRFEBELRLVSYSGVLFLLKQSQFLCLAVOGSLVLYLDFGALKKAVPLQPPPLTS 972
QY 276 KEGGIDTINDGDHSLITITGLQKRMWINVER---SVRIEGRIPFSTYLLGI--- 329
DB 973 ASKAIQ-----VFLLGSRKRVLYVERATVYSVEQNDLELADAYLGGVPPD 1021
QY 330 --PIAIRERFNISTPAFGCMKLNK---KTSGVRLNDTVGYTKKSEDMKLVRTASFSR 384
DB 1022 QLPPLRLRFP--TGSSVRCGVKGIKALGKYVDLKRNL--TTGVSAGCTADLLVGRAMTFHG 1079
QY 385 GG--QMSFTNLDPVSTRFQLSFGFOTFQPSGTLNLHQRRTSSLLVTEDEGHIELSTRDS 442
DB 1080 HGFRLALASNV-APLITGVNYSFGFHSADBSALLYRASPDGLCOVSLQOGVSVSLQLRT 1138
QY 443 NIPFSPGTYMDGLLHVSVISDTSGLRLIIDQV--LRNQRPLSPSMAQOS---LR 496
DB 1139 EV---KTOAGFADGAPHYAFYSNATGWMLYVDDQLQMKPHRGPPPLQPPBEPRL 1195
QY 497 LGG-----GHFEGCISNVLVGRFSQSPREVLDLASKSTKQDASLG 535
DB 1196 LGGLPESGTYVNFSGCISNVFQRLGPRVFDLQONLGSVNVSTG 1241

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RESULT 14

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US-10-312-352-22
; Sequence 22, Application US/10312352
; Publication No. US20040053824A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom
; APPLICANT: YUE, Henry; AZIMZAI, Yalda
; APPLICANT: HE, Amy; BATRA, Sajeev
; APPLICANT: LO, Terence P.; NGUYEN, Damien B.
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
; APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.
; APPLICANT: LAL, Preeti G.; KEARNEY, Liam
; APPLICANT: BURROD, Neil; YAO, Monique G.
; APPLICANT: CHAMLA, Narinder K.; ELIOT, Vicki S.
; APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.
; APPLICANT: BAUGHN, Mariah R.; HAFALIA, April, J.A.
; APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.
; APPLICANT: LU, Yan; BOROWSKY, Mark L.
; APPLICANT: LU, Dyrung Aina M.; RAMKUMAR, Jayalaxmi
; APPLICANT: YANG, Junning; GURURAJAN, Rajagopal
; APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.
; APPLICANT: XU, Yuning; KALLICK, Deborah A.

```

```
APPLICANT: LEE, Ernestine A.; THANGAVELU, Kavitha
APPLICANT: DELBERANE, Angelo M.; LEE, Sally
TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
FILE REFERENCE: EP-0794 USN
CURRENT APPLICATION NUMBER: US/10/312,352
PCT/US01/21067
PRIOR FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: 2001-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/215,454
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/219,462
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 60/240,111
PRIOR FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US 60/240,106
PRIOR FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US 60/244,021
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/248,887
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/249,570
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PERL Program
SEQ ID NO 22
LENGTH: 3695
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040053824A1 6382722CD1
US-10-312-352-22

Query Match      24.3%; Score 715; DB 15; Length 3695;
Best Local Similarity 33.1%; Pred. No. 1.9e-50;
Matches 194; Conservative 96; Mismatches 214; Indels 82; Gaps 21;

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DB      2737 MKFNSSGQVQLRTPRLADIATAAYTALKFYLGEPPEPGQTEPRFVMTGSRQATYDYM 2796
QY      61 MAVVDQGLTCVNYLGDRL-EAEVQIDQVLTSESQEAAMDVKFORLYQFAKLNTYKE--- 116
DB      2797 VSLRDKKVMHYVQLGEGRAVLSIDEDIGQ-----FAVSLDRTIQFGHMYTVYEROM 2850
QY      117 --ATSNKPKAPAVYDLEGSSNTLLNDPEDAVYVGYGPPDELPRLRPPYKGIETL 174
DB      2851 IQETKGDVYAPGA---EG-----LNLNRPDVYFYGYGPPSTFPPLLAFPGYRGCIEM 2902
QY      175 DDLENVLSLYNKKTPTNLTTEVEPCRRKEE-----SPKATFEGGYARIPIQPN-AP 228
DB      2903 DTNBEVVSLYNBERFQDLTAVDRCARSKSTGDPWLTGGSYLDGTGFARISFDQIST 2962
QY      229 FPNFIOTIOTTVDRGLLFFAENODNFI SLNIBOGNLMVRYKLS-----BPP----- 275
DB      2963 TKRPEQELRLVSYSGVLFYKQOSQFLCLAVQESGLVLYDPGAGLKAAPVLPQPPPLTS 3022
QY      276 KEGKIRDTINDKDHSLITIGKLQKRMWVNER---SVRIEGELFDFSTYYLIGI--- 329
DB      3023 ASRAIQ-----VFLGSGRRKVLVRVERATVYSVEQNDDELADAYVIGVPPD 3071
QY      330 --PLAIRERNISTPAFOGCMKNIK---KTSGVRLNDTVGVTKKSEDMKLVRTASFSR 384
DB      3072 QLPESLRRLRP--TGSVRGCVKGIKALGKYVDLKRLL--TTGVSACTADLLVGRAMTFHG 3129
QY      385 GG--QMSFTMLDVPSTDRFOLSPFQTFOPSGTLLNHQRTSSILVLTLEDGHIELSTRDS 442
DB      3130 HGFLRLALSNV-APLTGVNYSVGFPHASQDSALLVYASPDGLQVSLQGRVSLQILRT 3188
QY      443 NIPIKSPGTYMGDLHHVSVISDTSGLRLLIDQV--LRRNQLPSFSNAQOS---LR 496
DB      3189 EV---KTQAGPADGADPHYVAFVYSNATGVMVLYVDQOLQMKPHRGRPPELQPPGPPRL 3245
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QY      497 LGG-----GHFEGCISNVLYORFSGSPBVLDAKSTKQASLG 535
DB      3246 LGGLPESGTYNPFSSGISNVFVQRLGPPQVFLQNMGSVNVSTG 3291

RESULT 15
US-10-312-088-31
Sequence 31, Application US/10312088
Publication No. US20030219862A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Cogswell, John P.
APPLICANT: Kabinic, Karen S.
APPLICANT: Lai, Ying-Ta
APPLICANT: Martensen, Shelby A.
APPLICANT: Murdoch, Paul R.
APPLICANT: Smith, Randall P.
APPLICANT: Strum, Jay C.
APPLICANT: Xiang, Zhaoying
APPLICANT: Xie, Qing
APPLICANT: Rizni, Safia K.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50029
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: PCT/US01/19929
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/213,161
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/213,156
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Pascal for Windows Version 4.0
SEQ ID NO 31
LENGTH: 3696
TYPE: PRT
ORGANISM: Homo sapiens
US-10-312-088-31

Query Match      24.3%; Score 715; DB 15; Length 3696;
Best Local Similarity 33.1%; Pred. No. 1.9e-50;
Matches 194; Conservative 96; Mismatches 214; Indels 82; Gaps 21;

QY      1 MRNNGSGVEVRLPNLEDLKGYTSLSPFORDLAENGTEDMFWYLGKNAKSDYIG 60
DB      2738 MKFNSSGQVQLRTPRLADIATAAYTALKFYLGEPPEPGQTEPRFVMTGSRQATYDYM 2797
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DB      2852 IQETKGDVYAPGA---EG-----LNLNRPDVYFYGYGPPSTFPPLLAFPGYRGCIEM 2903
QY      175 DDLENVLSLYNKKTPTNLTTEVEPCRRKEE-----SPKATFEGGYARIPIQPN-AP 228
DB      2904 DTNBEVVSLYNBERFQDLTAVDRCARSKSTGDPWLTGGSYLDGTGFARISFDQIST 2963
QY      229 FPNFIOTIOTTVDRGLLFFAENODNFI SLNIBOGNLMVRYKLS-----BPP----- 275
DB      2964 TKRPEQELRLVSYSGVLFYKQOSQFLCLAVQESGLVLYDPGAGLKAAPVLPQPPPLTS 3023
QY      276 KEGKIRDTINDKDHSLITIGKLQKRMWVNER---SVRIEGELFDFSTYYLIGI--- 329
DB      3024 ASRAIQ-----VFLGSGRRKVLVRVERATVYSVEQNDDELADAYVIGVPPD 3072
QY      330 --PLAIRERNISTPAFOGCMKNIK---KTSGVRLNDTVGVTKKSEDMKLVRTASFSR 384
DB      3073 QLPESLRRLRP--TGSVRGCVKGIKALGKYVDLKRLL--TTGVSACTADLLVGRAMTFHG 3130
QY      385 GG--QMSFTMLDVPSTDRFOLSPFQTFOPSGTLLNHQRTSSILVLTLEDGHIELSTRDS 442
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Db 3131 HGFRLALSNV-APLTGNVYSGFGFHSADDSALLYTRASPDGICQVSLQGRVSLQLRT 3189
Qy 443 NIPFKSPGTNDGLHNVVISDTSGLRLIIDQV--LRNQRLPFSNAQOS---LR 496
Db 3190 BV---KTQAGPADGAPHYVAFYSNATGWLVYDDQLQMKPHRGPPPELQPEBPPRL 3246
Qy 497 LGG-----GHEGCTSNVLVORFSQSPBEVLDLASKSTKQASLG 535
Db 3247 LGGLPESGTIYNFSGCISNVFYORLGPORVFDLQONLGSVNVSTG 3292

Search completed: February 22, 2005, 08:44:42
Job time : 78.7216 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:13:40 ; Search time 26.3827 Seconds
(without alignments)
1598.653 Million cell updates/sec

Title: US-10-817-423-4

Perfect score: 2940

Sequence: 1 MRNGKSGVRLPNLEDL.....MLFKSPKPKRIFVNVQL 565

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Issued Patents AA:*

- 1: /cgnt_6/ptodata/1/1aa/5A COMB.pep:*
- 2: /cgnt_6/ptodata/1/1aa/5B COMB.pep:*
- 3: /cgnt_6/ptodata/1/1aa/6A COMB.pep:*
- 4: /cgnt_6/ptodata/1/1aa/6B COMB.pep:*
- 5: /cgnt_6/ptodata/1/1aa/PTUS COMB.pep:*
- 6: /cgnt_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB	ID
1	2940	100.0	1694 4 US-09-560-385A-12
2	2940	100.0	1725 4 US-09-560-385A-10
3	2439	83.0	1693 4 US-09-560-385A-4
4	2439	83.0	1693 4 US-09-560-385A-8
5	2439	83.0	1713 3 US-08-600-982-24
6	2439	83.0	1713 3 US-09-560-385A-6
7	2439	83.0	1713 3 US-09-538-092-1359
8	2439	83.0	1713 5 PCT-US94-10261A-24
9	2439	83.0	1724 4 US-09-560-385A-2
10	1310	44.6	770 1 US-08-445-135-2
11	715	24.3	3647 4 US-09-949-016-10932
12	694	23.6	1792 4 US-09-561-818A-4
13	694	23.6	1800 4 US-09-561-818A-8
14	694	23.6	1816 4 US-09-561-818A-2
15	685	23.6	1824 4 US-09-561-818A-6
16	685	23.3	953 4 US-09-845-583A-4
17	683	23.2	1792 4 US-09-561-818A-12
18	683	23.2	1816 4 US-09-561-818A-10
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20	302	10.3	3084 4 US-09-562-702A-12
21	302	10.3	3106 4 US-09-562-702A-10
22	297	10.1	1130 6 5444158-2
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24	294	10.0	1130 2 US-08-460-309-2
25	294	10.0	1130 2 US-08-125-077-2
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27	294	10.0	3089 4 US-09-562-702A-4

Description

28	294	10.0	3110 4 US-09-562-702A-2	Sequence 2, Appl
29	294	10.0	3110 4 US-09-562-702A-6	Sequence 6, Appl
30	294	10.0	3110 4 US-09-561-709B-7	Sequence 7, Appl
31	294	10.0	3110 4 US-09-917-254-86	Sequence 86, Appl
32	294	10.0	3110 4 US-09-949-016-5937	Sequence 5937, Ap
33	294	10.0	3111 2 US-08-460-309-4	Sequence 4, Appl
34	294	10.0	3111 2 US-08-125-077-4	Sequence 5, Appl
35	270	9.2	3075 2 US-08-460-309-5	Sequence 4, Appl
36	270	9.2	3075 2 US-08-125-077-5	Sequence 5, Appl
37	252	8.6	3070 4 US-09-949-016-7814	Sequence 7, Appl
38	182	6.2	1384 4 US-09-949-016-7814	Sequence 7814, Ap
39	153	5.2	705 4 US-10-006-011A-3	Sequence 3, Appl
40	153	5.2	4391 4 US-10-006-011A-2	Sequence 2, Appl
41	144	4.9	1331 4 US-09-949-016-6861	Sequence 6861, Ap
42	144	4.9	1523 3 US-09-182-024A-2	Sequence 2, Appl
43	139	4.7	1384 4 US-08-826-134-2	Sequence 2, Appl
44	139	4.7	1384 4 US-09-949-016-6395	Sequence 6395, Ap
45	139	4.7	1525 3 US-09-191-647-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-560-385A-12

Sequence 12, Application US/09560385A

Patent No. 6703363

GENERAL INFORMATION:

APPLICANT: Bouland, Ariel

TITLE OF INVENTION: Recombinant Laminin 5

FILE REFERENCE: 99-274-C

CURRENT APPLICATION NUMBER: US/09/560,385A

CURRENT FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 12

LENGTH: 1694

TYPE: PRT

ORGANISM: Rattus norvegicus

US-09-560-385A-12

Query Match

Best local Similarity 100.0%; Pred. No. 8.1e-285;

Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRNGKSGVRLPNLEDLKGYTSLFLQRPDLRNGGTEDMPVNYLGNKASXDYIG	60
DB	751	MRNGKSGVRLPNLEDLKGYTSLFLQRPDLRNGGTEDMPVNYLGNKASXDYIG	810
QY	61	MAVVDQQLTCVNYLGRREAVQIDQVLTSESGEAVMDRYKFORITQFALNTTKATSN	120
DB	811	MAVVDQQLTCVNYLGRREAVQIDQVLTSESGEAVMDRYKFORITQFALNTTKATSN	870
QY	121	KPAPAVYDLEGGSSNTLNLDPEDAVFYVGYGPPPELPSRLRPPPYKGCIEHLDLNN	180
DB	871	KPAPAVYDLEGGSSNTLNLDPEDAVFYVGYGPPPELPSRLRPPPYKGCIEHLDLNN	930
QY	181	VLSLVNFKTFNLTTEVEPCRRRKESEDNNGEGTYARIPQPNAPFPNFIQTITV	240
DB	931	VLSLVNFKTFNLTTEVEPCRRRKESEDNNGEGTYARIPQPNAPFPNFIQTITV	990
QY	241	DRGLLPPAEQNDPFIISLNTEDGNLARYKLNSEPPYKGRITDINDKSHIITIGKIQ	300
DB	991	DRGLLPPAEQNDPFIISLNTEDGNLARYKLNSEPPYKGRITDINDKSHIITIGKIQ	1050
QY	301	KRMWNNERSVRIEBSIFDFTYYIGTPIAIRERFNISTPAFOGCMKRLKKTSGVRL	360
DB	1051	KRMWNNERSVRIEBSIFDFTYYIGTPIAIRERFNISTPAFOGCMKRLKKTSGVRL	1110
QY	361	NDTVGVTKKCSBDKLVRTASFSRGQMSFTNLDVPSDFOLSPFGQTFQPSGTLNHQ	420
DB	1111	NDTVGVTKKCSBDKLVRTASFSRGQMSFTNLDVPSDFOLSPFGQTFQPSGTLNHQ	1170

QY 421 TRTSSLLVLTLEDGHIELSTRDSNIPIFKSPGTYMDGLHHVSVISPTSGRLIIDQVLR 480
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Db 1171 TRTSSLLVLTLEDGHIELSTRDSNIPIFKSPGTYMDGLHHVSVISPTSGRLIIDQVLR 1230
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QY 481 RNQRLPSFSAQOOSLRLGGHFEBCISNVLVORFOSPEVLDLASKSTKDAISLGGCSLN 540
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Db 1231 RNQRLPSFSAQOOSLRLGGHFEBCISNVLVORFOSPEVLDLASKSTKDAISLGGCSLN 1290
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QY 541 KPPFLMLFKSPKPFNKGRIFNNQL 565
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Db 1291 KPPFLMLFKSPKPFNKGRIFNNQL 1315
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RESULT 2
US-09-560-385A-10
; Sequence 10; Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Boutand, Arlet
; TITLE OF INVENTION: Recombinant laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-560-385A-10

Query Match 100.0%; Score 2940; DB 4; Length 1725;
Best Local Similarity 100.0%; Pred. No. 8.3e-285;
Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPNKSGVEVRLPNLDELKGYTSLFLQRPDLRENGTEDMFVMTLGNKDAKDYIG 60
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QY 61 MAVVDGQLTCVYMLGDRAEAVQIDQVLTSESQOAVMDRVKFORIYQPAKLNTYKATSN 120
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Db 842 MAVVDGQLTCVYMLGDRAEAVQIDQVLTSESQOAVMDRVKFORIYQPAKLNTYKATSN 901
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Db 902 KPRAPAVYDLGEGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKGCIELDLNEN 961
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QY 181 VLSVNFKTFNLTTEVEPCRRKESDKNYFEGTGYARIPTQPNAPFPNF1QTIQTV 240
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Db 962 VLSVNFKTFNLTTEVEPCRRKESDKNYFEGTGYARIPTQPNAPFPNF1QTIQTV 1021
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QY 241 DRGLLFFAENQDNFISLINEDGNLMRYKLNSEPPKRGIRDTINDGKHSILITIGKQ 300
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QY 301 KRWMINNERSVRIEGEIFDPSTYYLGGIPIAIRERFNIPTPAFOGCMKLNKKTSGVRL 360
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Db 1202 TRTSSLLVLTLEDGHIELSTRDSNIPIFKSPGTYMDGLHHVSVISPTSGRLIIDQVLR 1261
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QY 481 RNQRLPSFSAQOOSLRLGGHFEBCISNVLVORFOSPEVLDLASKSTKDAISLGGCSLN 540
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Db 1262 RNQRLPSFSAQOOSLRLGGHFEBCISNVLVORFOSPEVLDLASKSTKDAISLGGCSLN 1321
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QY 541 KPPFLMLFKSPKPFNKGRIFNNQL 565
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Db 1322 KPPFLMLFKSPKPFNKGRIFNNQL 1346
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RESULT 3
US-09-560-385A-4
; Sequence 4; Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Boutand, Arlet
; TITLE OF INVENTION: Recombinant laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1693
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-385A-4

Query Match 83.0%; Score 2439; DB 4; Length 1693;
Best Local Similarity 81.9%; Pred. No. 1.4e-234;
Matches 463; Conservative 47; Mismatches 35; Indels 0; Gaps 0;

QY 1 MRPNKSGVEVRLPNLDELKGYTSLFLQRPDLRENGTEDMFVMTLGNKDAKDYIG 60
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Db 751 MRPNKSGVEVRLPNLDELKGYTSLFLQRPDLRENGTEDMFVMTLGNKDAKDYIG 810
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QY 61 MAVVDGQLTCVYMLGDRAEAVQIDQVLTSESQOAVMDRVKFORIYQPAKLNTYKATSN 120
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Db 811 MAVVDGQLTCVYMLGDRAEAVQIDQVLTSESQOAVMDRVKFORIYQPAKLNTYKATSN 870
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QY 121 KPRAPAVYDLGEGSSNTLNLDPEDAVFYVGYPPDFELPSRLRPPYKGCIELDLNEN 180
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QY 241 DRGLLFFAENQDNFISLINEDGNLMRYKLNSEPPKRGIRDTINDGKHSILITIGKQ 300
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Db 991 DRGLLFFAENQDNFISLINEDGNLMRYKLNSEPPKRGIRDTINDGKHSILITIGKQ 1050
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QY 301 KRWMINNERSVRIEGEIFDPSTYYLGGIPIAIRERFNIPTPAFOGCMKLNKKTSGVRL 360
| | | | |
Db 1051 KRWMINNERSVRIEGEIFDPSTYYLGGIPIAIRERFNIPTPAFOGCMKLNKKTSGVRL 1110
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QY 361 NDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVSTDRFQLSFGQTFQPSGTLNMQ 420
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QY 421 TRTSSLLVLTLEDGHIELSTRDSNIPIFKSPGTYMDGLHHVSVISPTSGRLIIDQVLR 480
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QY 481 RNQRLPSFSAQOOSLRLGGHFEBCISNVLVORFOSPEVLDLASKSTKDAISLGGCSLN 540
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Db 1231 RNQRLPSFSAQOOSLRLGGHFEBCISNVLVORFOSPEVLDLASKSTKDAISLGGCSLN 1290
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QY 541 KPPFLMLFKSPKPFNKGRIFNNQL 565
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Db 1291 KPPFLMLFKSPKPFNKGRIFNNQL 1315
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RESULT 4
US-09-560-385A-8
; Sequence 8; Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Boutand, Arlet
; TITLE OF INVENTION: Recombinant laminin 5

FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560,385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 8
LENGTH: 1693
TYPE: PRT
ORGANISM: Homo sapiens
US-09-560-385A-8

Query Match 83.0%; Score 2439; DB 4; Length 1693;
Best Local Similarity 81.9%; Pred. No. 1,4e-234;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRNFGSGVRLPNDLBDKGYTSLFLQRPDLRENGTDMFWYLGNDKASDYIG 60
DB 751 MRNFGSGVRLPNDLBDKGYTSLFLQRPDLRENGTDMFWYLGNDKASDYIG 810
QY 61 MAVVDQQLTCVYMLGDRBAEVOIDVLTSESOEAVMDRKFQRIYQFALNTTKATSN 120
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DB 871 KKPAPAVYDLEGGSSNTLNLDPEDAVFYGYGYPDPFELPSRLRFPYKGCIELDLNEN 930
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DB 931 VLSLYNFKTFTNLTTEVEBCRRRKEESDKNVEGTYARIPTQPNAPFPNFIQTITV 990
QY 241 DRGLLFAEAGQDNFISLNTEDGMLNRYKLNSEPPKEGIRDTINDKSHLITIGKQ 300
DB 991 DRGLLFAEAGQDNFISLNTEDGMLNRYKLNSEPPKEGIRDTINDKSHLITIGKQ 1050
QY 301 KRWMINNERSVRIEGEIPDFTYIAGIPAIIRERNISTPAFGCKMLKXTSGVRL 360
DB 1051 KRWMINNERSVRIEGEIPDFTYIAGIPAIIRERNISTPAFGCKMLKXTSGVRL 1110
QY 361 NDTVGYTKKCSSEWKLVRASFSRGGQMSFTNLDVSTDRFOLSFGQTQPSGTLNMQ 420
DB 1111 NDTVGYTKKCSSEWKLVRASFSRGGQMSFTNLDVSTDRFOLSFGQTQPSGTLNMQ 1170
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DB 1171 TRTSSLLVLTEDGHIESTDSNIPFKSPGTMDGLHHVSYISDPSGRLIIDQVLR 1230
QY 481 RNRRLPSFNAOQSLRIGGHPFGCISNVLVORPSPEVLDLASKSTKQDASLGCCSLN 540
DB 1231 RNRRLPSFNAOQSLRIGGHPFGCISNVLVORPSPEVLDLASKSTKQDASLGCCSLN 1290
QY 541 KPPFLMLFKSPKRFNKGRIFNVOQL 565
DB 1291 KPPFLMLFKSPKRFNKGRIFNVOQL 1315

RESULT 5
US-08-600-982-24
Sequence 24, Application US/08600982
Patent No. 6120991
GENERAL INFORMATION:
APPLICANT: Carter, William G.
APPLICANT: Gili, Susanna A.
APPLICANT: Ryan, Maureen C.
TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
STREET: 1420 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA

ZIP: 98101-8100
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,982
FILING DATE: 02-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: E170 protein as translated from sequence
of FIGURES 15A-15F, and as shown also in FIGURES
DESCRIPTION: 15A-19R
US-08-600-982-24

Query Match 83.0%; Score 2439; DB 3; Length 1713;
Best Local Similarity 81.9%; Pred. No. 1,4e-234;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRNFGSGVRLPNDLBDKGYTSLFLQRPDLRENGTDMFWYLGNDKASDYIG 60
DB 771 MRNFGSGVRLPNDLBDKGYTSLFLQRPDLRENGTDMFWYLGNDKASDYIG 830
QY 61 MAVVDQQLTCVYMLGDRBAEVOIDVLTSESOEAVMDRKFQRIYQFALNTTKATSN 120
DB 831 MAVVDQQLTCVYMLGDRBAEVOIDVLTSESOEAVMDRKFQRIYQFALNTTKATSN 890
QY 121 KKPAPAVYDLEGGSSNTLNLDPEDAVFYGYGYPDPFELPSRLRFPYKGCIELDLNEN 180
DB 891 KKPAPAVYDLEGGSSNTLNLDPEDAVFYGYGYPDPFELPSRLRFPYKGCIELDLNEN 950
QY 181 VLSLYNFKTFTNLTTEVEBCRRRKEESDKNVEGTYARIPTQPNAPFPNFIQTITV 240
DB 951 VLSLYNFKTFTNLTTEVEBCRRRKEESDKNVEGTYARIPTQPNAPFPNFIQTITV 1010
QY 241 DRGLLFAEAGQDNFISLNTEDGMLNRYKLNSEPPKEGIRDTINDKSHLITIGKQ 300
DB 1011 DRGLLFAEAGQDNFISLNTEDGMLNRYKLNSEPPKEGIRDTINDKSHLITIGKQ 1070
QY 301 KRWMINNERSVRIEGEIPDFTYIAGIPAIIRERNISTPAFGCKMLKXTSGVRL 360
DB 1071 KRWMINNERSVRIEGEIPDFTYIAGIPAIIRERNISTPAFGCKMLKXTSGVRL 1130
QY 361 NDTVGYTKKCSSEWKLVRASFSRGGQMSFTNLDVSTDRFOLSFGQTQPSGTLNMQ 420
DB 1131 NDTVGYTKKCSSEWKLVRASFSRGGQMSFTNLDVSTDRFOLSFGQTQPSGTLNMQ 1190
QY 421 TRTSSLLVLTEDGHIESTDSNIPFKSPGTMDGLHHVSYISDPSGRLIIDQVLR 480
DB 1191 TRTSSLLVLTEDGHIESTDSNIPFKSPGTMDGLHHVSYISDPSGRLIIDQVLR 1250
QY 481 RNRRLPSFNAOQSLRIGGHPFGCISNVLVORPSPEVLDLASKSTKQDASLGCCSLN 540
DB 1251 RNRRLPSFNAOQSLRIGGHPFGCISNVLVORPSPEVLDLASKSTKQDASLGCCSLN 1310
QY 541 KPPFLMLFKSPKRFNKGRIFNVOQL 565
DB 1311 KPPFLMLFKSPKRFNKGRIFNVOQL 1335

RESULT 6

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US-09-560-385A-6
; Sequence 6, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Bontand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1713
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-385A-6

Query Match      83.0%; Score 2439; DB 4; Length 1713;
Best Local Similarity 81.9%; Pred. No. 1.4e-234;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY      1 MRFNKSGVEVRLPNDLEDKGYTSLFLQRPDLRENGSTEDMFVMTLGAKNDASRDYIG 60
DB      771 MRFNKSGVEVRLPNDLEDKGYTSLFLQRPNSRNGSTENMFVMTLGAKNDASRDYIG 830
QY      61 MAVVDGQLTCVYNLDGREAEVQIDQVLTSESSQEAAMDVRVKFORIYQPAKLNTYKATSN 120
DB      831 MAVVDGQLTCVYNLDGREAEVQIDQVLTSESSQEAAMDVRVKFORIYQPAKLNTYKATSN 890
QY      121 KPKAPAVYDLEGSSNTLNLDPEDAVFYGVYPPDFLPSRLRPPYKGCIELDLNEN 180
DB      891 KPTPGVYDMDGRNSNTLNLDPENVVYGVYPPDFLPSRLRPPYKGCIELDLNEN 950
QY      181 VLSLNFKTFYMLNTTEVEPCRRKESDKNYFEGTGVARIPQPNAPFPNFIQTIQTV 240
DB      951 VLSLNFKTFYMLNTTEVEPCRRKESDKNYFEGTGVARIPQPNAPFPNFIQTIQTV 1010
QY      241 DRGLFPFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIKIDTINDGKHSILITIGKIQ 300
DB      1011 DRGLFPFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIKIDTINDGKHSILITIGKIQ 1070
QY      301 KRMWIVNERSVRIEGERFDPSTYLLGGIPLAIRERNISTPAFGCKMNLKKTSGVYRL 360
DB      1071 KRMWIVNQNTIIDGEVDFPSTYLLGGIPLAIRERNISTPAFGCKMNLKKTSGVYRL 1130
QY      361 NDTVGYTKKCSBDMKLVRTASFSRGGOMSFYNLDVPTDRFQLSFGFQTFQPSGTLINHQ 420
DB      1131 NDTVGYTKKCSBDMKLVRTASFSRGGOMSFYNLDVPTDRFQLSFGFQTFQPSGTLINHQ 1190
QY      421 TRTSSLLVTLBDGHIELSTRDSNIPFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 480
DB      1191 TWTRNLQVTLBDGYIELSTDSGGPIFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 1250
QY      481 RNRQLPSFSAOQSRLGGGHEGCIISNVLVQRFQSPBEVLDLAKSTYKQASLGCCSLN 540
DB      1251 NSKRRLKHISRSQSLRLLGGSNFGCISNVFQRLSLSPVLDLTNSLKRQVSLGGCSLN 1310
QY      541 KPFFMLFKSPKPKRGRIFFVNOI 565
DB      1311 KPFFMLFKSTFRNKTKTFRINOL 1335

RESULT 7
US-09-538-092-1359
; Sequence 1359, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
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; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurafastSeqFormatter Version 0.9
; SEQ ID NO 1359
; LENGTH: 1713
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q16787
US-09-538-092-1359

Query Match      83.0%; Score 2439; DB 4; Length 1713;
Best Local Similarity 81.9%; Pred. No. 1.4e-234;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY      1 MRFNKSGVEVRLPNDLEDKGYTSLFLQRPDLRENGSTEDMFVMTLGAKNDASRDYIG 60
DB      771 MRFNKSGVEVRLPNDLEDKGYTSLFLQRPNSRNGSTENMFVMTLGAKNDASRDYIG 830
QY      61 MAVVDGQLTCVYNLDGREAEVQIDQVLTSESSQEAAMDVRVKFORIYQPAKLNTYKATSN 120
DB      831 MAVVDGQLTCVYNLDGREAEVQIDQVLTSESSQEAAMDVRVKFORIYQPAKLNTYKATSN 890
QY      121 KPKAPAVYDLEGSSNTLNLDPEDAVFYGVYPPDFLPSRLRPPYKGCIELDLNEN 180
DB      891 KPTPGVYDMDGRNSNTLNLDPENVVYGVYPPDFLPSRLRPPYKGCIELDLNEN 950
QY      181 VLSLNFKTFYMLNTTEVEPCRRKESDKNYFEGTGVARIPQPNAPFPNFIQTIQTV 240
DB      951 VLSLNFKTFYMLNTTEVEPCRRKESDKNYFEGTGVARIPQPNAPFPNFIQTIQTV 1010
QY      241 DRGLFPFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIKIDTINDGKHSILITIGKIQ 300
DB      1011 DRGLFPFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIKIDTINDGKHSILITIGKIQ 1070
QY      301 KRMWIVNERSVRIEGERFDPSTYLLGGIPLAIRERNISTPAFGCKMNLKKTSGVYRL 360
DB      1071 KRMWIVNQNTIIDGEVDFPSTYLLGGIPLAIRERNISTPAFGCKMNLKKTSGVYRL 1130
QY      361 NDTVGYTKKCSBDMKLVRTASFSRGGOMSFYNLDVPTDRFQLSFGFQTFQPSGTLINHQ 420
DB      1131 NDTVGYTKKCSBDMKLVRTASFSRGGOMSFYNLDVPTDRFQLSFGFQTFQPSGTLINHQ 1190
QY      421 TRTSSLLVTLBDGHIELSTRDSNIPFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 480
DB      1191 TWTRNLQVTLBDGYIELSTDSGGPIFKSPGYMDGLLHHVSVISDTSGLRLIIDQVLR 1250
QY      481 RNRQLPSFSAOQSRLGGGHEGCIISNVLVQRFQSPBEVLDLAKSTYKQASLGCCSLN 540
DB      1251 NSKRRLKHISRSQSLRLLGGSNFGCISNVFQRLSLSPVLDLTNSLKRQVSLGGCSLN 1310
QY      541 KPFFMLFKSPKPKRGRIFFVNOI 565
DB      1311 KPFFMLFKSTFRNKTKTFRINOL 1335

RESULT 8
PCT-US94-10261A-24
; Sequence 24, Application PC/TUS9410261A
; GENERAL INFORMATION:
; APPLICANT: Carter, William G.
; APPLICANT: Gyll, Susanna A.
; APPLICANT: Ryan, Maureen C.
; TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for
; TITLE OF INVENTION: Integrins
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Christensen, O'Connor, Johnson, and Kindness
```

STREET: 1420 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101-8100
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10261A
FILING DATE: 02-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: E170 protein as translated from sequence of
FIGURES 15A-15F, and as shown also in FIGURES 19A-19R
PCT-US94-10261A-24

Query Match 83.0%; Score 2439; DB 5; Length 1713;
Best Local Similarity 81.9%; Pred. No. 1.4e-234;

Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYTLGNKQASXDYIG 60
DB 771 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYTLGNKQASXDYIG 830
QY 61 MAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAAMDVKFORIYQPAKLNTYKATSN 120
DB 831 MAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAAMDVKFORIYQPAKLNTYKATSN 890
QY 121 KPRAPAVYDLGEGSSNTLNLDPEDAVFYVGYPPDFELPSRLAPPPYKGCIELDLNEN 180
DB 891 KPRAPAVYDLGEGSSNTLNLDPEDAVFYVGYPPDFELPSRLAPPPYKGCIELDLNEN 950
QY 181 VLSLYNFKTFNLTTEVEPCRRRKESDKNYFEGTGYARIPTQPNAPFNFIOITQTV 240
DB 951 VLSLYNFKTFNLTTEVEPCRRRKESDKNYFEGTGYARIPTQPNAPFNFIOITQTV 1010
QY 241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIKRTINDKSHLITIGKLQ 300
DB 1011 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIKRTINDKSHLITIGKLQ 1070
QY 301 KRWMINNERSVRIEGEIPDSFTYLLGIPAIIRERNISTPAPQGMKMLKKTSGVRL 360
DB 1071 KRWMINNERSVRIEGEIPDSFTYLLGIPAIIRERNISTPAPQGMKMLKKTSGVRL 1130
QY 361 NDIVGYTKKSEDMKLVRTASFSRGGOMSFNTLDVSTDRFOLSPFGOTOPSGTLLNHQ 420
DB 1131 NDIVGYTKKSEDMKLVRTASFSRGGOMSFNTLDVSTDRFOLSPFGOTOPSGTLLNHQ 1190
QY 421 TRTSSLLVLTLEDGHIESTDSNIPIFKSPGTMDGLLHHVSVISDTSGLRLIDDOVLR 480
DB 1191 TRTSSLLVLTLEDGHIESTDSNIPIFKSPGTMDGLLHHVSVISDTSGLRLIDDOVLR 1250
QY 481 RNORLPFSNAQOSLRIGGHEFGCISNVLYQRFSGSEPVLDLASXTKQDASLGGSIN 540
DB 1251 NSKRLKHIISSRSQSLRIGGHEFGCISNVLYQRFSGSEPVLDLASXTKQDASLGGSIN 1310
QY 541 KPPLMLFKSPKRNKRIFNVNQL 565
DB 1311 KPPLMLFKSPKRNKRIFNVNQL 1335

RESULT 9

US-09-560-385A-2
Sequence 2, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Bouland, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560,385A
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1724
TYPE: PRT
ORGANISM: Homo sapiens
US-09-560-385A-2

Query Match 83.0%; Score 2439; DB 4; Length 1724;
Best Local Similarity 81.9%; Pred. No. 1.4e-234;
Matches 463; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYTLGNKQASXDYIG 60
DB 782 MRFNGSGVEVRLPNDLEDKGYTSLFLQRPDLRNGGTEDMFVYTLGNKQASXDYIG 841
QY 61 MAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAAMDVKFORIYQPAKLNTYKATSN 120
DB 842 MAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAAMDVKFORIYQPAKLNTYKATSN 901
QY 121 KPRAPAVYDLGEGSSNTLNLDPEDAVFYVGYPPDFELPSRLAPPPYKGCIELDLNEN 180
DB 902 KPRAPAVYDLGEGSSNTLNLDPEDAVFYVGYPPDFELPSRLAPPPYKGCIELDLNEN 961
QY 181 VLSLYNFKTFNLTTEVEPCRRRKESDKNYFEGTGYARIPTQPNAPFNFIOITQTV 240
DB 962 VLSLYNFKTFNLTTEVEPCRRRKESDKNYFEGTGYARIPTQPNAPFNFIOITQTV 1021
QY 241 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIKRTINDKSHLITIGKLQ 300
DB 1022 DRGLLFFAENQDNFISLNIEDGNLMVRYKLNSEPPKEKGIKRTINDKSHLITIGKLQ 1081
QY 301 KRWMINNERSVRIEGEIPDSFTYLLGIPAIIRERNISTPAPQGMKMLKKTSGVRL 360
DB 1082 KRWMINNERSVRIEGEIPDSFTYLLGIPAIIRERNISTPAPQGMKMLKKTSGVRL 1141
QY 361 NDIVGYTKKSEDMKLVRTASFSRGGOMSFNTLDVSTDRFOLSPFGOTOPSGTLLNHQ 420
DB 1142 NDIVGYTKKSEDMKLVRTASFSRGGOMSFNTLDVSTDRFOLSPFGOTOPSGTLLNHQ 1201
QY 421 TRTSSLLVLTLEDGHIESTDSNIPIFKSPGTMDGLLHHVSVISDTSGLRLIDDOVLR 480
DB 1202 TRTSSLLVLTLEDGHIESTDSNIPIFKSPGTMDGLLHHVSVISDTSGLRLIDDOVLR 1261
QY 481 RNORLPFSNAQOSLRIGGHEFGCISNVLYQRFSGSEPVLDLASXTKQDASLGGSIN 540
DB 1262 NSKRLKHIISSRSQSLRIGGHEFGCISNVLYQRFSGSEPVLDLASXTKQDASLGGSIN 1321
QY 541 KPPLMLFKSPKRNKRIFNVNQL 565
DB 1322 KPPLMLFKSPKRNKRIFNVNQL 1346

RESULT 10
US-08-445-135-2
Sequence 2, Application US/08445135
Patent No. 5638789
GENERAL INFORMATION:
APPLICANT: Quaranta, Vito
TITLE OF INVENTION: Promotion of Epithelial Cell Adhesion

```

; TITLE OF INVENTION: and Hemidesmosome Assembly by a Laminin-Like Molecule
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,135
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/151,134
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelson, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: DESMOS.002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; IMMEDIATE SOURCE:
; CLONE: 150 KD
; US-08-445-135-2

Query Match 44.6%; Score 1310; DB 1; Length 770;
Best Local Similarity 90.9%; Pred. No. 5.7e-122;
Matches 259; Conservative 3; Mismatches 13; Indels 10; Gaps 4;

QY 1 MRNFGSGVETRLPNDLEDKGYTSLFLQRPDLRENGTETDMFVMTLGKNDASKDYIG 60
DB 491 MRNFGSGVETRLPNDLEDKGYTSLFLQRPDLRENGTETDMFVMTLGKNDASKDYIG 550
QY 61 MA-----VVDGQLTCVYNIAGDREAEVQIDQV-LTESESQEAAMDVKFORIYOPAKLNTYK 115
DB 551 IGGCRMPAD---VCLQPGGR--SVSSDRSLTESESQEAAMDVKFORIYOPAKLNTYK 605
QY 116 EATSNKPKAPAVYDLEGSSNTLNLDPEDAVFYVGYPDFELPSLRPPYKGCIEID 175
DB 606 EATSNKPKAPAVYDLEGSSNTLNLDPEDAVFYVGYPDFELPSLRPPYKGCIEID 665
QY 176 DLNENLSTLYNFKTTTTLNLTVEPCRRKRESDKYFEETGYARIPTQNAFPNFIQT 235
DB 666 DLNENLSTLYNFKTTTTLNLTVEPCRRKRESDKYFEETGYARIPTQNAFPNFIQT 725
QY 236 IQTTVDRLGLLFAENODNFISLNIEDGNLWVRYKLNSEPPKEXGI 280
DB 726 IQTTVDRLGLLFAENODNFISLNIEDGNLWVRYKLNSEPPKEXGI 770

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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10932
; LENGTH: 3647
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10932

Query Match 24.3%; Score 715; DB 4; Length 3647;
Best Local Similarity 33.1%; Pred. No. 3.5e-61;
Matches 194; Conservative 96; Mismatches 214; Indels 82; Gaps 21;

QY 1 MRNFGSGVETRLPNDLEDKGYTSLFLQRPDLRENGTETDMFVMTLGKNDASKDYIG 60
DB 2700 MRNFGSGVETRLPNDLEDKGYTSLFLQRPDLRENGTETDMFVMTLGKNDASKDYIG 2759
QY 61 MAVVDGQLTCVYNIAGDREAEVQIDQV-LTESESQEAAMDVKFORIYOPAKLNTYK--- 116
DB 2760 VSLRDKKRWVYQLDEBAGPAVLSIDEDIGEQ-----FAVSLDRTTLQFGHMSVTEVQOM 2813
QY 117 --ATSNKPKAPAVYDLEGSSNTLNLDPEDAVFYVGYPDFELPSLRPPYKGCIEI 174
DB 2814 IETGIDTVAPGA---EG-----LNLNRPDPVFVVGYPSTFTPLLRPFGRYGCIEI 2865
QY 175 DLNENLSTLYNFKTTTTLNLTVEPCRRKRE-----SDKNYFEETGYARIPTQNAFP 228
DB 2866 DLNENLSTLYNFKTTTTLNLTVEPCRRKRE-----SDKNYFEETGYARIPTQNAFP 2925
QY 229 FNNFIQTIQTTVDRLGLLFAENODNFISLNIEDGNLWVRYKLNSEPPKEXGI 275
DB 2926 TNRFEQELNLSVSGVLFPLKQSOPLCLAVQBSGLVLYDFGALKKAAPLQPPPLYS 2985
QY 276 KEKGIRDTINDKDSILITIGKLOKRWMINVER---SVRIEGRIFPSTYLLGI--- 329
DB 2986 ASKATQ-----VFLGGSKRVLVRRERTVYSVQDNDLELADAVYLGGVPPD 3034
QY 330 --PIAIRERENISTPAFOGCMKNLK---KTSGVRLNDTGVYTKKCSBDMKLVRTASFSR 384
DB 3035 QLPPLRLRLFP--TGGSVRCVVGIGIKALGYVDLKLNL--TTGVSACCTADLLVGRAMTFHG 3092
QY 385 GG--QMSFTNLDPVSTRFQSLSGFOTPOSGTTLNHDTRISLVLVTEDEGIEISTDS 442
DB 3093 HGPLRLALSNV-APLTGNVYSGFHSAQDSLLLYRASPDGLCOVSLQOGKVSILQLRT 3151
QY 443 NIPFKSPGTVDGGLHHVSVISDTSGLRLTIDQV--LRRNQRLPSPSMAQOS---LR 496
DB 3152 EV---KTQAGFADGAPHYAVFASNAATGWLIVDDQLQMKHRRGPPPELPQPEBEPRL 3208
QY 497 LGG-----GHFEGCISNVLVQFSPQSPBEVIDLASKSTKCDASIG 535
DB 3209 LGLPESGTYVNFSGCISNVFQRLILGPQVFDLQONLGSVNVSTG 3254

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RESULT 11
; US-09-949-016-10932
; Sequence 10932, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

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RESULT 12
; US-09-561-818A-4
; Sequence 4, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortsema, Jarkko
; APPLICANT: Tiggavaara, Kari
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D

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```
Query Match      23.6%; Score 694; DB 4; Length 1816;
Best Local Similarity 32.1%; Pred. No. 1.4e-59;
Matches 193; Conservative 101; Mismatches 246; Indels 62; Gaps 20;

QY 1 MRPNKSGVRLPNLEDLKGYTSLSLPL-----QRPDLRENGTMDMFMVTLGNDAK 56
DB 829 MAFDQSAVEHSRTSMDDLKAFSTLSLYMKPVPKRPBLTE---TADQFIIYLGSKNAK 885
QY 57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAVMDRVFORIYQPAKLNATYKE 116
DB 886 EYMGALIKNDNLVYVYNLGTQVLEIPLDS--KPVSSMPAYPSIVKIERVGRKGVFLTP 943
QY 117 ATSNKPKAPAVVDLEGGSSNTLNLDPDAVYVGYPPDFELPSRLRPPYKCIELDD 176
DB 944 SLSSTAEKFKIKGFEFGSDSLDLPEDVTFYVGVGSNFKLPTSLNLPGVGCLELAT 1003
QY 177 LNEENVLSLYNEKTFENLTTEVEPCRRK-----ESDKNYFEGTGARIPTOPN-----A 227
DB 1004 LNNDVISLYNFGHIYNDPSTSVPCARDKLAFTQSRASYPFDGSGYAVVRDI PRGRKG 1063
QY 228 PPNFPIQTIQTVDGGLFPAENQDNFISLNEGNLMVRY-----KLNSEPPKEGI 280
DB 1064 QVTRFDIEVRTPADNGLILMNVGSMFRLERNGYLHVFPYDFGSSGRVHLEDTLKA- 1122
QY 281 RDTINDGKDSILITIGKLOKRMWVNERSVRI---EGEIFDFSTYYLGIP-----I 331
DB 1123 --QINDAKYHEISI-IYHNDKMLLVDRRHVKSMDNEKKKIPFTDIYIGGAPPEILQSR 1179
QY 332 AIRBERFNISTPAFGCKMNL---KTSGVRLNDTVGYTKCSEDMKLVRTASFSRGQM 388
DB 1180 ALRAHLPLDI-NFRGCKMGFOFOKDFNLLEQTEETLGVGCGPEDSLISRAYFN--GQS 1236
QY 389 SFTNLD-VPSTDRFQLSFGFQFPQPSGTLNMQRTSSLLVTLDEGHIELSTRDNIPIF 447
DB 1237 FLASIOKISFPDFGFGNFRILQPNGLLFYASGSDVFSISLNDGTVIMDK--GIVQ 1294
QY 448 KSPGYTMDGLLHVSVISDTSGLR--LLID-DQVLRNRQRLPSFSNAQOSLR---LGG-- 499
DB 1295 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGIQTOASEKKFVFGGSP 1352
QY 500 -----GHFEGCISNVLVORPQSPEVLDLASKSTKXDSLGGCSLNKPPLMFRSPKRF 554
DB 1353 ISAOYANFTGCISNAYFTRVDVDEVEDFORYTEKVTSLYECPIESSPLFLHKKGNL 1412
QY 555 NK 556
DB 1413 SK 1414

RESULT 15
US-09-561-818A-6
; Sequence 6, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: KorteSmaa, Jarko
; APPLICANT: Tyygvaabon, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1824
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-6

Query Match      23.6%; Score 694; DB 4; Length 1824;
Best Local Similarity 32.1%; Pred. No. 1.4e-59;
Matches 193; Conservative 101; Mismatches 246; Indels 62; Gaps 20;

QY 1 MRPNKSGVRLPNLEDLKGYTSLSLPL-----QRPDLRENGTMDMFMVTLGNDAK 56
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DB 829 MAFDQSAVEHSRTSMDDLKAFSTLSLYMKPVPKRPBLTE---TADQFIIYLGSKNAK 885
QY 57 DYIGMAVVDGQLTCVYNLGDREAEVQIDQVLTSESQEAVMDRVFORIYQPAKLNATYKE 116
DB 886 EYMGALIKNDNLVYVYNLGTQVLEIPLDS--KPVSSMPAYPSIVKIERVGRKGVFLTP 943
QY 117 ATSNKPKAPAVVDLEGGSSNTLNLDPDAVYVGYPPDFELPSRLRPPYKCIELDD 176
DB 944 SLSSTAEKFKIKGFEFGSDSLDLPEDVTFYVGVGSNFKLPTSLNLPGVGCLELAT 1003
QY 177 LNEENVLSLYNEKTFENLTTEVEPCRRK-----ESDKNYFEGTGARIPTOPN-----A 227
DB 1004 LNNDVISLYNFGHIYNDPSTSVPCARDKLAFTQSRASYPFDGSGYAVVRDI PRGRKG 1063
QY 228 PPNFPIQTIQTVDGGLFPAENQDNFISLNEGNLMVRY-----KLNSEPPKEGI 280
DB 1064 QVTRFDIEVRTPADNGLILMNVGSMFRLERNGYLHVFPYDFGSSGRVHLEDTLKA- 1122
QY 281 RDTINDGKDSILITIGKLOKRMWVNERSVRI---EGEIFDFSTYYLGIP-----I 331
DB 1123 --QINDAKYHEISI-IYHNDKMLLVDRRHVKSMDNEKKKIPFTDIYIGGAPPEILQSR 1179
QY 332 AIRBERFNISTPAFGCKMNL---KTSGVRLNDTVGYTKCSEDMKLVRTASFSRGQM 388
DB 1180 ALRAHLPLDI-NFRGCKMGFOFOKDFNLLEQTEETLGVGCGPEDSLISRAYFN--GQS 1236
QY 389 SFTNLD-VPSTDRFQLSFGFQFPQPSGTLNMQRTSSLLVTLDEGHIELSTRDNIPIF 447
DB 1237 FLASIOKISFPDFGFGNFRILQPNGLLFYASGSDVFSISLNDGTVIMDK--GIVQ 1294
QY 448 KSPGYTMDGLLHVSVISDTSGLR--LLID-DQVLRNRQRLPSFSNAQOSLR---LGG-- 499
DB 1295 SVDKQYNDGLSHF--VISSVSPTRYELIVDKSRVGSKNPTKGIQTOASEKKFVFGGSP 1352
QY 500 -----GHFEGCISNVLVORPQSPEVLDLASKSTKXDSLGGCSLNKPPLMFRSPKRF 554
DB 1353 ISAOYANFTGCISNAYFTRVDVDEVEDFORYTEKVTSLYECPIESSPLFLHKKGNL 1412
QY 555 NK 556
DB 1413 SK 1414
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Search completed: February 22, 2005, 08:40:55
Job time : 29.3827 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:05:49 ; Search time 5.81686 Seconds
(without alignments)
3605.942 Million cell updates/sec

Title: US-10-817-423-6

Perfect score: 1118

Sequence: 1 MNKLKKTSGVRLNDTVGVTL.....MLFKSPKRFNKGRIFFVNVQL 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	850	76.0	1713	2 A55347	adhesive ligand ep
2	187	16.7	1816	1 S68960	laminin alpha-4 ch
3	186	16.6	3635	2 T10053	laminin alpha-5 ch
4	173.5	15.5	3712	2 S18253	laminin alpha-1 ch
5	144.5	12.9	3106	1 S53868	laminin alpha-2 ch
6	134.5	12.0	1751	1 M6H0M	laminin alpha-2 ch
7	115.5	10.3	3102	2 T43291	laminin alpha-1 ch
8	111.5	10.0	3084	1 M6M5A	laminin alpha-1 ch
9	107	9.6	3097	2 T00021	DN-cadherin - frut
10	105	9.4	5147	1 J1PFTM	cadherin-related t
11	101.5	9.1	3075	2 S14458	laminin alpha-1 ch
12	99.5	8.9	3672	2 T23433	hypothetical prote
13	99.5	8.9	3704	2 T73716	probable laminin a
14	99	8.9	1158	2 E86327	protein F18014.19
15	94.5	8.5	675	1 KXBO8	plasma protein S p
16	94	8.4	1722	2 E89753	protein F11C7.4 [1
17	92.5	8.3	487	2 P00259	hypothetical prote
18	91.5	8.2	403	2 A26371	sex steroid-bindin
19	91.5	8.2	714	2 S68603	hypothetical prote
20	91.5	8.2	882	2 A39030	androgen-binding p
21	91	8.1	510	2 P84459	hypothetical prote
22	91	8.1	506	1 S56640	ferredoxin-nitrite
23	91	8.1	729	2 P86308	stimilar to disease
24	91	8.1	2823	2 T22A3.8 [1	hypothetical prote
25	91	8.1	2823	2 T23064	protein T22A3.8 [1
26	90.5	8.1	4351	2 T00252	MEGF1 protein - ra
27	89.5	8.0	272	2 A61208	chondroitin sulfat
28	89.5	8.0	272	2 T30305	dnad protein - lac
29	89.5	8.0	1381	2 T31083	paranodin - rat

30	88	7.9	1264	2 T19545	hypothetical prote
31	87.5	7.8	1283	2 T13799	neurexin IV - frut
32	86.5	7.7	642	2 S53433	plasma protein S p
33	86.5	7.7	1531	2 T42218	slit-1 protein hom
34	85.5	7.6	935	2 A64608	exonuclease ABC c
35	84.5	7.6	776	2 T19900	hypothetical prote
36	84.5	7.6	1385	2 T14158	neurexin IV - mous
37	84	7.5	629	2 S63369	hypothetical prote
38	82.5	7.4	307	2 D90394	purine nucleosidas
39	82.5	7.4	468	2 B40228	neurexin I-beta pr
40	82.5	7.4	1530	2 T14594	neurexin I-alpha
41	82	7.3	428	1 E69044	diaminopimelate de
42	81.5	7.3	336	2 T27762	hypothetical prote
43	81.5	7.3	446	2 D64210	replicative DNA he
44	81.5	7.3	1365	2 A41483	glucosyltransferas
45	81.5	7.3	1507	2 A40228	neurexin I-alpha p

ALIGNMENTS

RESULT 1

A55347

adhesive ligand epiligrin, alpha-3 chain form A precursor - human

C/Species: Homo sapiens (man)

C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004

C/Accession: A55347

R/Ryan, M.C.; Tizard, R.; Vandevanter, D.R.; Carter, W.G.

J. Biol. Chem. 269, 22779-22787, 1994

A/Title: Cloning of the lam3 gene encoding the alpha3 chain of the adhesive ligand epi

A/Reference number: A55347, PMID:94357926, PMID:8077230

A/Accession: A55347

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1713 <RYA>

C/Superfamilies: UNIPROT:016787; GB:U34155; NID:9551596; PID:9551597

C/Keywords: alternative splicing

F/67-114/Domain: laminin-type EGF-like homology <LE2>

F/1392-1534/Domain: laminin G repeat homology <LG4>

Query Match 76.0%; Score 850; DB 2; Length 1713;
Best local similarity 76.6%; Pred. No. 1,1e-69;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY	1	MNKLKKTSGVRLNDTVGVTKKCEDWKLVRASFGGQMSFTNLDVPETRFQLSFGF	60
DB	1118	MNKLKKTSGVRLNDTVGVTKKCEDWKLVRASFGGQMSFTNLDVPETRFQLSFGF	1177
QY	61	QTPQSGTILNMQRTSSLLVTLQDGHIELSTRDSNIPFKSGCTTMDGILHHVSVISDT	120
DB	1178	QTPQSGTILNMQRTSSLLVTLQDGHIELSTRDSNIPFKSGCTTMDGILHHVSVISDT	1237
QY	121	SGRLIIDQVLRNORLSPFNAQOSLRGGHFGGCSNNVYVDFSGSPVTLDAASKS	180
DB	1238	SGRLIIDQVLRNORLSPFNAQOSLRGGHFGGCSNNVYVDFSGSPVTLDAASKS	1297
QY	181	TKKDAISLGGCSLNKPPFLMLFKSPKRFNKGRIFFVNVQL	218
DB	1298	LKRDVSLGGCSLNKPPFLMLFKSPKRFNKGRIFFVNVQL	1335

RESULT 2

S68960

laminin alpha-4 chain precursor - human

N/Alternate names: laminin Ah

C/Species: Homo sapiens (man)

C/Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004

C/Accession: S68960; S65926; S49149; S40150; I53516

R/Richards, A.; Al-Imara, L.; Pope, F.M.

Eur. J. Biochem. 238, 813-821, 1996

A/Title: The complete cDNA sequence of laminin alpha-4 and its relationship to the othe

A/Accession: S66960
A/Molecule type: mRNA
A/Residues: 1-1816 <RIC>
A/Cross-references: UNIPROT:Q16363; UNIPROT:Q14731; EMBL:X91171; NID:g1212962; PDB:CAA6
A/Experimental source: tissue type heart
R:Litvanen, A.; Sainio, K.; Sariola, H.; Tryggvason, K.
FEBS Lett. 365, 183-188, 1995
A/Title: Primary structure and expression of a novel human laminin alpha-4 chain.
A/Reference number: 153516; MUID:95300971; PMID:7781776
A/Accession: S65926
A/Molecule type: mRNA
A/Residues: 1-142, 'P', 144-177, 'P', 179-490, 'Y', 492-1056, 'P', 1058-1816 <ITV>
A/Cross-references: EMBL:S78569; NID:g1042081; PDB:AAB34635.1; PID:g1042082
R:Richard, A.J.; Al-Imara, L.; Carter, N.; Leverisha, M.; Lloyd, J.C.; Pope, F.M.
submitted to the EMBL Data Library, December 1993
A/Description: Localization of the gene (LAMA4) to chromosome 6q21 and isolation of a p
A/Reference number: S49149
A/Accession: S49149
A/Molecule type: mRNA
A/Residues: 236-1816 <R12>
A/Cross-references: EMBL:X76939; NID:g509805; PDB:CAA54258.1; PID:g509806
R:Richard, A.J.; Al-Imara, L.; Carter, N.; Lloyd, J.C.; Pope, F.M.
submitted to the EMBL Data Library, February 1993
A/Description: Isolation of a partial cDNA encoding a protein homologous to laminin A. A
A/Reference number: S40150
A/Accession: S40150
A/Molecule type: mRNA
A/Residues: 1403-1541, 'S', 1543-1816 <R13>
A/Cross-references: EMBL:X70904; NID:g437804; PDB:CAA50261.1; PID:g437805
C/Genetics:
A/Gene: GDB:LAMA4; LAMA3
A/Cross-references: GDB:203904; OMIM:600133
A/Map position: 6q21-6q21
C/Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C/Function: Laminins interact with cells and with other basement membrane proteins to promote
C/Superfamily: laminin alpha-4 chain; laminin G repeat homology; laminin-type EGF-like h
C/Keywords: basement membrane; cell binding; coiled coil; extracellular matrix; glycopro
F/1-24/Domain: signal sequence #status predicted <SIG>
F/25-1816/Product: laminin alpha-4 chain #status predicted <MAT>
F/82-129/Domain: laminin-type EGF-like homology <LE1>
F/132-184/Domain: laminin-type EGF-like homology <LE2>
F/187-338/Domain: laminin-type EGF-like homology <LE3>
F/241-265/Domain: laminin-type EGF-like homology #status atypical <LE4>
F/717-719/Region: cell attachment (R-G-D) motif
F/662-1031/Domain: laminin G repeat homology <LG1>
F/1068-1223/Domain: laminin G repeat homology <LG2>
F/1252-1398/Domain: laminin G repeat homology <LG3>
F/1488-1636/Domain: laminin G repeat homology <LG4>
F/1665-1816/Domain: laminin G repeat homology <LG5>
F/104, 215, 308, 458, 524, 550, 571, 574, 631, 639, 735, 751, 754, 780, 803, 1086, 1281, 1359, 1411/Bindin
F/266, 269/Disulfide bonds: interchain #status predicted

Query Match 16.7%; Score 187; DB 1; Length 1816;
Best Local Similarity 28.3%; Pred. No. 1.6e-08;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDYGVTKKCSSEDMKLVRTASFSRGSGMFTNLDV-VSTDRFQLSFGPQRF 63
DB 1202 KQFNLIEQTEYGVGCGEDSLISRAYFN--GGSFASIGIKISFDFEFGGFNFKTL 1259
QY 64 QPESGLTLMHQRTSLSLVLTLEDGHIELSTDSNIPFKSPGTMDGLLHVSVISDTGCL 123
DB 1260 QPGLGLFYVASSGSDVSIISDNTGLMDVK--GIKVSVDKQNDGSHF--VSSVSPT 1315
QY 124 R--LLID-DOVLRNRQRLPSFSNAQSLR--LGG-----GHFEGCISNVLVQPSQS 170
DB 1316 RYELIYDKSVKSGKNPKFKIGEQTQASEKKFYFGSGSPISAQVNFGCISNAFYTRVDRD 1375
QY 171 PEVLDLASKSTKMDASIGGSLKKPPLMLFKSPKPFNK 209
DB 1376 VEVEDFORVTEKVTSLYECPRISSPLFLHKKGKNLSK 1414

RESULT 3
T10053
laminin alpha 5 chain - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T10053
R:Miner, J.H.; Lewis, R.M.; Sannes, J.R.
submitted to the EMBL Data Library, November 1997
A/Reference number: Z16923
A/Accession: T10053
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-3635 <MIN>
A/Cross-references: UNIPROT:Q61001; EMBL:U37501; NID:g2599231; PID:g2599232
C/Genetics:
A/Gene: Lamas
C/Keywords: basement membrane; cell binding; extracellular matrix
F/1888-1939/Domain: laminin-type EGF-like homology <LEG>
F/1942-1970/Domain: EGF homology <EGF>

Query Match 16.6%; Score 186; DB 2; Length 3635;
Best Local Similarity 29.2%; Pred. No. 5.2e-08;
Matches 59; Conservative 34; Mismatches 91; Indels 18; Gaps 6;

QY 1 MKNLKTSGVRLNDYGVTKKCSSEDMKLVRTASFSRGSGMFTNLDV-PSTDRFQLSFG 59
DB 3015 IKALGKYVDLRLNLTGISFGCTADLLVGRTMFPHGGLPLALPDVAFTREVVSQFG 3073
QY 60 FQTPPQSGTLNHQRTSLSLVLTLEDGHIELSTDSNIPFKSPGTMDGLLHVSVISD 119
DB 3074 FQGTDDNMLLYRTSPDPGYQVSLREGHVTLRFNQEV---ETQVFPADGAPHYVAFYSN 3130
QY 120 TSGRLTLD--QVLRNRQRLPSFSNAQ-----QSLRLG-----GHFEGCISNVLVQ 166
DB 3131 VTGVALVYDDQLQVLSHRTTPTMLQLPBPSRLLLGLPVSGTFNFGCISNVFQR 3190
QY 167 FQSPQSEVLDLASKSTKMDASIG 188
DB 3191 LRGPQVRLDLMQMGSVNVSVG 3212

RESULT 4
S18253
laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C/Accession: S28399; S18253
R:Kusche-Guliberg, M.; Garrison, K.; Mackrell, A.J.; Fessler, L.I.; Fessler, J.H.
EMBO J. 11, 4519-4527, 1992
A/Title: Laminin A chain: expression during Drosophila development and genomic sequence
A/Reference number: S28399; MUID:93049203; PMID:1425586
A/Accession: S28399
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-3712 <KUS>
A/Cross-references: UNIPROT:Q00174; GB:M96388; NID:g157799; PDB:AAA28662.1; PID:g157800
R:Garrison, K.; Mackrell, A.J.; Fessler, J.H.
J. Biol. Chem. 266, 22899-22904, 1991
A/Title: Drosophila laminin A chain sequence, interspecies comparison, and domain struct
A/Reference number: S18253; MUID:92078147; PMID:1744083
A/Accession: S18253
A/Molecule type: mRNA
A/Residues: 1762-3712 <GAR>
A/Cross-references: EMBL:M75882; NID:g157797; PDB:AAA28661.1; PID:g157798
C/Genetics:
A/Gene: FlyBase:iana
A/Cross-references: FlyBase:FBgn0002526
C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C/Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular
F/273-330/Domain: laminin-type EGF-like homology <LEG>
F/333-400/Domain: laminin-type EGF-like homology <LEG2>
F/541-584/Domain: laminin-type EGF-like homology <LEG1>

F/1776-2115/Domain: III <DOM3>
 F/1776-1866/Domain: laminin-type EGF-like homology #status atypical <LE1>
 F/1809-1866/Domain: laminin-type EGF-like homology <LE2>
 F/1859-1914/Domain: laminin-type EGF-like homology <LE3>
 F/1917-1967/Domain: laminin-type EGF-like homology <LE4>
 F/1970-2014/Domain: laminin-type EGF-like homology <LE5>
 F/2017-2061/Domain: laminin-type EGF-like homology <LE6>
 F/2064-2109/Domain: laminin-type EGF-like homology <LE7>
 F/2116-2697/Domain: I/II, heptad repeats <DOM2>
 F/2698-3712/Domain: G <DOM3>
 F/2698-2863/Domain: repeat G1 <RG1>
 F/2864-3048/Domain: repeat G2 <RG2>
 F/3049-3223/Domain: repeat G3 <RG3>
 F/3079-3200/Domain: laminin G repeat homology <LG3>
 F/3334-3528/Domain: repeat G4 <RG4>
 F/3529-3712/Domain: repeat G5 <RG5>
 F/1847,1850,1943,2024,2196,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,3

Query Match 15.5%; Score 173.5; DB 2; Length 3712;
 Best Local Similarity 27.9%; Pred. No. 7.6e-07;
 Matches 65; Conservative 43; Mismatches 66; Indels 59; Gaps 12;

QY 3 NLKKTSGVYVLTNDVY---GVTKKCEBDKLVRTASPSRGQMSFTNLDVPSDTRFQLSFG 59
 3025 NVVINGGVVDLTXYVVGGVGEGCSAKFTVVSVAPEHYGFLRMNN--VSDNNLHVVLH 3082

DB 60 FQFQPSGTLT---NHQTRSSLLVTEEDGHISLSTDSNIPFKSPGYMDGLH--- 112
 3083 FKTQPGVGFYFANHD-QSSTIGLSQDGLKLNKMSGSLVLI-----DRIINDGED 3134

QY 113 HSEVISTSG-LRLIDDOVLRRNORLPSFNAQSLRLGG----- 153
 3135 HVTVQHTQELRLTVDDV---DNKRIGS---PQPLILSGDIFPAGLPDNTTRTPNAL 3187

DB 154 ----HFEQGISNVLVORFQSPREVLDLASKSTKQASLGCSLNKPPFLMLFK 202
 QY 3188 ASLAFYFGCISDVTY-----NEELINFANSAEKKNGNINCG-----PPHVLAYE 3231

RESULT 5
 553868
 laminin alpha-2 chain precursor - mouse
 N/Alternate names: laminin M chain; merosin heavy chain
 C/Species: Mus musculus (house mouse)
 C/Date: 21-Aug-1998 #sequence revision 21-Aug-1998 #text change 09-Jul-2004
 C/Accession: I49077; S50829; I48655; S31576; S53868
 R/Bernier, S.M.; Utani, A.; Sugiyama, S.; Doi, T.; Polsterna, C.; Yamada, Y.
 Matrix Biol. 14, 447-455, 1995
 A/Title: Cloning and expression of laminin alpha 2 chain (M-chain) in the mouse.
 A/Reference number: I49077; MUID:95316259; PMID:7795883
 A/Accession: I49077
 A/Status: preliminary; translated from GB/EMBL/DBD
 A/Molecule type: mRNA
 A/Residues: 1-3106 <RES>
 A/Cross-references: UNIPROT:Q60675; EMBL:U12147; NID:9699109; PIDN:AACS2165.1; PID:96991
 R/Xu, H.; Wu, X.R.; Wewer, U.M.; Engvall, E.
 Nature Genet. 8, 297-302, 1994
 A/Title: Murine muscular dystrophy caused by a mutation in the laminin alpha-2 (lama2) g
 A/Reference number: S50829; MUID:95179178; PMID:7874173
 A/Accession: S50829
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 64-281 <KUH>
 A/Cross-references: GB:S75315; NID:9833929; PIDN:AAB33573.1; PID:9833930
 R/Chang, A.C.; Madeworth, S.; Colligan, J.E.
 J. Immunol. 151, 1789-1801, 1993
 A/Title: Expression of merosin in the thymus and its interaction with thymocytes.
 A/Reference number: I48655; MUID:93346725; PMID:8345183
 A/Accession: I48655
 A/Status: preliminary; translated from GB/EMBL/DBD
 A/Molecule type: mRNA
 A/Residues: 2162-2204, 'D', 2206-2213, 'EY', 2216-2279 <RES>
 A/Cross-references: EMBL:X69869; NID:953055; PIDN:CAA9502.1; PID:953056

C/Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
 C/Function:
 A/Description: Interact with cells and with other basement membrane proteins to promote
 C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
 C/Keywords: Basement membrane; calcium binding; coiled coil; extracellular matrix; glyco
 F/1-22/Domain: signal sequence #status predicted <SIG>
 F/23-3106/Product: laminin alpha-2 chain #status predicted <MAT>
 F/283-337/Domain: laminin-type EGF-like homology <LE01>
 F/340-407/Domain: laminin-type EGF-like homology <LE02>
 F/410-462/Domain: laminin-type EGF-like homology <LE03>
 F/465-511/Domain: laminin-type EGF-like homology <LE04>
 F/514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>
 F/720-750/Domain: laminin-type EGF-like homology <LE06>
 F/753-800/Domain: laminin-type EGF-like homology <LE07>
 F/803-858/Domain: laminin-type EGF-like homology <LE08>
 F/861-911/Domain: laminin-type EGF-like homology <LE09>
 F/914-960/Domain: laminin-type EGF-like homology <LE10>
 F/963-1007/Domain: laminin-type EGF-like homology <LE11>
 F/1010-1053/Domain: laminin-type EGF-like homology <LE12>
 F/1056-1099/Domain: laminin-type EGF-like homology <LE13>
 F/1102-1121/Domain: laminin-type EGF-like homology #status atypical <LE14>
 F/1123-1159/Domain: laminin-type EGF-like homology #status atypical <LE15>
 F/1162-1171/Domain: laminin-type EGF-like homology #status atypical <LE16>
 F/1376-1413/Domain: laminin-type EGF-like homology #status atypical <LE17>
 F/1416-1462/Domain: laminin-type EGF-like homology <LE18>
 F/1465-1500/Domain: laminin-type EGF-like homology <LE19>
 F/1523-1567/Domain: laminin-type EGF-like homology <LE20>
 F/2166-2337/Domain: laminin G repeat homology <LG1>
 F/2360-2520/Domain: laminin G repeat homology <LG2>
 F/2546-2709/Domain: laminin G repeat homology <LG3>
 F/2785-2933/Domain: laminin G repeat homology <LG4>
 F/2960-3106/Domain: laminin G repeat homology <LG5>

Query Match 12.9%; Score 144.5; DB 1; Length 3106;
 Best Local Similarity 25.4%; Pred. No. 0.00028;
 Matches 61; Conservative 34; Mismatches 86; Indels 59; Gaps 11;

QY 3 NLKKTSG-----VVLNDTVGVTKKCEBDKLVRTASPSRG--QMSFTNLD 47
 DB 2484 NVKRYSGCLKLDIEISRPYNILSSPYGVTKGS--LEVNVTSPFKPEFVLAVSID 2541

QY 48 VPESTRFQLSFGFQTPQSGTLT-----NHQTRSSLLVTEEDG---HIEL 90
 DB 2542 VGF-----EINLSSTNBSGIIILGSGGTLTPRRKRQTYAVAFLNKGLVHLSS 2597

QY 91 STED-SNIPFKSPGYMDGLHRSVISTDSGLRLIDDOVLRRNORLPSFNAQ-QSL 148
 DB 2598 GTRTKRKIVKPEPNLFHDSRESHVY-ERTRGIFVQIDEDRRHQLNTEQPIFEVKL 2656

QY 149 RLGGG-----HFEQGISNVLVORFQSPREVLDLASKSTKQASLGCSLNK 195
 DB 2657 FVGGAPPEFQPSPELRNIPAFQGCVMVILNISP-----MDFAPIAFKNADIGRCYQKP 2711

RESULT 6
 554004
 laminin alpha-2 chain - human (fragment)
 N/Alternate names: laminin M chain; merosin heavy chain
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1991 #sequence revision 21-Aug-1998 #text change 09-Jul-2004
 C/Accession: PX0082; A35899; A38970; S14461
 R/Hori, H.; Kanamori, T.; Mizuta, T.; Yamaguchi, N.; Liu, Y.; Nagai, Y.
 J. Biochem. 116, 1212-1219, 1994
 A/Title: Human laminin M chain: Epitope analysis of its monoclonal antibodies by immuno-
 A/Reference number: PX0082; MUID:95221315; PMID:7535762
 A/Accession: PX0082
 A/Molecule type: mRNA
 A/Residues: 1-1751 <HOR>
 A/Cross-references: UNIPROT:P24043
 A/Experimental sources: Placenta
 R/Enrig, K.; Lelivo, I.; Argreaves, W.S.; Ruoslahti, E.; Engvall, E.
 Proc. Natl. Acad. Sci. U.S.A. 87, 3264-3268, 1990
 A/Title: Merosin, a tissue-specific basement membrane protein, is a laminin-like protein.

A:Reference number: A35899; UID:90238994; PMID:2185464
 A:Accession: A35899
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 'V', 623-1751 <EHR1>
 A:Cross-references: EMBL:MS9832
 A:Accession: A38970
 A:Molecule type: protein
 A:Residues: 1368-1384/1389-1406/1593-1607 <EHR2>
 A:Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in lacking 1599-1607.
 R:Harig, K.; Leivo, I.; Argraves, S.W.; Ruoslahti, E.; Engvall, E.
 A:Description: The tissue-specific basement membrane protein merosin is a laminin-like protein.
 A:Reference number: S14461
 A:Accession: S14461
 A:Molecule type: mRNA
 A:Residues: 'V', 623-1264, 'R', 1266-1751 <LE1>
 A:Cross-references: EMBL:MS9832; NID:G187520; PID:AAA63215.1; PID:G187521
 A:Comment: This protein is a prominent component of the basement membrane that mediates C:Genetics:
 A:Gene: GDB:LAMA2; LAMM
 A:Cross-references: GDB:132362; OMIM:156225
 A:Map position: 6q22-6q23
 C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
 C:Function:
 A:Description: Interact with cells and with other basement membrane proteins to promote C:Superfamily: laminin alpha-1 chain, laminin G repeat homology/ laminin-type EGF-like R
 C:Keywords: basement membrane; calcium binding; coiled coil; extracellular matrix; glyco
 F:21-58/Domain: laminin-type EGF-like homology #atypical <LE01>
 F:61-107/Domain: laminin-type EGF-like homology <LE02>
 F:110-165/Domain: laminin-type EGF-like homology <LE03>
 F:168-212/Domain: laminin-type EGF-like homology <LE04>
 F:527-567,1071-1300/Region: 3DM and 2D9 binding
 F:811-972/Domain: laminin G repeat homology <LG1>
 F:1005-1165/Domain: laminin G repeat homology <LG2>
 F:1191-1384/Domain: laminin G repeat homology <LG3>
 F:1430-1578/Domain: laminin G repeat homology <LG4>
 F:1605-1751/Domain: laminin G repeat homology <LG5>
 F:120,238,255,341,451,542,557,561,658,669,686,767,881,1001,1076,1119,1192,1199,1289,1509

Query Match 12.0%; Score 134.5; DB 1; Length 1751;
 Best Local Similarity 27.2%; Pred. No. 0.0011;
 Matches 65; Conservative 31; Mismatches 84; Indels 59; Gaps 11;

QY 3 NKKTSG-----VRLNDTVGVTKKSEDMKLVRTASFSRG--QMSFTND 47
 DB 1129 NKKYSGCKDKDIRSPVNIISPPYVGTGKCS--LENVTVSFPKGFVLSFVPID 1186
 QY 48 VESTDRFQUSFGQTQPSGTL-----NQTFTSSLLVLTEDGHR--LST 92
 DB 1187 VGT-----EINLSFTKNSGIIILGSGGTPAPRRRRKQCGAYVYILNLRGLVHLSLT 1242
 QY 93 ---RDSNIPFKSGGYVMGLHVGIVISPTSGRLRLIDQVLRNRQLPSPENAG--QSL 148
 DB 1243 GARTMKVIYRPPNLFPHDRHSVHV--ERTRGIFTVQDENRRYQNTLVEQPIVKKL 1301
 QY 149 RLGGG-----HREGISNVLVQRFSGSEVDLASKSTKCDASLGCSLTK 194
 DB 1302 FVGGAPPEPQPSLKNIPPEGICMVLVINSV-----MDFAPVFPKADIRCAHQK 1355

RESULT 7
 T43291
 Laminin alpha chain - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 11-Jan-2000 #sequence, revision 11-Jan-2000 #ext_change 09-Jul-2004
 C:Accession: T43291
 R:Zhu, X.; Kao, G.; Joh, K.; Hall, D.H.; Wadsworth, V.K.; Rutter, H.; Vogel, B.E.; Huang
 submitted to the EMBL Data Library, June 1998
 A:Description: Expression, function and evolution of laminin alpha chains.
 A:Reference number: Z22397
 A:Accession: T43291
 A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA
 A:Residues: 1-3102 <ZHU>
 A:Cross-references: UNIPROT:O45614; EMBL:AF074902; PID:AAAC26793.1
 C:Genetics:
 A:Map position: 1
 A:Note: lamal/2
 C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 10.3%; Score 115.5; DB 2; Length 3102;
 Best Local Similarity 23.1%; Pred. No. 0.13;
 Matches 53; Conservative 39; Mismatches 70; Indels 67; Gaps 11;

QY 6 KTSGLVRLNDTVGVTKKSEDMKLVRTASFSRGQMSFTNDVPSDFQUSFGQTFOP 65
 DB 2640 KIDGCSQVS---GVTDK-----ILGFPKGYLTIKGISIDNSSTF--AFSPRTRE 2685
 QY 66 SGTLLNMQTRSSSLVLTED-----GHT-----ELSTRDSNIPFKSPG 104
 DB 2686 NQTLVYQSSKQK--VSKRDEDDGKGYIATYLFPGYVLFHFKDASSR--KEVTFRSSH 2742
 QY 105 TYMDGILHVSIVISPTSGRLRLIDQVLRNRQL---PSFNAQSLRLG----- 152
 DB 2743 FVNDQVAVAFMERNGKLIYKVDKELGDSQSLDSFTSVGTSGRLILGFSDDLKRPN 2802
 QY 153 -----HREGISNVL--VQRFSGSEVDLASKSTKCDASLGCSLTK 193
 DB 2803 NEIPTSPFGICISDVFLNMRKVSIAPE-----KRNAQIGWCSMD 2842

RESULT 8
 MMSA
 Laminin alpha-1 chain precursor - mouse
 N:Alternate names: laminin chain A1
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1991 #sequence, revision 30-Jun-1991 #ext_change 09-Jul-2004
 C:Accession: A31771; A30449; S00624; A30450; S08895; S02678; S01790; A30451; S14670
 R:Sasaki, M.; Kleiman, H.K.; Huber, R.; Deutzmann, R.; Yamada, Y.
 J. Biol. Chem. 263, 16536-16544, 1988
 A:Title: Laminin, a multidomain protein. The A chain has a unique globular domain and hc
 A:Reference number: A31771; PMID:89034134; PMID:3182802
 A:Accession: A31771
 A:Molecule type: mRNA
 A:Residues: 1-3084 <SAS>
 A:Cross-references: UNIPROT:P19137; EMBL:U04064; NID:G309419; PID:AAA39410.1; PID:G3094
 A:Accession: A30449
 A:Molecule type: protein
 A:Residues: 183-195,570-571, 'A', 573-586,596-612, 'X', 614-617, 'EMK',630-646,1217-1222, 'YFP
 2466/2624-2639/2818-2843/3009-3033, 'V', 3035 <SA2>
 R:Harig, K.; Oberbauer, I.; Deutzmann, R.
 Eur. J. Biochem. 173, 629-635, 1988
 A:Title: The N terminus of laminin A chain is homologous to the B chains.
 A:Reference number: S00624; PMID:8825080; PMID:3267223
 A:Accession: S00624
 A:Molecule type: mRNA
 A:Residues: 1-208, 'T', 210-334 <HAR>
 A:Cross-references: EMBL:X07737; NID:G52857; PID:CAA30561.1; PID:G52858
 A:Accession: A30450
 A:Molecule type: protein
 A:Residues: 311-335, 'N', 337-339,630-642, 'D', 644,692-734,737-748, 'X', 750-760, 'G', 762-763,
 3-1389/1449-1459 <HA2>
 A:Note: the sequence from Fig. 7 is inconsistent with that from Fig. 5 in having 209-11e
 R:Mann, K.; Deutzmann, R.; Timpl, R.
 Eur. J. Biochem. 178, 71-80, 1988
 A:Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th
 A:Reference number: S08895; PMID:89078415; PMID:2462498
 A:Accession: S08895
 A:Molecule type: protein
 A:Residues: 153-169 <MAN>
 R:Fujitawa, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
 Biochem. J. 252, 453-461, 1988
 A:Title: Structure and distribution of N-linked oligosaccharide chains on various domain
 A:Reference number: S02678; PMID:88326259; PMID:2458101
 A:Accession: S02678

A:Molecule type: protein
 A:Residues: 630-642; 'D', 644; 2690-2704 <FUJ>
 R:Deuzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaumer, I.; Hartl, L.
 Eur. J. Biochem. 177, 35-45, 1988
 A>Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-
 A:Reference number: S01790; MID:89030693; PMID:3181157
 A:Molecule type: mRNA
 A:Residues: 2538-3084 <DEU>
 A:Cross-references: EMBL:X13459; NID:955499; PIDD:CA31807.1; PTD:9818014
 A:Accession: A30451
 A:Molecule type: protein
 A:Residues: 1911-1929; 1997-2006; 2033-2045; 'X', 2047-2054; 'X', 2056-2066; 'X', 2068-2105; 2120-
 470; 2487-2498; 2502-2525; 2538-2557; 2561-2591; 'X', 2593-2594; 2600-2610; 2616-2645; 2648-2655;
 93; 2998-3005; 'A', 3007-3033; 'V', 3035; 3068-3083 <DE2>
 A:Note: 2256-Val was also found
 R:Olsson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, L.
 Lab. Invest. 60, 772-782, 1989
 A>Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
 A:Reference number: A34961; MID:89280632; PMID:2733383
 A:Accession: S14670
 A:Molecule type: protein
 A:Residues: 2424-2436; 2440-2451; 2461-2467; 2487-2525; 2550-2557; 2561-2593; 2600-2610; 2616-2-
 -2942; 'T', 2944-2964; 2969-2976; 2980-2993; 2998-3000; 'I', 3002-3018; 'V', 3020-3034; 3068-3083
 C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
 C:Function:
 A:Description: interact with cells and with other basement membrane proteins to promote
 C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
 C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-1084/Product: laminin alpha-1 chain #status predicted <MAT>
 F:25-277/Domain: VI <DOM6>
 F:277-331/Domain: laminin-type EGF-like homology <LE01>
 F:378-519/Domain: V <DOM5>
 F:334-401/Domain: laminin-type EGF-like homology <LE02>
 F:404-458/Domain: laminin-type EGF-like homology <LE03>
 F:461-507/Domain: laminin-type EGF-like homology <LE04>
 F:510-519/Domain: laminin-type EGF-like homology #status atypical <LE05>
 F:520-715/Domain: IVB <DO4B>
 F:716-1166/Domain: IIIB <DO3B>
 F:716-746/Domain: laminin-type EGF-like homology #status atypical <LE06>
 F:749-795/Domain: laminin-type EGF-like homology <LE07>
 F:798-853/Domain: laminin-type EGF-like homology <LE08>
 F:830-834/Region: cell adhesion #status predicted
 F:856-906/Domain: laminin-type EGF-like homology <LE09>
 F:909-955/Domain: laminin-type EGF-like homology <LE10>
 F:958-1002/Domain: laminin-type EGF-like homology <LE11>
 F:1005-1048/Domain: laminin-type EGF-like homology <LE12>
 F:1051-1094/Domain: laminin-type EGF-like homology <LE13>
 F:1097-1116/Domain: laminin-type EGF-like homology #status atypical <LE14>
 F:1118-1134/Domain: laminin-type EGF-like homology #status atypical <LE15>
 F:1147-1149/Region: cell attachment (R-G-D) motif
 F:1157-1166/Domain: laminin-type EGF-like homology #status atypical <LE16>
 F:1167-1368/Domain: IVA <DO4A>
 F:1369-1561/Domain: IIIB <DO3A>
 F:1369-1407/Domain: laminin-type EGF-like homology #status atypical <LE17>
 F:1410-1456/Domain: laminin-type EGF-like homology <LE18>
 F:1459-1513/Domain: laminin-type EGF-like homology <LE19>
 F:1516-1560/Domain: laminin-type EGF-like homology <LE20>
 F:1562-2133/Domain: I/II <DOM2>
 F:1562-2133/Region: heptad repeats
 F:2134-3084/Domain: G <DOMG>
 F:2150-2308/Domain: laminin G repeat homology <LG1>
 F:2337-2492/Domain: laminin G repeat homology <LG2>
 F:2518-2683/Domain: laminin G repeat homology <LG3>
 F:2748-2897/Domain: laminin G repeat homology <LG4>
 F:2925-3082/Domain: laminin G repeat homology <LG5>
 F:25/Modified site: pyrolysine carboxylic acid (Gln) (in mature form) #status predicted
 F:45,79,370,374,531,562,672,808,914,959,969,1052,1344,1414,1586,1603,1659,1686,1706,1718
 e (Asn) (covalent) #status predicted
 F:304-312/Diulfide bonds: #status experimental
 F:770,857,1999,2055,2067,2835/Binding site: carbohydrate (Asn) (covalent) #status expected
 F:845,2102/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 10.0%; Score 111.5; DB 1; Length 3084;
 Best Local Similarity 20.2%; Pred. No. 0.31; Indels 95; Gaps 11;
 Matches 53; Conservative 39; Mismatches 75; VEMPP-----
 1 MKKLR-KTSGVRLNDVTGVTCKSEDMKLVRTASFSRGQMSFTNLDPSTDRFQSPQTFQPSGTL----- 101
 2466 IKKLRISSTPDLRLNSYGRKCA--LEPIQVSFLRGY-----VEMPP----- 2509
 60 FQTFQPSGTL-NHQTTS--LVTLDEGHILSTRDSNIPFK----- 101
 2510 -KSLSPSSILMTFAFKNSGTLVLGDAERAGAQHVPPFSIMLEGRIVHNSG 2568
 102 -----SPGYMDGLHVSIVISDTSGRLIPDQVLRNRQLPSFSAQGSAR 149
 2569 DGTSLKALLHAPTGSISDQSHSISLVNRNRVITTVQVE-----NSFEVKK 2615
 150 LG-----GG-----HFGCISNVLVGRFSQSPVTLDAKRS 180
 2616 LQPLTSGKTIIDSNLYIGLPEDKATPMLKMTSFGCIKNVTL-----DAQLDPTHTAT 2670
 181 TKKDALGGCSLNKPFLMLFK 202
 2671 GSEQVELDTCILAEHPQSLHR 2692
 RESULT 9
 T00021
 DN-cadherin - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #ext_change 09-Jul-2004
 C:Accession: T00021
 R:Iwata, Y.; Iwata, T.; Hirano, S.; Steward, R.; Takeichi, M.; Temura, T.
 Neuron 19, 77-89, 1997
 A>Title: Axon patterning requires DN-cadherin, a novel neuronal adhesion receptor, in t
 A:Reference number: Z14058; MID:97388431; PMID:9247265
 A:Accession: T00021
 A>Status: preliminary; translated from GB/EMBL/DDBL
 A:Molecule type: mRNA
 A:Residues: 1-3097 <IMA>
 A:Cross-references: UNIPROT:O15943; EMBL:AB002397; NID:92381491; PIDD:BA22151.1; PTD:9
 A:Experimental source: whole embryo and adult head
 C:Genetics:
 A:Cross-references: FlyBase:Fgmn015609
 A:Map position: 36D
 A:Note: 1(2)36Da
 F:2346-2377/Domain: EGF homology <EGF>
 F:2869-2902/Domain: EGF homology <EGF1>
 Query Match 9.6%; Score 107; DB 2; Length 3097;
 Best Local Similarity 21.1%; Pred. No. 0.81; Indels 84; Gaps 11;
 Matches 50; Conservative 34; Mismatches 69; VEMPP-----
 17 VGVLT-KKSGEDMKLVRTASFSRGQMSFTNLDPSTDRFQSPQTFQPSGTL----- 70
 2370 VGVLTGRCCQ-----TTSFRKNGMWTPELE--CDSHLSLFTTRKPDGLIINQPI 2422
 71 ----NHQTTS-----LVTLDEGHILSTRDSNIPFKSPGYMDGLHNV 114
 2423 VPPERBETLISDPIALBRLRGVPRLLIDPGSGTLRLRV-----KTKKTLDDGEWHRI 2474
 115 SVTSDTSGRLI-----DDQVLRNRQLPSFS--NAQSLRLGG 152
 2475 DLFMDTESIRMVDPFKSABIAEMEDGTPPEPDMSCQARQIPPNEXYLVNVAFLQVGG 2534
 153 GH-----FEGCISNVLVGRFSQSPVTLDAKSGTKKDALSGGC 190
 2535 LVHSGDQSLYFTHVWPTAKGPDGICRLNV-----HNSKLYDLAHGLGRN-SVAGC 2585
 RESULT 10
 IUPFTM
 cadherin-related tumor suppressor precursor - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
C/Accession: A41087, #A41087
R/Author: P. A. J. Weber, U. J. Onofrechuk, P. J. Blessmann, H. J. Bryant, P. J. Goodman, C. S. Cell 67, 853-868, 1991
A/Title: The fat tumor suppressor gene in Drosophila encodes a novel member of the cadherin family
A/Reference number: A41087, MUID:92069752, PMID:1959133
A/Accession: A41087
A/Molecule type: mRNA
A/Residues: 143-485;1279-5147 <MAH>
A/Cross-references: GB:M80537
A/Accession: B41087
A/Molecule type: DNA
A/Residues: 1-142;487-1278 <MA2>
A/Cross-references: GB:M80537
A/Note: 1229-Gly and 1233-Ser were also found
C/Genetics:
A/Genes: lac
A/Cross-references: FlyBase:FBgn0001075
C/Suprafamily: cadherin-related tumor suppressor; cadherin repeat homology; EGF homology
C/Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-5147/Product: cadherin-related tumor suppressor #status predicted <MAT>
F:36-4583/Domain: extracellular #status predicted <EXT>
F:51-156/Domain: cadherin repeat homology <CR1>
F:159-270/Domain: cadherin repeat homology <CR2>
F:371-382/Domain: cadherin repeat homology <CR3>
F:390-494/Domain: cadherin repeat homology <CR4>
F:497-599/Domain: cadherin repeat homology <CR5>
F:602-708/Domain: cadherin repeat homology <CR6>
F:718-822/Domain: cadherin repeat homology <CR7>
F:831-942/Domain: cadherin repeat homology <CR8>
F:948-1049/Domain: cadherin repeat homology <CR9>
F:1052-1153/Domain: cadherin repeat homology <CR10>
F:1156-1278/Domain: cadherin repeat homology <CR11>
F:1281-1384/Domain: cadherin repeat homology <CR12>
F:1387-1489/Domain: cadherin repeat homology <CR13>
F:1492-1601/Domain: cadherin repeat homology <CR14>
F:1607-1713/Domain: cadherin repeat homology <CR15>
F:1717-1823/Domain: cadherin repeat homology <CR16>
F:1826-1922/Domain: cadherin repeat homology <CR17>
F:1925-2027/Domain: cadherin repeat homology <CR18>
F:2028-2167/Domain: cadherin repeat homology <CR19>
F:2169-2278/Domain: cadherin repeat homology <CR20>
F:2281-2384/Domain: cadherin repeat homology <CR21>
F:2387-2491/Domain: cadherin repeat homology <CR22>
F:2494-2596/Domain: cadherin repeat homology <CR23>
F:2599-2703/Domain: cadherin repeat homology <CR24>
F:2707-2810/Domain: cadherin repeat homology <CR25>
F:2813-2913/Domain: cadherin repeat homology <CR26>
F:2915-3013/Domain: cadherin repeat homology <CR27>
F:3014-3124/Domain: cadherin repeat homology <CR28>
F:3127-3229/Domain: cadherin repeat homology <CR29>
F:3232-3334/Domain: cadherin repeat homology <CR30>
F:3337-3439/Domain: cadherin repeat homology <CR31>
F:3442-3545/Domain: cadherin repeat homology <CR32>
F:3548-3651/Domain: cadherin repeat homology <CR33>
F:3654-3756/Domain: cadherin repeat homology <CR34>
F:3954-4010/Domain: EGF homology <EG1>
F:4017-4048/Domain: EGF homology <EG2>
F:4056-4089/Domain: EGF homology <EG3>
F:4096-4127/Domain: EGF homology <EG4>
F:4584-4609/Domain: transmembrane #status predicted <TM>
F:4610-5147/Domain: intracellular #status predicted <INT>

Query Match 9.4%; Score 105; DB 1; Length 5147;
Best Local Similarity 24.4%; Pred. No. 2.5;
Matches 38; Conservative 30; Mismatches 64; Indels 24; Gaps 6;

33 ASPRSRGQMSFTLVDPSTRTFQSPGQFQSPGSLTNQRTSSLVTLTECHLESL 92
4413 SNFSTASQI---YAPK---MLSMFRTYKQGGQLVAVNTQMTSTSLRGRIVVYS 4464

Qy 93 RDS--NIPFKSPQTYMDGLHHVSVISDTSGRLIIDQVLRNRQPLPSPFSAQGS-- 147
Db 4465 KOHLTNTMTV-QETSLNDGKMHVSVLSPFSRSLRLIYDGRQVGEIDLIAVHFLDPLYL 4523
Qy 148 --LRIGGHHFEGCISNVLYQRFSGS-----PRV 173
Db 4524 TLINVGSAFVGCILANVTNNELDPLNGSGSIFPRV 4559

RESULT 11

S14458
1 laminin alpha-1 chain precursor - human
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C/Accession: S14458; S14663; A34961
R/Author: T. J. Uitto, J. J. Ruoslahti, E. J. Engvall, E. M. Meri, 151-160, 1991
A/Title: Molecular cloning of the cDNA encoding human laminin A chain.
A/Reference number: S14458; MUID:91333420; PMID:1714537
A/Accession: S14458
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-3075 <HAA>
A/Cross-references: UNIPROT:P25391
R/Author: M. J. Vlodavets, R. J. Boot-Handford, R. J. Kalunki, P. J. Tryggvason, K. Blochem. J. 276, 369-379, 1991
A/Title: Primary structure of the human laminin A chain. Limited expression in human tis
A/Reference number: S14663; MUID:91264789; PMID:2049067
A/Accession: S14663
A/Molecule type: mRNA
A/Residues: 1-227, 'FE', 230-251, 'MLP', 255-418, 'E', 420-518, 'L', 520-1022, 'V', 1024-1074, 'V',
A/Cross-references: EMBL:X58531; NID:G34225; PDB:CAA41418.1; PID:G34226
R/Author: D. J. Nagayoshi, T. J. Fazio, M. J. Peltonen, J. J. Jaakkola, S. J. Sanborn, D. J. Sasaki,
Lab. Invest. 60, 772-782, 1989
A/Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A/Reference number: A34961; MUID:89280632; PMID:2733383
A/Accession: A34961
A/Molecule type: mRNA
A/Status: not compared with conceptual translation
A/Residues: 'W', 2397-2745, 'L', 2747-3053, 'L', 3055-3072, 'PSP', <OLS>
A/Note: the authors translated the codon AGA for residue 2692 as Pro
C/Genetics:
A/Genes: GDB:1AMM1; LAMA
A/Cross-references: GDB:120135; OMIM:150320
C/Suprafamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
C/Keywords: basement membrane; calcium binding; cell binding; coiled coil; disulfide bon
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-3075/Product: laminin alpha-1 chain #status predicted <MAT>
F:18-269/Domain: VI <DOM6>
F:270-516/Domain: V <DOM5>
F:270-324/Domain: laminin-type EGF-like homology <LE1>
F:327-394/Domain: laminin-type EGF-like homology <LE2>
F:397-451/Domain: laminin-type EGF-like homology <LE3>
F:454-500/Domain: laminin-type EGF-like homology <LE4>
F:503-512/Domain: laminin-type EGF-like homology #status atypical <LE5>
F:517-708/Domain: IVB <DOM3>
F:709-1159/Domain: IIIB <DOM3>
F:709-739/Domain: laminin-type EGF-like homology #status atypical <LE6>
F:742-788/Domain: laminin-type EGF-like homology <LE7>
F:791-846/Domain: laminin-type EGF-like homology <LE8>
F:849-899/Domain: laminin-type EGF-like homology <LE9>
F:902-948/Domain: laminin-type EGF-like homology <LE10>
F:951-995/Domain: laminin-type EGF-like homology <LE11>
F:998-1041/Domain: laminin-type EGF-like homology <LE12>
F:1044-1087/Domain: laminin-type EGF-like homology <LE13>
F:1090-1109/Domain: laminin-type EGF-like homology #status atypical <LE14>
F:1111-1147/Domain: laminin-type EGF-like homology #status atypical <LE15>
F:1150-1159/Domain: laminin-type EGF-like homology #status atypical <LE16>
F:1160-1361/Domain: IIV <DOM4>
F:1362-1553/Domain: IIV <DOM4>
F:1362-1400/Domain: laminin-type EGF-like homology #status atypical <LE17>
F:1403-1449/Domain: laminin-type EGF-like homology <LE18>

F:1452-1506/Domain: laminin-type EGF-like homology <LE19>
 F:1509-1553/Domain: laminin-type EGF-like homology <LE20>
 F:1554-2125/Domain: I/II, heptad repeats <DOM2>
 F:2116-2120/Region: cell adhesion #status predicted
 F:2126-3075/Domain: G <DOM3>
 F:2142-2300/Domain: laminin G repeat homology <LG1>
 F:2329-2484/Domain: laminin G repeat homology <LG2>
 F:2510-2676/Domain: laminin G repeat homology <LG3>
 F:2534-2536/Region: cell attachment (R-G-D) motif
 F:2739-2888/Domain: laminin G repeat homology <LG4>
 F:2916-3073/Domain: laminin G repeat homology <LG5>
 F:38,164,555,665,763,801,858,926,952,1045,1407,1579,1596,1678,1689,1698,1717,1804,1894,1 rate (kDa) (covaleuc) #status predicted
 F:297-305/Disulfide bonds: #status predicted

Query Match 9.1%; Score 101.5; DB 2; Length 3075;
 Best Local Similarity 21.3%; Pred. No. 2.6;
 Matches 53; Conservative 43; Mismatches 102; Indels 51; Gaps 10;

QY 1 MKNLK-KTSGVRLNDVGVTKKSEDMKLVRTASFGQMSFTNIDVPSTDRFQSLG 59
 DB 2458 IKMLKSRSTFDDLRLNSGVKGL--LEPRSVSLKGYITLPPKSLPSEEMLVTF 2515
 QY 60 FQTFQPSGTL-----NHQRTSLVTLDEGHLESTRDSN-----IPFKS 102
 DB 2516 --TTNSGIIILALAGDVEKRGDEBAHVPPFSVMLIGNIEVAVNFGDGTGLKALLHA 2573
 QY 103 P-GTYMDGLLHVSVISDTSGRLIIDQ---VLRRNQLPFSFNAQSLRGG----- 152
 DB 2574 PTGCSGQAHSHISLVNRRITVQLDENNVEMKGLTVESRITVSNLYVGDIPIGEG 2633
 QY 153 -----GHREGCSNVLVQRFSGSPVLDLASKSTKQASLGCCSLANKPPFL----- 198
 DB 2634 TSLITWRSRPHGCIKMLIF-----NRLDPSNAGHGYVDLDTWLSERPCLAPDAEDS 2688
 QY 199 MLFSPKRF 207
 DB 2689 KILREPPAF 2697

RESULT 12

T23433
 hypothetical protein K08C7.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T23433

R/Berke, M.
 submitted to the EMBL Data Library, March 1996

A/Reference number: Z19740
 A/Accession: T23433

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA

A/Residues: 1-3672 <WIL>
 A/Cross-references: UNIPROT:Q21313; EMBL:Z70286; PIDD:CAA4293.1; GSPDB:GN00022; CESP:K0

A/Experimental source: clone K08C7
 A/Genetic:

A/Map position: 4
 A/Insertions: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 3

C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like

Query Match 8.9%; Score 99.5; DB 2; Length 3672;
 Best Local Similarity 27.1%; Pred. No. 5;
 Matches 60; Conservative 31; Mismatches 79; Indels 51; Gaps 12;

QY 1 MKNLKKTSGVRLND--TVGVTKKSEDMKLVRTASFGQMSFTNIDVPSTDRFQSL 56
 DB 3041 IKSVKLGSDNVDLSSHASKGVSGC--PLHSVTVFSLSDRTTASFNATRESFD--VSV 3097
 QY 57 SFGFQT---FQPSGTLNMQRTSSLLVTL-EDGHIELSTRD--SNIPFKSPGTMDGL 110
 DB 3098 TFFKTRTSIRQPSLFTVNDDEDSVLSVINEGDIILVTSGEDIATLELAASP-----DEK 3153

QY 111 LHHVSVISDTSGRLIIDQVLRNORLPFSFNAQSLRGCGH----- 154
 DB 3154 WHVYSIRKTYIIRIDAD-----SFSNEVARKHADNDNPDSFLSAFPGKSGRT 3203
 QY 155 --FEGCISNVLVQRFSGSPVLDLASKSTKQASLGCCSLN 193
 DB 3204 PSFVGCIGDVTL-----NGKLDLPAN-SRIKESLNGCSLS 3238

RESULT 13

T37316
 probable laminin alpha chain - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

A/Accession: T37316
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
 A/Residues: 1-3704 <JOH>

A/Cross-references: UNIPROT:P91904; EMBL:AB016806; PIDD:BAJ2347.1
 A/Experimental source: strain N2

C/Genetic:

A/Map position: IV
 A/Insertions: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3;

C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like

Query Match 8.9%; Score 99.5; DB 2; Length 3704;
 Best Local Similarity 27.1%; Pred. No. 5.1;
 Matches 60; Conservative 31; Mismatches 79; Indels 51; Gaps 12;

QY 1 MKNLKKTSGVRLND--TVGVTKKSEDMKLVRTASFGQMSFTNIDVPSTDRFQSL 56
 DB 3041 IKSVKLGSDNVDLSSHASKGVSGC--PLHSVTVFSLSDRTTASFNATRESFD--VSV 3097
 QY 57 SFGFQT---FQPSGTLNMQRTSSLLVTL-EDGHIELSTRD--SNIPFKSPGTMDGL 110
 DB 3098 TFFKTRTSIRQPSLFTVNDDEDSVLSVINEGDIILVTSGEDIATLELAASP-----DEK 3153
 QY 111 LHHVSVISDTSGRLIIDQVLRNORLPFSFNAQSLRGCGH----- 154
 DB 3154 WHVYSIRKTYIIRIDAD-----SFSNEVARKHADNDNPDSFLSAFPGKSGRT 3203
 QY 155 --FEGCISNVLVQRFSGSPVLDLASKSTKQASLGCCSLN 193
 DB 3204 PSFVGCIGDVTL-----NGKLDLPAN-SRIKESLNGCSLS 3238

RESULT 14

E86327
 protein F1B014.19 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

A/Accession: E86327
 R/Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
 anson, N.P.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Litov, J.S.; Maiti, R.; Marziani
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venier, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MIMD:21016719; PMID:11130712

A/Accession: E86327
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-1158 <STO>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:07:29 ; Search time 36.8842 Seconds
(without alignments)
3026.590 Million cell updates/sec

Title: US-10-817-423-6

Perfect score: 1118

Sequence: 1 MKNLKKTSGVRLNDTVGVT.....MLFKSPRRPKRGRFVNVQL 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1118	100.0	1725	2 P70570	P70570 ratlun norv
2	1033	92.4	3333	1 IMA3 MOUSE	Q61789 mus musculu
3	852	76.2	1668	2 Q6VU69	Q6VU69 homo sapien
4	852	76.2	3277	2 Q6VU67	Q6VU67 homo sapien
5	852	76.2	3333	2 Q6VU68	Q6VU68 homo sapien
6	850	76.0	1713	1 IMA3 HUMAN	Q16787 homo sapien
7	850	76.0	1806	2 Q6VU60	Q6VU60 homo sapien
8	850	76.0	3333	2 Q76E14	Q76E14 homo sapien
9	760.5	68.0	1725	2 Q6E7A1	Q6E7A1 canis famli
10	204	18.2	1254	2 Q91VVO	Q91VVO mus musculu
11	204	18.2	1816	1 IMA4 MOUSE	P97927 mus musculu
12	187	16.7	1816	1 IMA4 HUMAN	Q16363 homo sapien
13	186	16.6	794	2 Q6R37	Q6R37 mus musculu
14	186	16.6	1524	2 Q6ZQA1	Q6ZQA1 mus musculu
15	186	16.6	3718	1 IMA5 MOUSE	Q61001 mus musculu
16	174	15.6	670	2 Q9BT3	Q9BT3 homo sapien
17	174	15.6	3695	1 IMA5 HUMAN	Q15230 homo sapien
18	174	15.6	3695	2 Q6TD58	Q6TD58 homo sapien
19	173.5	15.5	3712	1 IMA DROME	Q00174 drosophila
20	173.5	15.5	3712	2 Q9VR00	Q9VR00 drosophila
21	143.5	12.9	3106	1 IMA2 MOUSE	Q60675 mus musculu
22	143.5	12.8	659	2 Q7TQ19	Q7TQ19 mus musculu
23	143.5	12.8	858	2 Q8R145	Q8R145 mus musculu
24	134.5	12.0	517	2 Q8MR7	Q8MR7 drosophila
25	134.5	12.0	1039	2 Q9VQB1	Q9VQB1 drosophila
26	134.5	12.0	3110	1 IMA2 HUMAN	P24043 homo sapien
27	130.5	11.7	211	2 Q712T9	Q712T9 homo sapien
28	128.5	11.5	2923	1 CLR2 HUMAN	Q9HC44 homo sapien
29	127	11.4	1247	2 Q7PT06	Q7PT06 anopheles g
30	124	11.1	2144	1 CLR2 RAT	Q9GY22 rattus norv
31	122.5	11.0	2920	1 CLR2 MOUSE	Q9T0M0 mus musculu

32	122.5	11.0	3616	2 Q7PPF9	Q7PPF9 anopheles g
33	115.5	10.3	3102	2 Q45614	Q45614 caenorhabdi
34	111.5	10.0	3084	1 IMA1 MOUSE	P19137 mus musculu
35	110	9.8	3367	2 Q9XZC9	Q9XZC9 drosophila
36	110	9.8	3375	2 Q81P51	Q81P51 drosophila
37	107	9.6	3097	1 CADN DROME	Q15943 drosophila
38	105	9.4	5147	1 FAT DROME	P33450 drosophila
39	104	9.3	1180	2 Q8BPF6	Q8BPF6 mus musculu
40	104	9.3	1310	1 CTA4 MOUSE	Q99547 mus musculu
41	104	9.3	1310	2 Q8K002	Q8K002 mus musculu
42	104	9.3	1330	2 Q69ZB1	Q69ZB1 mus musculu
43	101.5	9.1	3075	1 IMA1 HUMAN	P25391 homo sapien
44	101	9.0	1306	2 Q8WYK1	Q8WYK1 homo sapien
45	100	8.9	436	2 P91806	P91806 strongyloce

ALIGNMENTS

RESULT 1

P70570 PRELIMINARY; PRT; 1725 AA.

AC P70570;

DT 01-FEB-1997 (T-EMBLrel. 02, Created)

DT 01-FEB-1997 (T-EMBLrel. 02, Last sequence update)

DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)

DE Lamtin-5 alpha 3 chain.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97081969; PubMed=8923212;

RA Baker S.E., Hopkinson S.B., Fitchum M., Andreason G.L., Frasler F.,

RA Plopper G., Quaranta V., Jones J.C.R.;

RT "Lamtin-5 and hemidesmosomes: role of the alpha 3 chain subunit in

hemidesmosome stability and assembly.";

RL J. Cell Sci. 109:2509-2520 (1996).

DR HSSP; P35070; 11PO.

DR GO; GO:0005606; C:lamtin-1; IEA.

DR GO; GO:0005102; F:receptor binding; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0030155; P:regulation of cell adhesion; IEA.

DR GO; GO:0030334; P:regulation of cell migration; IEA.

DR GO; GO:0045995; P:regulation of embryonic development; IEA.

DR InterPro; IPR006985; Cona_Like_1ec_gl.

DR InterPro; IPR006209; EGF_Like.

DR InterPro; IPR002049; Lamtin_EGF.

DR InterPro; IPR001791; Lamtin_G.

DR InterPro; IPR009254; Lamtin_I.

DR InterPro; IPR010307; Lamtin_II.

DR InterPro; IPR003129; TSP_N.

DR Pfam; PF00053; Lamtin_EGF; 2.

DR Pfam; PF02210; Lamtin_G_2; 4.

DR Pfam; PF06008; Lamtin_I; 1.

DR Pfam; PF06009; Lamtin_II; 1.

DR SMART; SM00180; EGF_Lam; 2.

DR SMART; SM00282; LamG; 5.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 1.

DR PROSITE; PS01248; LAMTIN_TYPE_EGF; 2.

DR PROSITE; PS50025; LAM_G_DOMAIN; 5.

KW Lamtin EGF-like domain.

SQ SSQUNCE 1725 AA; 190392 MW; 02EB43B3B72B0FB CRC64;

Query Match 100.0%; Score 1118; DB 2; Length 1725;

Best Local Similarity 100.0%; Pred. No. 2.1e-87;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDTVGVTKKCEBMDKLVRTASFGGOMSPFTNIDVPSDFQSLFGF 60

DB 1129 MKNLKKTSGVRLNDITVGVTKKCSBDWKLVRTASFSRGQGFPTNLDPSTDFQLSPGF 1188
 QY QFPQPSGTLNHOGRTRSLVLTLEDGHIELSTDSNIPFKSPGTWMDGLHHVVSIDT 120
 DB 1189 QTFQPSGTLNHOGRTRSLVLTLEDGHIELSTDSNIPFKSPGTWMDGLHHVVSIDT 1248
 QY 121 SGIRLLIDQVLRNRQRLPSPSNAQSLRLGGHFGGCSISNVLVQRFSPSPVTLDAASKS 180
 DB 1249 SGIRLLIDQVLRNRQRLPSPSNAQSLRLGGHFGGCSISNVLVQRFSPSPVTLDAASKS 1308
 QY 181 TKKDAISLGGCSLNKPPFLMLFKSPKPKNKRIINYNOL 218
 DB 1309 TKKDAISLGGCSLNKPPFLMLFKSPKPKNKRIINYNOL 1346
 RESULT 2
 LMA3_MOUSE STANDARD, PRT, 3333 AA.
 ID LMA3_MOUSE
 AC Q61789; Q08751; Q61788; Q61966; Q9UHQ7;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Laminin alpha-3 chain precursor (Nicein alpha subunit).
 GN Name=Lama3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE OF 1-58 FROM N.A., AND SEQUENCE OF 32-38.
 RA MEDLINE=21818471; PubMed=11829758; DOI=10.1042/0264-6021:3620213;
 RX Garbe J.H., Gohring W., Mann K., Timpl R., Sasaki T.;
 RT "Complete sequence, recombinant analysis and binding to laminins and
 RT sulphated ligands of the N-terminal domains of laminin alpha3 and
 RT alpha5 chains.";
 RL Biochem. J. 362:213-221 (2002).
 RN [2]
 RP SEQUENCE OF 1-726 FROM N.A.
 RA STRAIN=ICR;
 RX MEDLINE=97296337; PubMed=9151674; DOI=10.1083/jcb.137.3.685;
 RT Miner J.H., Paton B.L., Lenz S.T., Gilbert D.J., Snider W.D.,
 RA Jenkins N.A., Copeland N.G., Sane J.R.;
 RT "The laminin alpha chains: expression, developmental transitions, and
 RT chromosomal locations of alpha1-5, identification of heterotimeric
 RT laminins 8-11, and cloning of a novel alpha3 isoform.";
 RL J. Cell Biol. 137:685-701 (1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM A), AND SEQUENCE OF 716-3284 FROM N.A.
 RA (ISOFORM B).
 RX MEDLINE=95394948; PubMed=7665604; DOI=10.1074/jbc.270.37.21820;
 RT Galliano M.-F., Aberdam D., Aguzzi A., Ortonne J.-P., Meneguzzi G.,
 RA "Cloning and complete primary structure of the mouse laminin alpha 3
 RT chain. Distinct expression pattern of the laminin alpha 3A and alpha
 RT 3B chain isoforms.";
 RL J. Biol. Chem. 270:21820-21826 (1995).
 RN [4]
 RP REVISIONS.
 RA Aberdam D.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1767-2485 FROM N.A.
 RA MEDLINE=94281750; PubMed=8012114;
 RX Aberdam D., Galliano M.-F., Mattei M.-G., Pisaní-Spadafora A.,
 RA Ortonne J.-P., Meneguzzi G.;
 RT "Assignment of mouse nicein genes to chromosomes 1 and 18.";
 RL Mamm. Genome 5:229-233 (1994).
 RN [6]
 RP SEQUENCE OF 1767-2485 FROM N.A.
 RA TISSUE=Lung;
 RX MEDLINE=94353405; PubMed=8081888;
 RA Aberdam D., Aguzzi A., Baudoin C., Galliano M.-F., Ortonne J.-P.,

RA Meneguzzi G.;
 RT "Developmental expression of nicein adhesion protein (laminin-5)
 RT subunits suggests multiple morphogenic roles.";
 RL Cell Adhes. Commun. 2:115-129 (1994).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
 CC via integrin alpha3/beta1 in focal adhesion and integrin alpha-
 CC 6/beta4 in hemidesmosomes, (2) signal transduction via tyrosine
 CC phosphorylation of p125-FAK and p80, (3) differentiation of
 CC keratinocytes (by similarity).
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end. The alpha-3 chain is a subunit of laminin-5
 CC (epiligrin/kalium/nicein), and possibly also a component of
 CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=B;
 CC Name=A;
 CC IsoId=Q61789-1; Sequence=Displayed;
 CC -1- ISOId=Q61789-2; Sequence=VSP_003038, VSP_003039;
 CC TISSUE SPECIFICITY: Basal membrane of the upper alimentary tract
 CC and urinary and nasal epithelia, salivary glands and teeth (both
 CC variants). Isoform A is predominantly expressed in skin, hair
 CC follicles and developing neurons of the trigeminal ganglion.
 CC Isoform B was found in bronchi, alveoli, stomach, intestinal
 CC crypts, whisker pad, CNS, telencephalic neuroectoderm, thalamus,
 CC Ratke's pouch and periventricular subependymal germinal layer.
 CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact
 CC with other laminin chains to form a coiled coil structure.
 CC -1- DOMAIN: Domains IV and V are globular.
 CC -1- SIMILARITY: Contains 15 laminin BGF-like domains.
 CC -1- SIMILARITY: Contains 5 laminin G-like domains.
 CC -1- SIMILARITY: Contains 1 laminin IV domain.
 CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.
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 CC -----
 DR EMBL, AJ293592; CAB99254.2; -.
 DR EMBL, U88353; AAC53179.1; -.
 DR EMBL, X84014; CA58837.1; -.
 DR EMBL, I20478; CAA58836.1; ALT_FRAME.
 DR HSSP, P02468; INPE.
 DR MGD, MG1:99909; Lama3.
 DR GO, GO:0005604; C:basement membrane, IDA.
 DR InterPro, IPR008985; ConA like_1ec_g1.
 DR InterPro, IPR006209; EGF like.
 DR InterPro, IPR008979; Gal_bind_like.
 DR InterPro, IPR009030; Grow_fac_recept.
 DR InterPro, IPR008212; Lam_N2.
 DR InterPro, IPR000034; Laminin_B.
 DR InterPro, IPR002049; Laminin_BGF.
 DR InterPro, IPR001791; Laminin_G.
 DR InterPro, IPR009254; Laminin_I.
 DR InterPro, IPR010307; Laminin_II.
 DR InterPro, IPR008211; Laminin_N.
 DR InterPro, IPR003129; TSP_N.
 DR Pfam, PF00052; Laminin_B_1.
 DR Pfam, PF00053; Laminin_BGF_10.

DR Pfam; PF00054; Laminin_G; 3.
 DR Pfam; PF06008; Laminin_I; 1.
 DR Pfam; PF06009; Laminin_II; 1.
 DR Pfam; PF00055; Laminin_N; 1.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR ProDom; PD003031; Laminin_B; 1.
 DR PROSITE; PS00022; EGF_1; 10.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PSS0025; LAM_G_DOMAIN; 5.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 10.
 DR Alternative splicing; Basement membrane; Cell adhesion; Coiled coil;
 DR Direct protein sequencing; Extracellular matrix; Glycoprotein;
 DR Laminin EGF-like domain; Repeat; Signal.
 KM Laminin EGF-like domain; Repeat; Signal.
 FT STGNL 1 31
 FT CHAIN 32 3333 Laminin alpha-3 chain.
 FT DOMAIN 32 294 Laminin N-terminal (domain VII).
 FT DOMAIN 295 725 Domain V.
 FT DOMAIN 296 350 Laminin EGF-like 1.
 FT DOMAIN 353 420 Laminin EGF-like 2.
 FT DOMAIN 423 464 Laminin EGF-like 3.
 FT DOMAIN 488 530 Laminin EGF-like 4.
 FT DOMAIN 533 576 Laminin EGF-like 5.
 FT DOMAIN 582 625 Laminin EGF-like 6.
 FT DOMAIN 628 678 Laminin EGF-like 7.
 FT DOMAIN 681 725 Laminin EGF-like 8.
 FT DOMAIN 793 1262 Laminin domain IV 1 (domain IV B).
 FT DOMAIN 1263 1464 Domain III B.
 FT DOMAIN 1310 1353 Laminin EGF-like 9.
 FT DOMAIN 1354 1403 Laminin EGF-like 10.
 FT DOMAIN 1404 1454 Laminin EGF-like 11.
 FT DOMAIN 1455 1464 Laminin EGF-like 12 (N-terminal).
 FT DOMAIN 1465 1653 Laminin domain IV (domain IV A).
 FT DOMAIN 1654 1821 Domain III A.
 FT DOMAIN 1654 1686 Laminin EGF-like 12 (C-terminal).
 FT DOMAIN 1687 1733 Laminin EGF-like 13.
 FT DOMAIN 1734 1786 Laminin EGF-like 14.
 FT DOMAIN 1787 1821 Laminin EGF-like 15 (incomplete).
 FT DOMAIN 1822 2388 Domain II and I.
 FT DOMAIN 2389 2590 Laminin G-like 1.
 FT DOMAIN 2591 2759 Laminin G-like 2.
 FT DOMAIN 2766 2926 Laminin G-like 3.
 FT DOMAIN 2986 3150 Laminin G-like 4.
 FT DOMAIN 3157 3330 Laminin G-like 5.
 FT DOMAIN 1854 1983 Coiled coil (potential).
 FT DOMAIN 2015 2060 Coiled coil (potential).
 FT DOMAIN 2091 2168 Coiled coil (potential).
 FT DOMAIN 2214 2241 Coiled coil (potential).
 FT DOMAIN 2321 2386 Cell attachment site (potential).
 FT SITE 2277 2279
 FT DISULFID 1310 1317 By similarity.
 FT DISULFID 1312 1324 By similarity.
 FT DISULFID 1326 1335 By similarity.
 FT DISULFID 1338 1351 By similarity.
 FT DISULFID 1354 1369 By similarity.
 FT DISULFID 1356 1376 By similarity.
 FT DISULFID 1378 1387 By similarity.
 FT DISULFID 1390 1401 By similarity.
 FT DISULFID 1404 1416 By similarity.
 FT DISULFID 1406 1423 By similarity.
 FT DISULFID 1425 1434 By similarity.
 FT DISULFID 1437 1452 By similarity.
 FT DISULFID 1487 1496 By similarity.
 FT DISULFID 1689 1703 By similarity.
 FT DISULFID 1706 1715 By similarity.
 FT DISULFID 1718 1731 By similarity.
 FT DISULFID 1734 1746 By similarity.
 FT DISULFID 1736 1755 By similarity.
 FT DISULFID 1757 1766 By similarity.
 FT DISULFID 1769 1784 By similarity.
 FT DISULFID 1822 1825 Interchain (Probable).
 FT DISULFID 1825 1825 Interchain (Probable).

Query Match

92.4%; Score 1033; DB 1; Length 3333;

Best Local Similarity 92.7%; Pred. No. 1,le-79;
 Matches 202; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 MKRLKTSGVVRLNDVGVTKKSEPMKVRTPSPRGOMSTPNDVSTDFQISFGP 60
 DB 2737 MKRLKTSGVVRLNDVGVTKKSEPMKVRTPSPRGOMSTPNDVSTDFQISFGP 2796
 QY 61 QTFQPSGTLNHOVRTSSLVLTLEDEHLESTDSNIPFSPQTYMDGLHHVSVISDT 120
 DB 2797 QTFQPSGTLNHOVRTSSLVLTLEDEHLESTDSNIPFSPQTYMDGLHHVSVISDT 2856
 QY 121 SGRLRLIDQVLRNRORLPSPNAQSLRGHGFEGCISNVLVGRFSQSPVLDLASKS 180
 DB 2857 SGRLRLIDQVLRNRORLPSPNAQSLRGHGFEGCISNVLVGRFSQSPVLDLASKS 2916
 QY 181 TKRDASLGGCSLNKPPFLMFKSPKPKNGRIYNNQL 218
 DB 2917 TKRDASLGGCSLNKPPFLMFKSPKPKNGRIYNNQL 2954
 RESULT 3
 ID Q6VU69 PRELIMINARY; PRT; 1668 AA.
 AC Q6VU69;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Laminin alpha 3 splice variant a.
 GN Name=LAMA3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=42833568; Pubmed=12915477; DOI=10.1093/hmg/ddg234;
 RA McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
 RA Dopling-Hepensetal P.U., Bady R.A., Jamil T., Phillips R.J.,
 RA Shabir S.G., Haroon T.S., Knurshid K., Moore J.B., Page B.,
 RA Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
 RA McGrath J.A.;
 RT "An unusual N-terminal deletion of the laminin (alpha)3a isoform leads
 RT to the chronic granulation tissue disorder laryngo-onycho-cutaneous
 RT syndrome.";
 RL Hum. Mol. Genet. 12:2395-2409 (2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RU McLean W.H.I.;
 RU Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY327114; AAQ72569.1; -;
 DR GO; GO:0005606; C:Laminin-1; IEA.
 DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0030155; P:regulation of cell migration; IEA.
 DR GO; GO:0030334; P:regulation of cell adhesion; IEA.
 DR GO; GO:0045995; P:regulation of embryonic development; IEA.
 DR InterPro; IPR001844; Chaprin Cpn60.
 DR InterPro; IPR008985; Cona like_1ec_g1.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR009254; Laminin_I.
 DR InterPro; IPR010307; Laminin_II.
 DR InterPro; IPR003129; TSP N.
 DR Pfam; PF00053; Laminin_EGF; 1.
 DR Pfam; PF02210; Laminin_G; 2; 4.
 DR Pfam; PF06008; Laminin_I; 1.
 DR Pfam; PF00054; Laminin_II; 1.
 DR SMART; SM00180; EGF_Lam; 2.
 DR SMART; SM00282; LamG; 5.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF 2; 1.
 DR PROSITE; PS01248; LAMININ TYPE EGF; 2.
 DR PROSITE; PS50025; LAM G DOMAIN; 5.
 KW Laminin EGF-like domain.
 SQ SEQUENCE 1668 AA; 184053 MW; 98BF5FC45637645C CRC64;
 Query Match 76.2%; Score 852; DB 2; Length 1668;
 Best Local Similarity 76.6%; Pred. No. 1.9e-64;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MNKLKTSQVRLNDVGVYTKKCSBDMKLVRTASPSRGGMSFTNLDVSTDRFQLSPGF 60
 DB 1073 MNKLKTSQVRLNDVGVYTKKCSBDMKLVRSASPSRGGQLSTDLGLPTDHLQASFGF 1132
 QY 61 QTFQPSGTLNMQRTSSILVLTEDGHIELSTRDSNIPFSPGTYMDGLAHVSVISDT 120
 DB 1133 QTFQPSGTLNMQRTSSILVLTEDGHIELSTRDSNIPFSPGTYMDGLAHVSVISDN 1192
 QY 121 SGLRLIIDQVLRNRQLPSFSNAQSLRIGGHEGCGISNVLVQFSPQSPVLDLASKS 180
 DB 1193 SGLRLIIDQVLRNRQLPSFSNAQSLRIGGHEGCGISNVLVQFSLSPVLDLTSNS 1252
 QY 181 TKKDAISLGGCSLNKPPFLMLFKSPKPKNGRIENNVQL 218
 DB 1253 LKRDVSLGGCSLNKPPFLMLKSGTRFNKTKTFRINQL 1290
 RESULT 4
 Q6VU67 PRELIMINARY; PRT; 3277 AA.
 ID Q6VU67
 AC Q6VU67
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Laminin alpha 3 splice variant b2.
 GN Name=LAMA3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
 RX McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
 RA Dopping-Hepenstall P.J., Bady R.A., Jamil T., Phillips R.J.,
 RA Shabibi S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
 RA Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
 RA McGrath J.A.;
 RT "An unusual N-terminal deletion of the laminin (alpha)3a isoform leads
 RT to the chronic granulacion tissue disorder laryngo-oncho-cutaneous
 RT syndrome.";
 RT Hum. Mol. Genet. 12:2395-2409 (2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX McLean W.H.I.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY327116; AAC72571.1; -;
 DR GO; GO:0005578; Extracellular matrix (sensu Metazoa); IEA.
 DR GO; GO:0005506; Cilaminin-1; IEA.
 DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0003034; P:regulation of cell adhesion; IEA.
 DR GO; GO:0045955; P:regulation of cell migration; IEA.
 DR GO; GO:0045955; P:regulation of embryonic development; IEA.
 DR InterPro; IPR001844; Chaplin_Cp60.
 DR InterPro; IPR008985; Con_Like_Iec_g1.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR008979; Gal_bind_Like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000034; Laminin_B.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001791; Laminin_G.

DR InterPro; IPR009254; Laminin_I.
 DR InterPro; IPR010307; Laminin_II.
 DR InterPro; IPR008211; Laminin_N.
 DR InterPro; IPR003129; TSP_N.
 DR Pfam; PF00052; Laminin_B_1.
 DR Pfam; PF00053; Laminin_EGF; 8.
 DR Pfam; PF02210; Laminin_G_2; 4.
 DR Pfam; PF06008; Laminin_I_1.
 DR Pfam; PF06009; Laminin_II; 1.
 DR Pfam; PF00055; Laminin_N; 1.
 DR PRINTS; PD00011; EGF_LAMININ.
 DR ProDom; PD003031; Laminin_B; 1.
 DR SMART; SM00181; EGF; 8.
 DR SMART; SM00180; EGF_Lam; 14.
 DR SMART; SM00281; Lamg; 1.
 DR SMART; SM00282; Lamg; 5.
 DR SMART; SM00135; Lamnt; 1.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; 12.
 DR PROSITE; PS01186; EGF 2; 1.
 DR PROSITE; PS01248; LAMININ TYPE EGF; 13.
 DR PROSITE; PS50025; LAM G DOMAIN; 5.
 KW Laminin EGF-like domain.
 SQ SEQUENCE 3277 AA; 360209 MW; 3ACFEB98357122B CRC64;
 Query Match 76.2%; Score 852; DB 2; Length 3277;
 Best Local Similarity 76.6%; Pred. No. 4.5e-64;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;
 QY 1 MNKLKTSQVRLNDVGVYTKKCSBDMKLVRTASPSRGGMSFTNLDVSTDRFQLSPGF 60
 DB 2682 MNKLKTSQVRLNDVGVYTKKCSBDMKLVRSASPSRGGQLSTDLGLPTDHLQASFGF 2741
 QY 61 QTFQPSGTLNMQRTSSILVLTEDGHIELSTRDSNIPFSPGTYMDGLAHVSVISDT 120
 DB 2742 QTFQPSGTLNMQRTSSILVLTEDGHIELSTRDSNIPFSPGTYMDGLAHVSVISDN 2801
 QY 121 SGLRLIIDQVLRNRQLPSFSNAQSLRIGGHEGCGISNVLVQFSPQSPVLDLASKS 180
 DB 2802 SGLRLIIDQVLRNRQLPSFSNAQSLRIGGHEGCGISNVLVQFSLSPVLDLTSNS 2861
 QY 181 TKKDAISLGGCSLNKPPFLMLFKSPKPKNGRIENNVQL 218
 DB 2862 LKRDVSLGGCSLNKPPFLMLKSGTRFNKTKTFRINQL 2899
 RESULT 5
 Q6VU68 PRELIMINARY; PRT; 3333 AA.
 ID Q6VU68
 AC Q6VU68
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Laminin alpha 3 splice variant b1.
 GN Name=LAMA3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2833568; PubMed=12915477; DOI=10.1093/hmg/ddg234;
 RX McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
 RA Dopping-Hepenstall P.J., Bady R.A., Jamil T., Phillips R.J.,
 RA Shabibi S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
 RA Darling J., Atherton D.J., Van Steensel M.A., Munro C.S., Smith F.J.,
 RA McGrath J.A.;
 RT "An unusual N-terminal deletion of the laminin (alpha)3a isoform leads
 RT to the chronic granulacion tissue disorder laryngo-oncho-cutaneous
 RT syndrome.";
 RT Hum. Mol. Genet. 12:2395-2409 (2003).
 RN [2]

RP SEQUENCE FROM N.A.
 RL McLean W.H.I. to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY327115; AA072570.1; -
 DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO: GO:0005606; C:laminin-1; IEA.
 DR GO: GO:0005102; F:receptor binding; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR GO: GO:0030334; P:regulation of cell adhesion; IEA.
 DR GO: GO:0045595; P:regulation of cell migration; IEA.
 DR InterPro: IPR001844; Chaprin Cpn60.
 DR InterPro: IPR008985; Cona like_1ec_g1.
 DR InterPro: IPR006209; EGF like_1ec_g1.
 DR InterPro: IPR008979; Gal_bind_like.
 DR InterPro: IPR006210; IEGF.
 DR InterPro: IPR000034; Laminin_B.
 DR InterPro: IPR002049; Laminin_EGF.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR009254; Laminin_I.
 DR InterPro: IPR010307; Laminin_II.
 DR InterPro: IPR008211; Laminin_N.
 DR InterPro: IPR003129; TSP_N.
 DR Pfam: PF00052; Laminin_B; 1.
 DR Pfam: PF00053; Laminin_EGF; 8.
 DR Pfam: PF02210; Laminin_G; 2; 4.
 DR Pfam: PF06008; Laminin_I; 1.
 DR Pfam: PF06009; Laminin_II; 1.
 DR Pfam: PF00055; Laminin_N; 1.
 DR PRINTS: PR00011; EGF_LAMININ.
 DR ProDom: PD003031; Laminin_B; 1.
 DR SMART: SM00181; EGF; 8.
 DR SMART: SM00180; EGF_Lam; 14.
 DR SMART: SM00281; LamB; 1.
 DR SMART: SM00282; LamG; 5.
 DR SMART: SM00136; LamT; 1.
 DR PROSITE: PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE: PS00022; EGF_1; 12.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01248; LAMININ_TYPE_EGF; 13.
 DR PROSITE: PS00025; LAM_G_DOMAIN; 5.
 DR KMW Laminin_EGF-like domain.
 DR SEQUENCE 3333 AA; 366646 MW; 9P99AF49B8EP27DD CRC64;

Query Match 76.2%; Score 852; DB 2; Length 3333;
 Best Local Similarity 76.6%; Pred. No. 4.ee-64;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKRLKKTSGVRLNDTVGVTKKCEDEKLVRTASFSFGQMSFTNLDVPESTRFQLSRGF 60
 DB 2738 MKRLKKTSGVRLNDTVGVTKKCEDEKLVRSASFSGQLSFTDGLPTDHLQASFGF 2797
 QY 61 QTFQPSGTLNHOHRTSSLVLTLEDGHIESTRDSNPIFKSPQTVWDGLLHVSVISDT 120
 DB 2798 QTFQPSGTLNHOHRTSSLVLTLEDGHIESTRDSNPIFKSPQTVWDGLLHVSVISDN 2857
 QY 121 SGLRLILDQVLRNORLPSPFSAQSLRGCGHFECISNVTVQRFPSQSEPVLDLASKS 180
 DB 2858 SGLRLILDQVLRNORLPSPFSAQSLRGCGHFECISNVTVQRFPSQSEPVLDLASKS 180
 QY 181 TKRDASLGGCSLKKPPIAMFKSKPRPKRGRIRVNDL 218
 DB 2918 LKRDVSLGGCSLKKPPIAMFKSKPRPKRGRIRVNDL 2955

DE (Nlcein alpha subunit).
 GN Name=LAM3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Keratinocytes;
 RX MEDLINE=94357926; PubMed=8077230;
 RA Ryan M.C., Tizard R., Vandevanter D.R., Carter W.G.;
 RT "Cloning of the Lam3 gene encoding the alpha 3 chain of the adhesive
 RT ligand epiligrin. Expression in wound repair.";
 RL J. Biol. Chem. 269:22779-22787(1994).
 RN [2]
 RP SEQUENCE OF 1-1331 FROM N.A. (ISOFORMS A AND B).
 RX MEDLINE=96163880; PubMed=8586427;
 RA Vidal F., Baudouin C., Miguel C., Galliano M.-F., Christiano A.M.,
 RA Vltio J., Ortonne J.-P., Meneguzzi G.;
 RT "Cloning of the laminin alpha 3 chain gene (LAMA3) and identification
 RT of a homozygous deletion in a patient with Herlitz junctional
 RT epidermolysis bullosa.";
 RL Genomics 30:273-280(1995).
 RN [3]
 RP DISBASE.
 RX PubMed=12915477; DOI=10.1093/hmg/ddg234;
 RA Irwin McLean W.H., Irvine A.D., Hamill K.J., Whitlock N.V.,
 RA Coleman-Campbell C.M., Mellerio J.E., Ashton G.S.,
 RA Dopping-Hepenstall P.J.H., Bady R.A.J., Jamil T., Phillips R.J.,
 RA Shabir S.G., Haroon T.S., Khurshid K., Moore J.E., Page B.,
 RA Darling J., Atherton D.J., Van Steensel M.A.M., Munro C.S.,
 RA Smith F.J.D., McGrath J.A.;
 RT "An unusual N-terminal deletion of the laminin alpha3 isoform leads
 RT to the chronic granulation tissue disorder laryngo-oncho-cutaneous
 RT syndrome.";
 RL Hum. Mol. Genet. 12:2395-2409(2003).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- FUNCTION: Laminin-5 is thought to be involved in (1) cell adhesion
 CC via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-
 CC 6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine
 CC phosphorylation of p125-FAK and p80, (3) differentiation of
 CC keratinocytes.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end. The alpha-3 chain is a subunit of laminin-5
 CC (epiligrin/kalinin/nlcein), and possibly also a component of
 CC laminin-6 (K-laminin) and laminin-7 (KS-laminin).
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=A;
 CC Name=B;
 CC Name=C;
 CC Name=D;
 CC Name=E;
 CC Name=F;
 CC Name=G;
 CC Name=H;
 CC Name=I;
 CC Name=J;
 CC Name=K;
 CC Name=L;
 CC Name=M;
 CC Name=N;
 CC Name=O;
 CC Name=P;
 CC Name=Q;
 CC Name=R;
 CC Name=S;
 CC Name=T;
 CC Name=U;
 CC Name=V;
 CC Name=W;
 CC Name=X;
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 CC Name=AA;
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 CC Name=CB;
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 CC Name=CD;
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 CC Name=CR;
 CC Name=CS;
 CC Name=CT;
 CC Name=CU;
 CC Name=CV;
 CC Name=CW;
 CC Name=CX;
 CC Name=CY;
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CC	epidermolysis bullosa Herlitz-Pearson type,JB3 is a blistering disorder in skin that is characterized by a separation of basal cells from the basement membrane due to a decreased number of hemidesmosomes. Laminin-5 is missing from the basement membrane of patients with the gravus form of epidermolysis bullosa.
CC	-1 DISEASE: Defects in LAMA3 are the cause of laryngoconjunctiveus syndrome (LOCS) [MIM:245660]. LOCS is an autosomal recessive epithelial disorder confined to the Punjabi Maslin population. The condition is characterized by cutaneous erosions, nail dystrophy and exuberant vascular granulation tissue in certain epithelia, especially conjunctiva and larynx.
CC	-1 SIMILARITY: Contains 3 laminin EGF-like domains.
CC	-1 SIMILARITY: Contains 5 laminin G-like domains.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL, L34155; AAA59483.1; -.
DR	EMBL, X85107; CAAS9428.1; -.
DR	EMBL, X85108; CAAS9429.1; -.
DR	PIR, A55347; A55347.
DR	HSSP, P02468; INPE.
DR	GeneW, HGNC:6483; LAMA3.
DR	MIM, 600805; -.
DR	MIM, 226700; -.
DR	MIM, 245660; -.
DR	GO, GO:0005604; C:basement membrane, TAS.
DR	GO, GO:0008544; E:epidermal differentiation, TAS.
DR	InterPro, IPR008985; ConA_1ike_1ec_g1.
DR	InterPro, IPR006209; EGF_1ike.
DR	InterPro, IPR009030; Grow_fac_recept.
DR	InterPro, IPR002049; Laminin_EGF.
DR	InterPro, IPR001791; Laminin_G.
DR	InterPro, IPR009254; Laminin_I.
DR	InterPro, IPR010307; Laminin_II.
DR	InterPro, IPR003129; TSP_N.
DR	Pfam, PF00053; Laminin_EGF_2.
DR	Pfam, PF00054; Laminin_G_2.
DR	Pfam, PF06008; Laminin_I_1.
DR	Pfam, PF06009; Laminin_II_1.
DR	PROSITE, PS00022; EGF_1_1.
DR	PROSITE, PS01186; EGF_2_1.
DR	PROSITE, PS01248; LAMININ TYPE EGF; 2.
DR	PROSITE, PS50025; LAM_G_DOMAIN_5.
KW	Alternative splicing; Basement membrane; Cell adhesion; Coiled coil; Epidermolysis bullosa; Extracellular matrix; Glycoprotein; Laminin EGF-like domain; Repeat; Signal.
KW	Laminin EGF-like domain; Repeat; Signal.
FT	SIGNAL 1 20 Potential.
FT	CHAIN 21 1713 laminin alpha-3 chain.
FT	DOMAIN 46 201 Domain III A.
FT	DOMAIN 67 113 laminin EGF-like 1.
FT	DOMAIN 114 166 laminin EGF-like 2.
FT	DOMAIN 167 185 laminin EGF-like 3 (incomplete).
FT	DOMAIN 186 769 Domain II and I.
FT	DOMAIN 770 971 laminin G-like 1.
FT	DOMAIN 978 1140 laminin G-like 2.
FT	DOMAIN 1147 1307 laminin G-like 3.
FT	DOMAIN 1366 1530 laminin G-like 4.
FT	DOMAIN 1537 1710 laminin G-like 5.
FT	DOMAIN 231 327 Coiled coil (Potential).
FT	DOMAIN 396 548 coiled coil (Potential).
FT	DOMAIN 594 621 Coiled coil (Potential).
FT	DOMAIN 702 765 Coiled coil (Potential).
FT	DOMAIN 1686 1713 Coiled coil (Potential).
FT	DISULFID 67 76 By similarity.
FT	DISULFID 69 83 By similarity.
FT	DISULFID 86 95 By similarity.
FT	DISULFID 98 111 By similarity.

FT	DISULFID	114	126	By similarity.
FT <th>DISULFID</th> <td>116</td> <td>135</td> <td>By similarity.</td>	DISULFID	116	135	By similarity.
FT <th>DISULFID</th> <td>137</td> <td>146</td> <td>By similarity.</td>	DISULFID	137	146	By similarity.
FT <th>DISULFID</th> <td>149</td> <td>164</td> <td>By similarity.</td>	DISULFID	149	164	By similarity.
FT <th>DISULFID</th> <td>202</td> <td>202</td> <td>Interchain (Probable).</td>	DISULFID	202	202	Interchain (Probable).
FT <th>DISULFID</th> <td>205</td> <td>205</td> <td>Interchain (Probable).</td>	DISULFID	205	205	Interchain (Probable).
FT <th>SITE</th> <td>658</td> <td>660</td> <td>Cell attachment site (Potential).</td>	SITE	658	660	Cell attachment site (Potential).
FT <th>CARBOHYD</th> <td>542</td> <td>542</td> <td>N-linked (GLCNAC. . .) (Potential).</td>	CARBOHYD	542	542	N-linked (GLCNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>645</td> <td>645</td> <td>N-linked (GLCNAC. . .) (Potential).</td>	CARBOHYD	645	645	N-linked (GLCNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>745</td> <td>745</td> <td>N-linked (GLCNAC. . .) (Potential).</td>	CARBOHYD	745	745	N-linked (GLCNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>882</td> <td>882</td> <td>N-linked (GLCNAC. . .) (Potential).</td>	CARBOHYD	882	882	N-linked (GLCNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>964</td> <td>964</td> <td>N-linked (GLCNAC. . .) (Potential).</td>	CARBOHYD	964	964	N-linked (GLCNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>1108</td> <td>1108</td> <td>N-linked (GLCNAC. . .) (Potential).</td>	CARBOHYD	1108	1108	N-linked (GLCNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>1131</td> <td>1131</td> <td>N-linked (GLCNAC. . .) (Potential).</td>	CARBOHYD	1131	1131	N-linked (GLCNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>1125</td> <td>1125</td> <td>N-linked (GLCNAC. . .) (Potential).</td>	CARBOHYD	1125	1125	N-linked (GLCNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>1477</td> <td>1477</td> <td>N-linked (GLCNAC. . .) (Potential).</td>	CARBOHYD	1477	1477	N-linked (GLCNAC. . .) (Potential).
FT <th>CARBOHYD</th> <td>1667</td> <td>1667</td> <td>N-linked (GLCNAC. . .) (Potential).</td>	CARBOHYD	1667	1667	N-linked (GLCNAC. . .) (Potential).
FT <th>VARSPLIC</th> <td>1</td> <td>45</td> <td>MGWIRFGALGCGCLGVSSQQQAVPLPQPGQSQLOASLYE FRPS -> KVSVSGVLYYQAKSGFALPGDWLLEKRPDYV TCGQMSIIYEETNPAPRDRLAHGKVHYVEGNFRASSRAP SREELATVLSRLADVRIQGLYFTETRLTVLSVEVLEASDT GSGRIALVAEICACPPAPVAGDSC (in isoform B).</td>	VARSPLIC	1	45	MGWIRFGALGCGCLGVSSQQQAVPLPQPGQSQLOASLYE FRPS -> KVSVSGVLYYQAKSGFALPGDWLLEKRPDYV TCGQMSIIYEETNPAPRDRLAHGKVHYVEGNFRASSRAP SREELATVLSRLADVRIQGLYFTETRLTVLSVEVLEASDT GSGRIALVAEICACPPAPVAGDSC (in isoform B).
FT <th>CONFLICT</th> <td>5</td> <td>5</td> <td>/Frrid=VSP_003037.</td>	CONFLICT	5	5	/Frrid=VSP_003037.
FT <th>CONFLICT</th> <td>123</td> <td>125</td> <td>W -> R (in Ref. 2).</td>	CONFLICT	123	125	W -> R (in Ref. 2).
FT <th>CONFLICT</th> <td>481</td> <td>481</td> <td>ATG -> GMC (in Ref. 2).</td>	CONFLICT	481	481	ATG -> GMC (in Ref. 2).
FT <th>CONFLICT</th> <td>754</td> <td>754</td> <td>M -> K (in Ref. 2).</td>	CONFLICT	754	754	M -> K (in Ref. 2).
FT <th>CONFLICT</th> <td>969</td> <td>969</td> <td>R -> L (in Ref. 2).</td>	CONFLICT	969	969	R -> L (in Ref. 2).
FT <th>CONFLICT</th> <td>1052</td> <td>1052</td> <td>E -> Q (in Ref. 2).</td>	CONFLICT	1052	1052	E -> Q (in Ref. 2).
FT <th>CONFLICT</th> <td>1184</td> <td>1184</td> <td>D -> A (in Ref. 2).</td>	CONFLICT	1184	1184	D -> A (in Ref. 2).
FT <th>CONFLICT</th> <td>1184</td> <td>1184</td> <td>G -> A (in Ref. 2).</td>	CONFLICT	1184	1184	G -> A (in Ref. 2).
FT <th>SEQUENCE</th> <td>1713 AA;</td> <td>189304 MW;</td> <td>45EAB9B1017B60D3 CRC64;</td>	SEQUENCE	1713 AA;	189304 MW;	45EAB9B1017B60D3 CRC64;
Query Match		76.0%;	Score 850;	DB 1; Length 1713;
Best Local Similarity		76.6%;	Pred. No. 3e-64;	
Matches 167;	Conservative 16;	Mismatches 33;	Indels 0;	Gaps 0;
QY	1	MKNLKTSGVRLNDYGVYTKKCEBDMKLVRTAFSGGQMSFNNLDVPSYDRQLSFRG	60	
DB	1118	MKNLKTSGVRLNDYGVYTKKCEBDMKLVASAFSGGQLSFTDLGLPPDHLQASRFG	1177	
QY	61	QTPOSGTLNHOVRTSSLVLTLEDGHELESTRSNPIFKSPGYMDGLLHYSVISTD	120	
DB	1178	QTPOSGTLNHOVRTSSLVLTLEDGHELESTRSNPIFKSPGYMDGLLHYSVISTD	1237	
QY	121	SGILRLIDDOVLARNQRLPSEFSNAQSLRLGGHPECCISNVLYORFSQSEVLDLASKS	180	
DB	1238	SGILRLIDDOVLARNQRLPSEFSNAQSLRLGGHPECCISNVLYORFSQSEVLDLASKS	1297	
QY	181	TKKQASLGGGSLNPPFLMLFKSKRPNKGRHIFNVNOL	218	
DB	1298	LKRDVSLGGCSLNKPFLMLLKGSTRFNPKTKTFRIINOL	1335	
RESULT 7				
Q96TG0	PRELIMINARY;	PRT;	1806 AA.	
AC	Q96TG0;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Alpha 3B chain of Laminin-5 (Fragment).			
GN	Name=LAMA3;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Aberdam D., Vidal, Baudoin, Miguel, Ortime, Meneguzzi;			
RL	Submitted (FEB-1995) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; X84900; CA559325.1; -.			
DR	HSSP; P02468; INPE.			
DR	GO; GO:0005606; C:laminin-1; IEA.			

DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0005195; P:regulation of cell adhesion; IEA.
 DR GO; GO:0030334; P:regulation of cell migration; IEA.
 DR GO; GO:0045595; P:regulation of embryonic development; IEA.
 DR InterPro; IPR001844; Chaprinin_Cpn60.
 DR InterPro; IPR008985; Cona_1like_1ec_g1.
 DR InterPro; IPR006209; EGF_1like.
 DR InterPro; IPR000034; laminin_B.
 DR InterPro; IPR002049; laminin_EGF.
 DR InterPro; IPR001791; laminin_G.
 DR InterPro; IPR009254; laminin_I.
 DR InterPro; IPR010307; laminin_II.
 DR InterPro; IPR003129; TSP_N.
 DR Pfam; PF00052; laminin_B_1.
 DR Pfam; PF00053; laminin_EGF_2.
 DR Pfam; PF02210; laminin_G_2; 4.
 DR Pfam; PF06008; laminin_I_1.
 DR Pfam; PF06009; laminin_II_1.
 DR ProDom; PD003031; laminin_B; 1.
 DR SMART; SM00180; EGF_Lam; 2.
 DR SMART; SM00281; EGF_Lam; 1.
 DR SMART; SM00282; LamG; 5.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
 DR Laminin_EGF-like domain.
 FT NON TER 1
 SQ SEQUENCE 1806 AA; 199411 MW; 8F94CDE2A5A52B93 CRC64;

Query Match 76.0%; Score 850; DB 2; Length 1806;
 Best Local Similarity 76.6%; Pred. No. 3.2e-64;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKTSGVVRLNDVGVTKKCEDMKLVRTASFSRGGQMSFTNLDPSTDRFQLSFGF 60
 DB 1211 MKNLKTSGVVRLNDVGVTKKCEDMKLVRSASFSGQUSFTDLGLPTDHLQASFGF 1270
 QY 61 QTFQPSGTLINHOQTRTSLVLTLEDGHIELSTRDSNIPFKSPGTMDGLLHVSVISDT 120
 DB 1271 QTFQPSGTLINHOQTRTSLVLTLEDGHIELSTRDSNIPFKSPGTMDGLLHVSVISDN 1330
 QY 121 SGRLLIDQVLRNRQRLRPFSSNAQSLRLGGHFGECISNVLVQRFSSPEVLDLASKS 180
 DB 1331 SGRLLIDQVLRNRQRLRPFSSNAQSLRLGGHFGECISNVLVQRFSSPEVLDLASKS 1390
 QY 181 TKKDAISGGCSLNKPPFLMFKSPKRFNKGRIPNVNQL 218
 DB 1391 LKRDVSLGGCSLNKPPFLMFKSPKRFNKGRIPNVNQL 1428

RESULT 8

ID Q76E14 PRELIMINARY; PRT; 3333 AA.
 AC Q76E14;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Laminin alpha 3b chain.
 GN Name=LAMA3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kariya Y., Yasuda C., Nakashima Y., Ishida K., Tsubota Y.,
 RA Miyazaki K.,
 RT "Characterization of laminin 5B and NH2-terminal proteolytic fragment
 of its alpha3b chain: promotion of cellular adhesion, migration, and
 proliferation.";

RL J. Biol. Chem. 279:24774-24784(2004).
 DR EMBL; AB107369; BAD13428.1; -
 DR GO; GO:0005578; Extracellular matrix (sensu Metazoa); IEA.
 DR GO; GO:0005606; C1laminin-1; IEA.
 DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0030334; P:regulation of cell adhesion; IEA.
 DR GO; GO:0030334; P:regulation of cell migration; IEA.
 DR GO; GO:0045595; P:regulation of embryonic development; IEA.
 DR InterPro; IPR001844; Chaprinin_Cpn60.
 DR InterPro; IPR008985; Cona_1like_1ec_g1.
 DR InterPro; IPR006209; EGF_1like.
 DR InterPro; IPR008979; Gal_bind_1like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000034; laminin_B.
 DR InterPro; IPR002049; laminin_EGF.
 DR InterPro; IPR001791; laminin_G.
 DR InterPro; IPR009254; laminin_I.
 DR InterPro; IPR010307; laminin_II.
 DR InterPro; IPR008211; laminin_N.
 DR InterPro; IPR003129; TSP_N.
 DR Pfam; PF00052; laminin_B_1.
 DR Pfam; PF00053; laminin_EGF_8.
 DR Pfam; PF02210; laminin_G_2; 4.
 DR Pfam; PF06008; laminin_I_1.
 DR Pfam; PF06009; laminin_II_1.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR ProDom; PD003031; laminin_B; 1.
 DR SMART; SM00181; EGF; 8.
 DR SMART; SM00180; EGF_Lam; 14.
 DR SMART; SM00281; LamE; 1.
 DR SMART; SM00282; LamG; 5.
 DR SMART; SM00136; LamNT; 1.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 13.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
 DR Laminin_EGF-like domain.
 SQ SEQUENCE 3333 AA; 366616 MW; 6F99A4D4B99FCB0 CRC64;

Query Match 76.0%; Score 850; DB 2; Length 3333;
 Best Local Similarity 76.6%; Pred. No. 6.9e-64;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKTSGVVRLNDVGVTKKCEDMKLVRTASFSRGGQMSFTNLDPSTDRFQLSFGF 60
 DB 2738 MKNLKTSGVVRLNDVGVTKKCEDMKLVRSASFSGQUSFTDLGLPTDHLQASFGF 2797
 QY 61 QTFQPSGTLINHOQTRTSLVLTLEDGHIELSTRDSNIPFKSPGTMDGLLHVSVISDT 120
 DB 2798 QTFQPSGTLINHOQTRTSLVLTLEDGHIELSTRDSNIPFKSPGTMDGLLHVSVISDN 2857
 QY 121 SGRLLIDQVLRNRQRLRPFSSNAQSLRLGGHFGECISNVLVQRFSSPEVLDLASKS 180
 DB 2858 SGRLLIDQVLRNRQRLRPFSSNAQSLRLGGHFGECISNVLVQRFSSPEVLDLASKS 2917
 QY 181 TKKDAISGGCSLNKPPFLMFKSPKRFNKGRIPNVNQL 218
 DB 2918 LKRDVSLGGCSLNKPPFLMFKSPKRFNKGRIPNVNQL 2955

RESULT 9

ID Q867A1 PRELIMINARY; PRT; 1725 AA.
 AC Q867A1;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Laminin alpha 3 (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Spizito F., Capt A., Guagnere F., Ortonne J.-P., Meneguzzi G.;
 RL Submitted (FEF-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF236865; AAL54876.1; -.
 DR HSSP; P11209; IG2C.
 DR GO; GO:0005606; C:lamnin-1; IEA.
 DR GO; GO:0005102; P:receptor binding; IEA.
 DR GO; GO:0005198; P:structural molecule activity; IEA.
 DR GO; GO:0030155; P:regulation of cell adhesion; IEA.
 DR GO; GO:0030334; P:regulation of cell migration; IEA.
 DR GO; GO:0045395; P:regulation of embryonic development; IEA.
 DR InterPro; IPR008985; Cons like _lec_g1.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR009254; Laminin_I.
 DR InterPro; IPR010307; Laminin_II.
 DR InterPro; IPR003129; TSP N.
 DR Pfam; PF00053; Laminin_EGF; 2.
 DR Pfam; PF02210; Laminin_G_2; 4.
 DR Pfam; PF06008; Laminin_I; 1.
 DR Pfam; PF06009; Laminin_II; 1.
 DR SMART; SM00282; LamG; 2.
 DR SMART; SM00180; EGF Lam; 5.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
 KW Laminin EGF-like domain.
 FT NON_TER 1725 1725
 SQ SEQUENCE 1725 AA; 191053 MW; DF71BE0E1FB5134C CRC64;

Query Match 68.0%; Score 760.5; DB 2; Length 1725;
 Best Local Similarity 69.1%; Pred. No. 1,6e-56;
 Matches 150; Conservative 20; Mismatches 46; Indels 1; Gaps 1;

QY 1 MKNLKTTSGVRLNDVGVYTKKCEBWKLVRTASFSRGQMSFTNLDVSTDRFQSLSPFG 60
 DB 1129 MKNLKTTGVRLNDVGVYTKKCEBWKLVRSASFSRDGLRTGLDPLPSEFQSLSPFG 1188
 QY 61 QTFQPSGTLNMQRTSSLVLTLEDGHELESTRDSNPIFKSPGTYMDGLLHHVSYISPT 120
 DB 1189 QTFQPSGTLNMQRTSSLVLTLEDGHELESTRDSNPIFKSPGTYMDGLLHHVSYISPT 1247
 QY 121 SGRLIIDQVLRNQLPSFSNAQOSLRIGGHPGECISNVLVQRFPSQPEVLDLASKS 180
 DB 1248 SGRLIIDQVLRNQLPSFSNAQOSLRIGGHPGECISNVLVQRFPSQPEVLDLASKS 1307
 QY 181 TKKDAISGGCSLNKPPLMFKSPKPKNGKIRFNVNO 217
 DB 1308 FKRDVSLGGCSLNKPPLMFKSPKPKNGKIRFNVNO 1344

RESULT 10
 Q91VVO PRELIMINARY; PRT; 1254 AA.

AC Q91VVO 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DB Lama4 protein (Fragment).
 GN Name=Lama4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Useth T.B., Toshiyuki S., Carrinck P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Raithe J., Helton B., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilmour J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzyminski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC008533; AA08533.1; -.
 DR HSSP; O60675; IQUO.
 DR MGI; MGI:109321; Lama4.
 DR GO; GO:0005605; C:basal lamina; IDA.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0001568; P:blood vessel development; IMP.
 DR Pfam; PF02210; Laminin_G_2; 5.
 DR Pfam; PF06009; Laminin_I; 1.
 DR SMART; SM00282; LamG; 5.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
 FT NON_TER 1 1
 SQ SEQUENCE 1254 AA; 139723 MW; 54D49EF76D37CD9 CRC64;

Query Match 18.2%; Score 204; DB 2; Length 1254;
 Best Local Similarity 29.1%; Pred. No. 1.3e-08;
 Matches 64; Conservative 35; Mismatches 99; Indels 22; Gaps 8;

QY 5 KXTSGVRLNDVGVYTKKCEBWKLVRTASFSRGQMSFTNLDVSTDRFQSLSPFG 63
 DB 642 KDFNLLEQTERLGVYGGCPEDSLISRAVFN--GQSFASIQKISFDFGFGGNNFRL 699
 QY 64 QPSGTLNMQRTSSLVLTLEDGHELESTRDSNPIFKSPGTYMDGLLHHVSYISPT 122
 DB 700 QPSGTLNMQRTSSLVLTLEDGHELESTRDSNPIFKSPGTYMDGLLHHVSYISPT 756
 QY 122 LRLIIDQVLRNQLPSFSNAQOS-----LRLG-----GHPGECISNVLVQRFPSQ 169
 DB 757 YELVVDKSRIRKGN--PTKGRABQOTTEKKEFYFGSPISPOYANFTGCISNAYFTRLD 814
 QY 170 SPEVLDLASKSTKKDASISGGCSLNKPPLMFKSPKPKNGKIRFNVNO 209
 DB 815 DVEVEDPQREYSEKVTSTLYECPTESSPLFLHKKGKNSK 854

RESULT 11
 LMA4 MOUSE STANDARD; PRT; 1816 AA.

AC P97927; O88785; P70409;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DB Laminin alpha-4 chain precursor.
 GN Name=Lama4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]


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FT CARBOHYD 1283 1283 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1361 1361 N-linked (GlcNAc...) (Potential).
FT CONFLICT 8 8 C->S (in Ref. 2).
FT CONFLICT 18 18 C->Y (in Ref. 2).
FT CONFLICT 248 248 C->R (in Ref. 3).
FT CONFLICT 297 297 G->A (in Ref. 3).
FT CONFLICT 431 431 THR->HIS (in Ref. 2).
FT CONFLICT 679 679 S->C (in Ref. 3).
FT CONFLICT 703 703 D->G (in Ref. 2).
FT CONFLICT 706 706 N->H (in Ref. 2).
FT CONFLICT 728 728 K->R (in Ref. 2).
FT CONFLICT 730 730 F->I (in Ref. 2).
FT CONFLICT 779 779 R->G (in Ref. 1; AA sequence).
FT CONFLICT 810 810 R->S (in Ref. 3).
FT CONFLICT 865 865 AEP->QT (in Ref. 2).
FT CONFLICT 936 936 K->E (in Ref. 3).
FT CONFLICT 970 970 L->V (in Ref. 3).
FT CONFLICT 1132 1132 H->R (in Ref. 3).
FT CONFLICT 1200 1200 F->I (in Ref. 2).
FT CONFLICT 1382 1382 D->A (in Ref. 2).
FT CONFLICT 1413 1414 NS->EF (in Ref. 1).
FT CONFLICT 1489 1489 A->S (in Ref. 2).
SO SEQUENCE 1816 AA; 201818 MM; B49C45F3A45999D8 CXC64;

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Query Match 18.2%; Score 204; DB 1; Length 1816;
Best Local Similarity 29.1%; Pred. No. 2e-08;
Matches 64; Conservative 35; Mismatches 99; Indels 22; Gaps 8;

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QY 5 KKTSGVRLNDYGVYKKGSEDKLVRTASFSRGCGMSFVND-VSTDRFQLSPFGQFP 63
DB 1204 KQDFNLBQTEVGVYGCEDLSIRAYFN--GQSFLASIQKISFFGEGGFNFRYL 1261
QY 64 QPSGTLNQTSTSLVLTEDGHIELSTSDSNIPFKSPGTMDGLHH-VSVIDSTSG 122
DB 1262 QPWGLLFYTTSGSDVSIENCTVMDYK--GIKMSSTDQVHDGLPHVVTISIDTR- 1318
QY 123 LRLIIDQVLRNRNRLPSFNSAQS-----LRLGG-----GHREGCISNVLVGRFSQ 169
DB 1319 YELVVDKSLRGKRN--PTKGAKEQOTTEKKFYFGSPISPYQVNFPGCISNAYFTRLDR 1376
QY 170 SPFVLDLASKSTYKDKASLGCCSLNKPPLMLPKSPKRFK 209
DB 1377 DVEVEDPQRYSEKVTSLYCEPLSSPLFLHKKGNSSK 1416

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RESULT 12

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ID LMA4_HUMAN STANDARD; PRT; 1816 AA.
AC Q16363; Q14735; Q15335; Q9UB18; Q9JUN9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Laminin alpha-4 chain precursor.
GN Name=LAMA4;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal Lung;
RX MEDLINE=95300971; PubMed=7781776; DOI=10.1016/0014-5793(95)00462-1;
RA Iivanainen A., Sainio K., Sariola H., Tryggvason K.;
RT "Primary structure and expression of a novel human laminin alpha 4
RT chain."
RL FEBS Lett. 365:183-188(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=97454279; PubMed=9310354;
RA Richards A.J., Lucarini C., Pope F.M.;
RT "The structural organisation of LAMA4, the gene encoding laminin
RT alpha4."

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RL Eur. J. Biochem. 248:15-23(1997).
RN [3]
RP SEQUENCE OF 236-1816 FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95048381; PubMed=7959779;
RA Richards A.J., Al-Inara L., Carter N.P., Lloyd J.C., Leversha M.A.,
RA Pope F.M.;
RT "Localization of the gene (LAMA4) to chromosome 6q21 and isolation of
RT a partial cDNA encoding a variant laminin A chain."
RL Genomics 22:237-239(1994).
RN [4]
RP SEQUENCE OF 66-1816 FROM N.A.
RL Tubbey B.;
CC Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
CC -! FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -! SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end.
CC -! SUBCELLULAR LOCATION: Extracellular; found in the basement
CC membranes (major component).
CC -! TISSUE SPECIFICITY: In adult, strong expression in heart, lung,
CC ovary small and large intestines, placenta, liver; weak or no
CC expression in skeletal muscle, kidney, pancreas, testis, prostate,
CC brain. High expression in fetal lung and kidney. Expression in
CC fetal and newborn tissues is observed in certain mesenchymal cells
CC in tissues such as smooth muscle and dermis.
CC -! DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -! DOMAIN: Domain G is globular.
CC -! SIMILARITY: Contains 4 laminin EGF-like domains.
CC -! SIMILARITY: Contains 5 laminin G-like domains.
CC -! CAUTION: Gene LAMA4 was formerly called LAMA3.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@ib-sib.ch).
CC
DR EMBL, S78569; AAB34635.1; -.
DR EMBL, X91171; CAA62596.1; -.
DR EMBL, Y14240; CAA74636.1; -.
DR EMBL, X76939; CAA54258.1; -.
DR EMBL, Z99289; -; NOT_ANNOTATED_CDS.
DR PIR, S68960; S68960.
DR HSPF, F02468; INPB.
DR Genew, HGNC:6484; LAMA4.
DR MIM, 600133; -.
DR GO, GO:0005605; C:basal lamina; TAS.
DR GO, GO:0005201; F:extracellular matrix structural constituent; TAS.
DR InterPro, IPR008985; CoLA-like_1ec_g1.
DR InterPro, IPR006209; EGF-like.
DR InterPro, IPR002049; Laminin_EGF.
DR InterPro, IPR001791; Laminin_G.
DR InterPro, IPR009254; Laminin_I.
DR InterPro, IPR010307; Laminin_II.
DR InterPro, IPR003129; TSP_N.
DR Pfam, PF00053; Laminin_EGF; 3.
DR Pfam, PF00054; Laminin_G; 3.
DR Pfam, PF06008; Laminin_I; 1.
DR Pfam, PF06009; Laminin_II; 1.
DR PROSITE, PS00022; EGF_1; UNKNOWN 1.
DR PROSITE, PS50025; LAM_G_DOMAIN; 5.
DR PROSITE, PS01248; LAMININ_TYRP_EGF; 3.
DR Basemem membrane; Cell adhesion; Coiled coil; Extracellular matrix;
KW Glycoprotein; Laminin EGF-like domain; Repeat; Signal.

```


FT SIGNAL 1 24 Potential.

FT CHAIN 25 1816 laminin alpha-4 chain.

FT DOMAIN 82 131 laminin EGF-like 1.

FT DOMAIN 132 186 laminin EGF-like 2.

FT DOMAIN 187 240 laminin EGF-like 3.

FT DOMAIN 241 255 laminin EGF-like 4 (incomplete).

FT DOMAIN 256 825 laminin II and I.

FT DOMAIN 826 1028 laminin G-like 1.

FT DOMAIN 1040 1220 laminin G-like 2.

FT DOMAIN 1227 1395 laminin G-like 3.

FT DOMAIN 1462 1633 laminin G-like 4.

FT DOMAIN 1640 1813 laminin G-like 5.

FT DOMAIN 313 396 Coiled coil (Potential).

FT DOMAIN 466 521 Coiled coil (Potential).

FT DOMAIN 574 607 Coiled coil (Potential).

FT DOMAIN 655 717 Coiled coil (Potential).

FT DOMAIN 770 799 Coiled coil (Potential).

FT SITE 717 719 Cell attachment site (Potential).

FT DISULFID 82 98 By similarity.

FT DISULFID 84 98 By similarity.

FT DISULFID 101 110 By similarity.

FT DISULFID 113 129 By similarity.

FT DISULFID 132 146 By similarity.

FT DISULFID 134 155 By similarity.

FT DISULFID 157 166 By similarity.

FT DISULFID 169 184 By similarity.

FT DISULFID 187 202 By similarity.

FT DISULFID 189 209 By similarity.

FT DISULFID 212 221 By similarity.

FT DISULFID 224 238 By similarity.

FT DISULFID 266 266 Interchain (Probable).

FT DISULFID 269 269 Interchain (Probable).

FT CARBOHYD 104 104 N-linked (GlcNAc).

FT CARBOHYD 215 215 N-linked (GlcNAc).

FT CARBOHYD 308 308 N-linked (GlcNAc).

FT CARBOHYD 458 458 N-linked (GlcNAc).

FT CARBOHYD 524 524 N-linked (GlcNAc).

FT CARBOHYD 550 550 N-linked (GlcNAc).

FT CARBOHYD 571 571 N-linked (GlcNAc).

FT CARBOHYD 574 574 N-linked (GlcNAc).

FT CARBOHYD 631 631 N-linked (GlcNAc).

FT CARBOHYD 639 639 N-linked (GlcNAc).

FT CARBOHYD 735 735 N-linked (GlcNAc).

FT CARBOHYD 751 751 N-linked (GlcNAc).

FT CARBOHYD 754 754 N-linked (GlcNAc).

FT CARBOHYD 780 780 N-linked (GlcNAc).

FT CARBOHYD 803 803 N-linked (GlcNAc).

FT CARBOHYD 1086 1086 N-linked (GlcNAc).

FT CARBOHYD 1281 1281 N-linked (GlcNAc).

FT CARBOHYD 1359 1359 N-linked (GlcNAc).

FT CARBOHYD 1411 1411 N-linked (GlcNAc).

FT CARBOHYD 143 143 A -> P (in Ref. 1).

FT CONFLICT 178 178 L -> G (in Ref. 1).

FT CONFLICT 265 265 G -> C (in Ref. 4).

FT CONFLICT 276 276 D -> A (in Ref. 4).

FT CONFLICT 491 491 Y -> H (in Ref. 2 and 3).

FT CONFLICT 1057 1057 T -> P (in Ref. 1).

FT CONFLICT 1110 1112 SGR -> GGP (in Ref. 4).

SO SEQUENCE 1816 AA; 201908 MW; 0489AF379A0FAAD CRC64;

Query Match 16.7%; Score 187; DB 1; Length 1816;

Best Local Similarity 28.3%; Pred. No. 6e-07;

Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDYGVTKKSGEDWLVTAFAFRGGGFTNLD-VPTDRFQSLFQFQTF 63

DB 1202 KQPNLLQETETLGVGCGCEDSLISRATFN--GQFASISQIKLSFDFEGGFNRTL 1259

QY 64 QPSGTLNQTSTSLVLTLEDGHILSTRDSNIPFKSPGTWMDGLHHVSVISDTSG 123

DB 1260 QPGLLFFYASGSDVFSISLDNGTVIMDK--GIKVSVDKQYVDGLSHF--VYSSVSPT 1315

QY 124 R--LLID-DGYLRNQLLPFSNAQSLR---LGG-----GHFECINVLVQRSSQ 170

DB 1316 RYELIYDKSVKSNFTKGIETQASSEKFFYGGSPISAGVANFTGCSISNAFTYDRD 1375

QY 171 PEVLDAKSTKQASLGCGSLNKPPLMLFKSPKPKFNK 209

DB 1376 VEVEDFORYTEKVTSLYECPRISSPLFLHKKGNLSK 1414

RESULT 13

Q8R3Y7 ID Q8R3Y7 PRELIMINARY; PRT; 794 AA.

AC Q8R3Y7; 01-JUN-2002 (T-EMBLrel. 21, Created)

DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Lama5 protein (Fragment).

GN Name=Lama5;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CZECH II; TISSUE=Mammary tumor;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L., Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Ueda T.B., Tomihata S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J., Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Ray J., Helton E., Kettman M., Madan A., Rodriguez R., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalek U., Smaluk D.E., Scherch A., Schein J.E., Jones S.J., Matra M.A.;

RT "generation and initial analysis of more than 15,000 full-length human

RL and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CZECH II; TISSUE=Mammary tumor;

RA Strausberg R.,

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC020313; AAH20313.1; -.

DR HSSP; Q14393; IH30.

DR MGD; MGI:105382; Lama5.

DR GO; GO:0005604; C:basement membrane; IDA.

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0005178; F:protein binding; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0001763; P:branching morphogenesis; IDA.

DR GO; GO:0030324; P:lung development; IMP.

DR GO; GO:0007517; P:muscle development; IMP.

DR InterPro; IPR008985; Cona_like_rec_91.

DR InterPro; IPR001791; Laminin_G.

DR InterPro; IPR003129; TSP_N.

DR Pfam; PF02210; Laminin_G_2; 4.

DR SMART; SM00282; Lamg; 4.

DR PROSITE; PSS0025; LAM_G_DOMAIN; 4.

FT NON_TER 1

SO SEQUENCE 794 AA; 86936 MW; 5316391F38E5662C CRC64;

Query Match 16.6%; Score 186; DB 2; Length 794;

Best Local Similarity 29.2%; Pred. No. 2.6e-07;

Matches 59; Conservative 34; Mismatches 91; Indels 18; Gaps 6;


```

CC -1- DOMAIN: Domains VI, IV and G are globular.
CC -1- SIMILARITY: Contains 22 laminin EGF-like domains.
CC -1- SIMILARITY: Contains 5 laminin G-like domains.
CC -1- SIMILARITY: Contains 2 laminin IV domains.
CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.1sb-sib.ch/announce/
CC or send an email to license@1sb-sib.ch).
CC -----
DR EMBL: A193593; CAB9255.1; -.
DR EMBL: U37501; AAC53430.1; -.
DR PIR: T10053; T10053.
DR HSSP: P02468; 1NPE.
DR MGD: MGI:105382; Lama5.
DR GO: GO:0005604; C:basement membrane; IDA.
DR GO: GO:0005178; F:integrin binding; IDA.
DR GO: GO:0005151; F:protein binding; IPT.
DR GO: GO:0001763; P:branching morphogenesis; IDA.
DR GO: GO:0030324; P:lung development; IMP.
DR GO: GO:0007517; P:muscle development; IMP.
DR InterPro: IPR008985; Cona_like_1ec_g1.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR008979; Gal_bind_like.
DR InterPro: IPR009030; Grow_fac_recept.
DR InterPro: IPR000034; Laminin_B.
DR InterPro: IPR002049; Laminin_G.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR009254; Laminin_I.
DR InterPro: IPR010307; Laminin_II.
DR InterPro: IPR008211; Laminin_N.
DR InterPro: IPR008212; Lam_N2.
DR InterPro: IPR003129; TSP_N.
DR Pfam: PF00052; Laminin_B_1.
DR Pfam: PF00053; Laminin_EGF_17.
DR Pfam: PF00054; Laminin_G_2.
DR Pfam: PF06008; Laminin_I_1.
DR Pfam: PF06009; Laminin_II_1.
DR Pfam: PF00055; Laminin_N_1.
DR PRINTS: PR00011; EGF_LAMININ.
DR ProDom: PD003031; Laminin_B_1.
DR PROSITE: PS00022; EGF_1; 19.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01248; LAMININ_TYPE_EGF_19.
DR PROSITE: PS50025; LAM_G_DOMAIN_5.
KW Basement membrane; Cell adhesion; Coiled coil;
KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
KW Laminin EGF-like domain; Repeat; Signal.
FT CHAIN 1 40 Laminin alpha-5 chain.
FT SIGNAL 1 40 Laminin N-terminal (domain VI).
FT DOMAIN 305 363 Laminin EGF-like 1.
FT DOMAIN 364 433 Laminin EGF-like 2.
FT DOMAIN 434 479 Laminin EGF-like 3.
FT DOMAIN 500 546 Laminin EGF-like 4.
FT DOMAIN 547 592 Laminin EGF-like 5.
FT DOMAIN 593 637 Laminin EGF-like 6.
FT DOMAIN 638 682 Laminin EGF-like 7.
FT DOMAIN 683 728 Laminin EGF-like 8.
FT DOMAIN 729 781 Laminin EGF-like 9.
FT DOMAIN 782 833 Laminin EGF-like 10.
FT DOMAIN 834 855 Laminin EGF-like 11.
FT DOMAIN 856 1442 Laminin EGF-like 12. (incomplete).
FT DOMAIN 1443 1488 Laminin EGF-like 13.
FT DOMAIN 1489 1532 Laminin EGF-like 14.
FT DOMAIN 1533 1581 Laminin EGF-like 15.
FT DOMAIN 1582 1632 Laminin EGF-like 16.
FT DOMAIN 1633 1642 Laminin EGF-like 16 (N-terminal).
FT DOMAIN 1643 1831 Laminin domain IV 2 (domain IV A).
FT DOMAIN 1832 1864 Laminin EGF-like 16 (C-terminal).
FT DOMAIN 1865 1914 Laminin EGF-like 17.
FT DOMAIN 1915 1970 Laminin EGF-like 18.
FT DOMAIN 1971 2024 Laminin EGF-like 19.
FT DOMAIN 2025 2072 Laminin EGF-like 20.
FT DOMAIN 2072 2118 Laminin EGF-like 21.
FT DOMAIN 2119 2168 Laminin EGF-like 22.
FT DOMAIN 2169 2735 Domain II and I.
FT DOMAIN 2736 2933 Laminin G-like 1.
FT DOMAIN 2947 3119 Laminin G-like 2.
FT DOMAIN 3128 3296 Laminin G-like 3.
FT DOMAIN 3337 3511 Laminin G-like 4.
FT DOMAIN 3518 3689 Laminin G-like 5.
FT DOMAIN 2205 2257 Coiled coil (Potential).
FT DOMAIN 2330 2464 Coiled coil (Potential).
FT DOMAIN 2604 2621 Coiled coil (Potential).
FT DOMAIN 2639 2705 Coiled coil (Potential).
FT DOMAIN 1723 1725 Cell attachment site (Potential).
FT SITE 1839 1841 Cell attachment site (Potential).
FT DISULFID 305 314 By similarity.
FT DISULFID 307 327 By similarity.
FT DISULFID 329 338 By similarity.
FT DISULFID 341 361 By similarity.
FT DISULFID 364 373 By similarity.
FT DISULFID 366 398 By similarity.
FT DISULFID 401 410 By similarity.
FT DISULFID 413 431 By similarity.
FT DISULFID 434 445 By similarity.
FT DISULFID 436 452 By similarity.
FT DISULFID 454 463 By similarity.
FT DISULFID 466 475 By similarity.
FT DISULFID 500 512 By similarity.
FT DISULFID 502 521 By similarity.
FT DISULFID 523 532 By similarity.
FT DISULFID 535 544 By similarity.
FT DISULFID 547 559 By similarity.
FT DISULFID 549 566 By similarity.
FT DISULFID 568 577 By similarity.
FT DISULFID 580 590 By similarity.
FT DISULFID 593 605 By similarity.
FT DISULFID 595 611 By similarity.
FT DISULFID 613 622 By similarity.
FT DISULFID 625 635 By similarity.
FT DISULFID 638 650 By similarity.
FT DISULFID 640 656 By similarity.
FT DISULFID 658 667 By similarity.
FT DISULFID 670 680 By similarity.
FT DISULFID 683 695 By similarity.
FT DISULFID 685 702 By similarity.
FT DISULFID 704 713 By similarity.
FT DISULFID 716 726 By similarity.
FT DISULFID 1443 1455 By similarity.
FT DISULFID 1445 1462 By similarity.
FT DISULFID 1464 1473 By similarity.
FT DISULFID 1476 1486 By similarity.
FT DISULFID 1533 1548 By similarity.
FT DISULFID 1535 1555 By similarity.
FT DISULFID 1557 1566 By similarity.
FT DISULFID 1569 1579 By similarity.
FT DISULFID 1582 1594 By similarity.
FT DISULFID 1584 1601 By similarity.
FT DISULFID 1603 1612 By similarity.
FT DISULFID 1615 1630 By similarity.
FT DISULFID 1865 1874 By similarity.
FT DISULFID 1867 1881 By similarity.
FT DISULFID 1884 1893 By similarity.
FT DISULFID 1896 1912 By similarity.
FT DISULFID 1915 1930 By similarity.
FT DISULFID 1917 1939 By similarity.
FT DISULFID 1941 1950 By similarity.
FT DISULFID 1953 1968 By similarity.
FT DISULFID 1971 1986 By similarity.
FT DISULFID 1973 1993 By similarity.

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FT	DISULFID	1996	2005	By similarity.
FT	DISULFID	2008	2022	By similarity.
FT	DISULFID	2072	2083	By similarity.
FT	DISULFID	2074	2090	By similarity.
FT	DISULFID	2092	2101	By similarity.

Query Match 16.6%; Score 186; DB 1; Length 3718;
Best Local Similarity 29.2%; Pred. No. 1.8e-06;
Matches 59; Conservative 34; Mismatches 91; Indels 18; Gaps 6;

Qy	1	MKNLKKTSGVRLNDVGVTKKCEMDKLVRTASFSRGGMFTNLDV--PSTDRFQLSPG	59
Db	3098	IKALGKYVDLKRIN--TTGISFGCTADLVGRITFHGHGFLPALPDVAPITEVVTSGPG	3156
Qy	60	PQTFQPSGTLNHNQRTSSILVTLBDGHIELSTRDSNIPIFKSPGTMDGLHHVSVISD	119
Db	3157	FRGTQNNLLYRTSPDPYQVSLRSGHTLRFMNQE---ETQRYFADGAPHYVAFYEN	3213
Qy	120	TSGRLRLID--QVLRNRQRLPSFSNAQ---OSLRIG-----GHFEGCISNVLVOR	166
Db	3214	VTGVMLYVDOLQVLVKSHERITPMLQLQEBEPSRLILGGLPVSGTFHNFSGCISNVFOR	3273
Qy	167	FSQSPFVLPLASKSTKQASIG	188
Db	3274	LRGPQRFVPLRHQMGSVNVSVG	3295

Search completed: February 22, 2005, 08:24:24
Job time : 37.8842 secs

CC prior art cell lines have been created that produce but do not secrete
CC only one or two chain laminins
XX
SQ Sequence 1694 AA;

Query Match 100.0%; Score 1118; DB 3; Length 1694;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRLKKTSGVRLNDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVPSIDRFQLSGF 60
DB 1098 MNRLKKTSGVRLNDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVPSIDRFQLSGF 1157
QY 61 QTFQPSGTLNMQRTSSILVTLBEGHIELSTRDSNIPFSPGTYMDGLHHSVISDT 120
DB 1158 QTFQPSGTLNMQRTSSILVTLBEGHIELSTRDSNIPFSPGTYMDGLHHSVISDT 1217
QY 121 SGLRLIIDQVLRNRQLPFSFNAQOSLRIGGHEGCGISNVLVQRFQSPPEVLDAKS 180
DB 1218 SGLRLIIDQVLRNRQLPFSFNAQOSLRIGGHEGCGISNVLVQRFQSPPEVLDAKS 1277
QY 181 TKKDAISLGCGSLNKPPFLMLFKSPKRFNKGRIFFNNQL 218
DB 1278 TKKDAISLGCGSLNKPPFLMLFKSPKRFNKGRIFFNNQL 1315

RESULT 2

AAB48460
ID AAB48460 standard; protein; 1725 AA.

AC AAB48460;

DT 02-MAR-2001 (first entry)

DE Rat laminin 5 polypeptide, SEQ ID NO: 10.

XX Rat; laminin 5; vulnery; antilucer; antinflammatory; antidiabetic;
XX cell adhesion promoter; wound healing; ulcers; burn; skin graft;
XX periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
OS Rattus norvegicus.

XX WO200066731-A2.

XX 09-NOV-2000.

PF 28-APR-2000; 2000MO-US011459.

PR 30-APR-1999; 99US-0131720P.

PR 21-AUG-1999; 99US-0149738P.

PR 24-SEP-1999; 99US-0155945P.

XX (BIOS-) BIOSTATUM INC.

XX Boutaud A;

PI MPI; 2000-687538/67.

DR N-PSDB; AAC83721.

PT Laminin 5-expressing cells, used to accelerate wound healing associated
with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
burns, acute wounds and skin grafts.

XX Claim 3; Page 104-109; 232pp; English.

XX The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type
CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell

CC line produces and secretes recombinant heterotrimeric laminin, whereas
CC prior art cell lines have been created that produce but do not secrete
CC only one or two chain laminins
XX

SQ Sequence 1725 AA;

Query Match 100.0%; Score 1118; DB 3; Length 1725;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRLKKTSGVRLNDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVPSIDRFQLSGF 60
DB 1129 MNRLKKTSGVRLNDTVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVPSIDRFQLSGF 1188
QY 61 QTFQPSGTLNMQRTSSILVTLBEGHIELSTRDSNIPFSPGTYMDGLHHSVISDT 120
DB 1189 QTFQPSGTLNMQRTSSILVTLBEGHIELSTRDSNIPFSPGTYMDGLHHSVISDT 1248
QY 121 SGLRLIIDQVLRNRQLPFSFNAQOSLRIGGHEGCGISNVLVQRFQSPPEVLDAKS 180
DB 1249 SGLRLIIDQVLRNRQLPFSFNAQOSLRIGGHEGCGISNVLVQRFQSPPEVLDAKS 1308
QY 181 TKKDAISLGCGSLNKPPFLMLFKSPKRFNKGRIFFNNQL 218
DB 1309 TKKDAISLGCGSLNKPPFLMLFKSPKRFNKGRIFFNNQL 1346

RESULT 3

AAB48459
ID AAB48459 standard; protein; 1693 AA.

AC AAB48459;

DT 02-MAR-2001 (first entry)

DE Human laminin 5 polypeptide, SEQ ID NO: 8.

XX Human; laminin 5; vulnery; antilucer; antinflammatory; antidiabetic;
XX cell adhesion promoter; wound healing; ulcers; burn; skin graft;
XX periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX Homo sapiens.

XX WO200066731-A2.

XX 09-NOV-2000.

PF 28-APR-2000; 2000MO-US011459.

PR 30-APR-1999; 99US-0131720P.

PR 21-AUG-1999; 99US-0149738P.

PR 24-SEP-1999; 99US-0155945P.

XX (BIOS-) BIOSTATUM INC.

XX Boutaud A;

PI MPI; 2000-687538/67.

DR N-PSDB; AAC83720.

PT Laminin 5-expressing cells, used to accelerate wound healing associated
with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
burns, acute wounds and skin grafts.

XX Claim 3; Page 91-97; 232pp; English.

XX The present sequence is a laminin 5 chain polypeptide. Recombinant
CC laminin 5-expressing cells are used to accelerate wound healing,
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
intestinal ulcers, periodontitis, and gingivitis. They are also used to
CC improve the biocompatibility of medical devices, and to promote cell
CC adhesion to a surface. They can be used for the ex vivo treatment of Type

CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
 CC line produces and secretes recombinant heterotrimeric laminin, whereas
 CC prior art cell lines have been created that produce but do not secrete
 CC only one or two chain laminins
 XX
 SQ Sequence 1693 AA;

Query Match 76.0%; Score 850; DB 3; Length 1693;
 Best Local Similarity 76.6%; Pred. No. 2.6e-91;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKTSGVRLNDIVGVTKKCEDEMKLVRTASFSFGQMSFTNLDVSTDFQSLSGF 60
 DB 1098 MKNLKTSGVRLNDIVGVTKKCEDEMKLVRSASFSFGQSLSTFDGLPPTDHLQASFG 1157
 QY 61 QTFQPSGTLNHQRTSSLVLTLEDGHIELSTDSNIPFKSPGTMDGLHHVSVISDT 120
 DB 1158 QTFQPSGTLNHQRTSSLVLTLEDGHIELSTDSGPIFKSPGTMDGLHHVSVISDN 1217
 QY 121 SGRLIIDQVLRNRQLPFSNAQSLRIGGHEFCISNVLYORFSQSPVLDLASKS 180
 DB 1218 SGRLIIDQVLRNRQLPFSNAQSLRIGGHEFCISNVLYORFSQSPVLDLASKS 1277
 QY 181 TKKDAISLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
 DB 1278 LKRDVSLGGCSLNKPPFLMLKSTRPNKTKTRINQL 1315

RESULT 4

AAB48457 standard; protein; 1693 AA.

AAAB48457;

02-MAR-2001 (first entry)

Human laminin 5 polypeptide, SEQ ID NO: 4.

Human; laminin 5; vulneryary; antiulcer; antiinflammatory; antidiabetic;

cell adhesion promoter; wound healing; ulcers; burn; skin graft;

periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.

Homo sapiens.

WO200066731-A2.

09-NOV-2000.

28-APR-2000; 2000WO-US011459.

30-APR-1999; 99US-0131720P.

21-AUG-1999; 99US-0149738P.

24-SEP-1999; 99US-0155945P.

(BIOS-) BIOSTATUM INC.

Boutaud A;

WPI; 2000-687538/67.

N-PSDB; AAC83718.

Claim 3; Page 66-71; 232pp; English.

The present sequence is a laminin 5 chain polypeptide. Recombinant
 laminin 5-expressing cells are used to accelerate wound healing,
 especially diabetic foot ulcers, venous ulcers, pressure sores, skin
 surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
 intestinal ulcers, periodontitis, and gingivitis. They are also used to
 improve the biocompatibility of medical devices, and to promote cell

CC adhesion to a surface. They can be used for the ex vivo treatment of Type
 CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
 CC line produces and secretes recombinant heterotrimeric laminin, whereas
 CC prior art cell lines have been created that produce but do not secrete
 CC only one or two chain laminins
 XX
 SQ Sequence 1693 AA;

Query Match 76.0%; Score 850; DB 3; Length 1693;
 Best Local Similarity 76.6%; Pred. No. 2.6e-91;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKTSGVRLNDIVGVTKKCEDEMKLVRTASFSFGQMSFTNLDVSTDFQSLSGF 60
 DB 1098 MKNLKTSGVRLNDIVGVTKKCEDEMKLVRSASFSFGQSLSTFDGLPPTDHLQASFG 1157
 QY 61 QTFQPSGTLNHQRTSSLVLTLEDGHIELSTDSNIPFKSPGTMDGLHHVSVISDT 120
 DB 1158 QTFQPSGTLNHQRTSSLVLTLEDGHIELSTDSGPIFKSPGTMDGLHHVSVISDN 1217
 QY 121 SGRLIIDQVLRNRQLPFSNAQSLRIGGHEFCISNVLYORFSQSPVLDLASKS 180
 DB 1218 SGRLIIDQVLRNRQLPFSNAQSLRIGGHEFCISNVLYORFSQSPVLDLASKS 1277
 QY 181 TKKDAISLGGCSLNKPPFLMLFKSPKRFNKGRIFNVNQL 218
 DB 1278 LKRDVSLGGCSLNKPPFLMLKSTRPNKTKTRINQL 1315

RESULT 5

AAR70148 standard; protein; 1713 AA.

AAR70148;

25-MAR-2003 (revised)

05-OCT-1995 (first entry)

Deduced sequence of cDNA corresp. to the alpha-3BPA transcript.

E170; epithelial ligand glycoprotein; epiligrin complex;

epithelial cell binding.

Homo sapiens.

WO9506660-A1.

09-MAR-1995.

02-SEP-1994; 94WO-US010261.

02-SEP-1993; 93US-00115918.

(HUTC-) HUTCHINSON CANCER RES CENT FRID.

Carter WG, Gil SG, Ryan MC;

WPI; 1995-115398/15.

N-PSDB; AAQ83236.

Claim 12; Fig 15A-F; 187pp; English.

AAQ83235 depicts the nt. sequence compiled from sequencing cDNA clones
 corresp. to the alpha-3 BPA transcript. The invention includes nt
 sequences in the gp. comprising the nt sequence shown in AAQ83235, the
 cDNA clone Bp-1 (ATCC No. 75540) shown in AAQ83234, the cDNA clone 1-1
 (ATCC No. 75539), and the cDNA clone 8-6 (ATCC No. 75538), or the nt.
 sequences shown in AAQ83236. The entire nt region encoding E170 is

CC depicted in AA083236, and corresp. to the SQ of alpha-3. AA083236
 CC consists of a composite sequence derived from several overlapping clones.
 CC A synthetic polypeptide of at least 5 AAs that corresp. to part or all of
 CC the nt. sequence shown in AA083236 is claimed. (Updated on 25-MAR-2003 to
 CC correct PN field.)

XX SQ Sequence 1713 AA;

Query Match 76.0%; Score 850; DB 2; Length 1713;
 Best Local Similarity 76.6%; Pred. No. 2.6e-91;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKTTSGVRLNDVTGVTKKCSDEWKLVRKASFSRGGQMSFTNLDVSTDRFQLSPGF 60
 DB 1118 MKNLKTTSGVRLNDVTGVTKKCSDEWKLVRKASFSRGGQMSFTNLDVSTDRFQLSPGF 1177
 QY 61 QTFQPSGTLNHOQRTSSLVLTLEDGHIETSDSNIPFKSGTMDGLHHVSVISDT 120
 DB 1178 QTFQPSGTLNHOQRTSSLVLTLEDGHIETSDSNIPFKSGTMDGLHHVSVISDN 1237
 QY 121 SGRLILDDQVLRNRQLPSFSNAQSLRLGGHREGCISNVLVORFSGSPFVLDLASKS 180
 DB 1238 SGRLILDDQVLRNRQLPSFSNAQSLRLGGHREGCISNVLVORFSGSPFVLDLASKS 1297
 QY 181 TKDASLGGCSLNKPPFLMTFKSPKRPNGRIFFVNQL 218
 DB 1298 LKRDVSLGGCSLNKPPFLMTFKSGTRFNKTKTFRINQL 1335

RESULT 6
 AAB48458

ID AAB48458 standard; protein; 1713 AA.

AC AAB48458;

XX 02-MAR-2001 (first entry)

DT Human laminin 5 polypeptide, SEQ ID NO: 6.

XX Human laminin 5; vulnereary; antiulcer; antiinflammatory; antidiabetic;

KM cell adhesion promoter; wound healing; ulcer; burn; skin graft;

KW periodontitis; gingivitis; type I diabetes; angiogenesis regulation.

XX Homo sapiens.

OS WO200066731-A2.

PN 09-NOV-2000.

PD 28-APR-2000; 2000WO-US011459.

XX 30-APR-1999; 99US-0131720P.

PR 21-AUG-1999; 99US-0149738P.

PR 24-SEP-1999; 99US-0155945P.

XX (BIOG-) BIOSTATUM INC.

XX Boutaud A;

PI WPI; 2000-687538/67.

DR N-PSDB; AAC83719.

XX Laminin 5-expressing cells, used to accelerate wound healing associated

PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,

XX burns, acute wounds and skin grafts.

PS Claim 3; Page 79-84; 232pp; English.

XX The present sequence is a laminin 5 chain polypeptide. Recombinant

CC laminin 5-expressing cells are used to accelerate wound healing,

CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin

CC surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-

CC intestinal ulcers, periodontitis, and gingivitis. They are also used to

CC Improve the biocompatibility of medical devices, and to promote cell
 CC adhesion to a surface. They can be used for the ex vivo treatment of type
 CC I diabetes. Laminin can also be used to regulate angiogenesis. The cell
 CC line produces and secretes recombinant heterotimeric laminin, whereas
 CC prior art cell lines have been created that produce but do not secrete
 CC only one or two chain laminins

XX SQ Sequence 1713 AA;

Query Match 76.0%; Score 850; DB 3; Length 1713;
 Best Local Similarity 76.6%; Pred. No. 2.6e-91;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKTTSGVRLNDVTGVTKKCSDEWKLVRKASFSRGGQMSFTNLDVSTDRFQLSPGF 60
 DB 1118 MKNLKTTSGVRLNDVTGVTKKCSDEWKLVRKASFSRGGQMSFTNLDVSTDRFQLSPGF 1177
 QY 61 QTFQPSGTLNHOQRTSSLVLTLEDGHIETSDSNIPFKSGTMDGLHHVSVISDT 120
 DB 1178 QTFQPSGTLNHOQRTSSLVLTLEDGHIETSDSNIPFKSGTMDGLHHVSVISDN 1237
 QY 121 SGRLILDDQVLRNRQLPSFSNAQSLRLGGHREGCISNVLVORFSGSPFVLDLASKS 180
 DB 1238 SGRLILDDQVLRNRQLPSFSNAQSLRLGGHREGCISNVLVORFSGSPFVLDLASKS 1297
 QY 181 TKDASLGGCSLNKPPFLMTFKSPKRPNGRIFFVNQL 218
 DB 1298 LKRDVSLGGCSLNKPPFLMTFKSGTRFNKTKTFRINQL 1335

RESULT 7
 ABR92102

ID ABR92102 standard; protein; 1713 AA.

AC ABR92102;

XX 10-SEP-2003 (first entry)

DT Human cervical cancer cell marker encoding cDNA SEQ ID NO:113.

XX Human, cervical cancer; cervical cancer marker; cancer therapy;

KM detection; gene therapy; vaccine.

XX Homo sapiens.

OS WO2002101075-A2.

PN 19-DEC-2002.

PD 12-JUN-2002; 2002WO-US018638.

XX 13-JUN-2001; 2001US-0298155P.

PR 13-JUN-2001; 2001US-0298155P.

PR 14-NOV-2001; 2001US-0335936P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Schlegel R, Chen Y, Zhao X, Monahan JB, Kamatkar S;

PI Gamavartapu M, Glatt K, Hoersch S;

DR WPI; 2003-156967/15.

DR N-PSDB; ACF12884.

XX New isolated nucleic acid molecule useful for detecting, characterizing,

PT preventing and treating human cervical cancers, in various prognostic and

PT diagnostic assays, in pharmacogenomics and in monitoring clinical trials.

XX Claim 4; Page 269-273; 386pp; English.

CC ACF12882 to ACF12947 encode the human cervical cancer marker proteins (I)

CC given in ABR92047 to ABR92164. A higher level of expression of (I) than

CC normal indicates the presence of cervical cancer. Also described: (1) a

CC vector (II) containing (I); (2) a host cell (III) containing (I); and (3)

CC assessing (M1) whether a patient is afflicted with cervical cancer,
CC comprising comparing the level of expression of a marker in a patient's
CC sample, and the normal level of expression of the marker in a control non
CC cervical cancer sample, where a significant increase in the level of
CC expression of the marker in the patient's sample relative to that in the
CC control sample is an indication that the patient is afflicted with
CC cervical cancer. (1) has cytostatic activity, and can be used in gene
CC therapy and in vaccines. (1) is useful in detecting, characterizing,
CC preventing and treating human cervical cancers. (1) may also be used in
CC various prognostic and diagnostic assays, pharmacogenomics and in
CC monitoring clinical trials

SQ Sequence 1713 AA;

Query Match 76.0%; Score 850; DB 6; Length 1713;
Best Local Similarity 76.6%; Pred. No. 2.6e-91;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDVGVTKKSEBWKLVRTASFSFGQMSFTNLDVSTDFPQLSFGF 60
DB 1118 MKNLKKTSGVRLNDVGVTKKSEBWKLVRTASFSFGQMSFTNLDVSTDFPQLSFGF 1177
QY 61 QTFPQSGTLLNHQTRTSLLVLTLEDGHIELSTRDSNIPFKSPQTYMDGLLHVSVISDT 120
DB 1178 QTFPQSGTLLNHQTRTSLLVLTLEDGHIELSTRDSNIPFKSPQTYMDGLLHVSVISDT 1237
QY 121 SGRLRLIDQVLRNRQRLPSFNAQOSLRIGGHEGECISNVLVORFSQSPFVLDLASKS 180
DB 1238 SGRLRLIDQVLRNRQRLPSFNAQOSLRIGGHEGECISNVLVORFSQSPFVLDLASKS 1297
QY 181 TKKDAALGGCSLNKPPFLMFKSPKRNKRIFNVNOL 218
DB 1298 LKRDVSLGGCSLNKPPFLMFKSPKRNKRIFNVNOL 1335

RESULT 8

ADD29904 ID ADD29904 standard; protein; 1713 AA.

XX AC ADD29904;

XX DT 15-JAN-2004 (first entry)

XX DE Human laminin alpha 3 seq id 2.

XX KM ophthalmological; dermatological; laminin alpha 3; G3 domain;

XX KW cell adhesion function; cell movement effect; epithelial tissue function;

XX OS Homo sapiens.

XX PN JP2003093064-A.

XX PD 02-APR-2003.

XX PF 20-SEP-2001; 2001JP-00287519.

XX PR 20-SEP-2001; 2001JP-00287519.

XX PA (KAGA-) KAGAKU GIUTTSU SHINKO JIGYODAN.

XX DR (KIHA-) ZH KIHARA KINEN YOKOHAMA SEIMEI KAGAKU.

XX DT WPI; 2003-817304/77.

XX DR N-PSDB; ADD29903.

XX PT Novel modified G3 domain of laminin alpha 3 chain useful for controlling

XX PS Claim 1; SEQ ID NO 2; 49pp; Japanese.

XX CC The invention describes a modified laminin alpha3 chain comprising one or

XX CC more amino acid deletions, substitutions or additions at region

XX CC corresponding to a region of G3 domain having amino acids 1214-1324 of

CC laminin alpha3 chain having a fully defined sequence of 1713 amino acids
CC as given in the specification. (1) can control cell adhesion function and
CC cell movement effect. A composition comprising laminin is useful for
CC maintaining or treating the function of epithelial tissue and for
CC treatment or prevention of retinal detachment and in cosmetic surgery and
CC skin graft. The modified region of laminin alpha3 chain can control cell
CC adhesion function and cell movement effect. This is the amino acid
CC sequence of human laminin alpha 3.

SQ Sequence 1713 AA;

Query Match 76.0%; Score 850; DB 7; Length 1713;
Best Local Similarity 76.6%; Pred. No. 2.6e-91;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDVGVTKKSEBWKLVRTASFSFGQMSFTNLDVSTDFPQLSFGF 60
DB 1118 MKNLKKTSGVRLNDVGVTKKSEBWKLVRTASFSFGQMSFTNLDVSTDFPQLSFGF 1177
QY 61 QTFPQSGTLLNHQTRTSLLVLTLEDGHIELSTRDSNIPFKSPQTYMDGLLHVSVISDT 120
DB 1178 QTFPQSGTLLNHQTRTSLLVLTLEDGHIELSTRDSNIPFKSPQTYMDGLLHVSVISDT 1237
QY 121 SGRLRLIDQVLRNRQRLPSFNAQOSLRIGGHEGECISNVLVORFSQSPFVLDLASKS 180
DB 1238 SGRLRLIDQVLRNRQRLPSFNAQOSLRIGGHEGECISNVLVORFSQSPFVLDLASKS 1297
QY 181 TKKDAALGGCSLNKPPFLMFKSPKRNKRIFNVNOL 218
DB 1298 LKRDVSLGGCSLNKPPFLMFKSPKRNKRIFNVNOL 1335

RESULT 9

ADG37225 ID ADG37225 standard; protein; 1713 AA.

XX AC ADG37225;

XX DT 26-FEB-2004 (first entry)

XX DE Human laminin-6 alpha 3 subunit.

XX KM human; laminin-6; alpha 3; B1 subunit; B2 subunit; cell-movement;

XX KW cell-adhesion; dermatological; neuroprotective; muscular;

XX OS Homo sapiens.

XX PN JP2003212791-A.

XX PD 30-JUL-2003.

XX PF 17-JAN-2002; 2002JP-00009227.

XX PR 17-JAN-2002; 2002JP-00009227.

XX PA (KAGA-) KAGAKU GIUTTSU SHINKO JIGYODAN.

XX DR WPI; 2003-819867/77.

XX DT N-PSDB; ADG37224.

XX PT Composition comprising laminin-6 for regulation of cell-movement activity

XX PS function of epithelial tissue, nervous tissue and muscles.

XX PS Claim 2; SEQ ID NO 2; 55pp; Japanese.

XX CC This invention describes a novel composition comprising the human laminin

XX CC -6 alpha 3; B1 or B2 subunits for regulation of cell-movement activity

XX CC and/or cell-adhesion activity. The products of the invention have

XX CC dermatological, neuroprotective and muscular activity. The composition of

XX CC the invention is useful for treating or maintaining the function of the

XX CC epithelial tissue, the nervous tissue and muscles and is also useful for

CC treatment or prevention of varicella disease.
 XX Sequence 1713 AA;
 SQ Query Match 76.0%; Score 850; DB 7; Length 1713;
 Best Local Similarity 76.6%; Pred. No. 2.6e-91; Indels 0; Gaps 0;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MNLLKKTSGVRLNDVTGVTKKCSSEDMKLVRTASFSRGGQMSFTNLDVPSDFQLSFGF 60
 DB 1118 MNLLKKTSGVRLNDVTGVTKKCSSEDMKLVRSASFSRGGQLSTDLGLPTDHLQASFGF 1177

QY 61 QTFQPSGTLNMQRTSSLLVLTEDGHIELSTRDSNIPFKSPGYTMDGLAHVSVISDT 120
 DB 1178 QTFQPSGTLNMQRTSSLLVLTEDGHIELSTRDSNIPFKSPGYTMDGLAHVSVISDN 1237

QY 121 SGLRLIIDQVLRNRQLPSFSNAQSLRLGGHFGECISNVTVORFSQSPETLDLASKS 180
 DB 1238 SGLRLIIDQVLRNRQLPSFSNAQSLRLGGHFGECISNVTVORLSLSPVLDLTSNS 1297

QY 181 TKKDALGGCSLNKPPFLMLFKSPKRFNKGRIFFNNQL 218
 DB 1298 LKRDVSLGGCSLNKPPFLMLKGSTRFNKTKTFIRINQL 1335

RESULT 10
 ABM81957
 ID ABM81957 standard; protein; 1713 AA.
 XX
 AC ABM81957;
 DT 18-NOV-2004 (first entry)
 DE Tumour-associated antigenic target (TAT) polypeptide PRO2799, SEQ:5041.
 XX
 KM Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KM tumour; diagnosis; cell proliferative disorder; breast cancer;
 KM colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KM central nervous system cancer; bladder cancer; pancreatic cancer;
 KM cervical cancer; melanoma; leukemia; hybridisation probe;
 KM chromosome identification; chromosome mapping; gene mapping;
 KM gene therapy; cytostatic.
 XX
 OS Homo sapiens.
 PN WO2004030615-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 29-SEP-2003; 2003WO-US028547.
 XX
 PR 02-OCT-2002; 2002US-0414971P.
 XX
 PA (GETH) GENENTECH INC.
 PI Wu TD, Zhang Z, Zhou Y;
 DR WPI; 2004-347921/32.
 DR N-PSDB; ACN40327.
 XX
 PT New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 PS Claim 12; SEQ ID NO 5041; 7273bp; English.
 CC The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to the nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and

CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT polypeptide of the invention

SQ Sequence 1713 AA;
 Query Match 76.0%; Score 850; DB 8; Length 1713;
 Best Local Similarity 76.6%; Pred. No. 2.6e-91; Indels 0; Gaps 0;
 Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MNLLKKTSGVRLNDVTGVTKKCSSEDMKLVRTASFSRGGQMSFTNLDVPSDFQLSFGF 60
 DB 1118 MNLLKKTSGVRLNDVTGVTKKCSSEDMKLVRSASFSRGGQLSTDLGLPTDHLQASFGF 1177

QY 61 QTFQPSGTLNMQRTSSLLVLTEDGHIELSTRDSNIPFKSPGYTMDGLAHVSVISDT 120
 DB 1178 QTFQPSGTLNMQRTSSLLVLTEDGHIELSTRDSNIPFKSPGYTMDGLAHVSVISDN 1237

QY 121 SGLRLIIDQVLRNRQLPSFSNAQSLRLGGHFGECISNVTVORFSQSPETLDLASKS 180
 DB 1238 SGLRLIIDQVLRNRQLPSFSNAQSLRLGGHFGECISNVTVORLSLSPVLDLTSNS 1297

QY 181 TKKDALGGCSLNKPPFLMLFKSPKRFNKGRIFFNNQL 218
 DB 1298 LKRDVSLGGCSLNKPPFLMLKGSTRFNKTKTFIRINQL 1335

RESULT 11
 ADR87606
 ID ADR87606 standard; protein; 1713 AA.
 XX
 AC ADR87606;
 DT 02-DEC-2004 (first entry)
 DE Human Laminin alpha 3 (nicein), SEQ ID 10.
 XX
 KM Cytostatic; Gene Therapy; renal cell carcinoma; Wilms tumour; human;
 KM Laminin alpha 3; nicein.
 XX
 OS Homo sapiens.
 PN WO2004075835-A2.
 XX
 PD 10-SEP-2004.
 XX
 PF 20-FEB-2004; 2004WO-US005042.
 XX
 PR 21-FEB-2003; 2003US-00372683.
 XX
 PA (GETH) GENENTECH INC.
 PI Gerlitsen ME, Peale FV, Wu TD;
 DR WPI; 2004-676901/66.
 DR N-PSDB; ADR87605.
 XX
 PT New anti-EDNRA antibody, useful in preparing a composition for diagnosing
 PT or inhibiting the growth of renal cell carcinoma or Wilms tumor.
 XX
 PS Example 1; SEQ ID NO 10; 257bp; English.
 XX

CC The present invention relates to novel antibodies which bind to proteins
CC which are overexpressed in renal cell carcinomas or Wilms tumour. The
CC antibody can bind to a protein comprising CXCR4 (ADR87598), laminin alpha
CC 4 (ADR87600), TIMP1 (ADR87602), Type IV collagen alpha 1 (ADR87604),
CC laminin alpha 3 (nuclein) (ADR87606), Adrenomedullin (ADR87608), Type IV
CC collagen alpha 2 (ADR87610), Thrombospondin 2 (ADR87612), Type I collagen
CC alpha 2 (ADR87614), Type VI collagen alpha 3 (ADR87616), Latent TGFbeta
CC binding protein 2 (LTPB2) (ADR87618), Serine or cysteine protease
CC inhibitor heat shock protein 47 (HSP47) (ADR87620), Procollagen-lysine, 2
CC -oxoglutarate 5-dioxygenase (ADR87622), connexin 43 (ADR87624), Type IV
CC collagen alpha 2 (ADR87626), Connexin 37 (ADR87628), Ephrin A1
CC (ADR87630), Laminin beta 2 (ADR87632), Integrin alpha 1, hevin
CC (ADR87635), Stanniocalcin 1 (ADR87637), Thrombospondin 4 (ADR87639), CD36
CC polypeptide (ADR87641), Endothelin receptor A (EDNRA, ADR87643) or
CC Endothelin receptor B (EDNRB, ADR87645). The proteins of ADR87598-ADR87641
CC and ADR87645 are all overexpressed in renal cell carcinoma, and ADR87643
CC (EDNRA) is overexpressed in Wilms tumour. The antibodies are useful in
CC preparing a composition for diagnosing or inhibiting the growth of renal
CC cell carcinoma or Wilms tumour. The present sequence is one such protein
CC of the invention.

XX SQ Sequence 1713 AA;

Query Match 76.0%; Score 850; DB 8; Length 1713;
Best Local Similarity 76.6%; Pred. No. 2.6e-91;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDVTVGTVKCSBDMKLVRTASFSRGGQMSFTNLDVPSDFRQSLSGFG 60
DB 1118 MKNLKKTSGVRLNDVTVGTVKCSBDMKLVRTASFSRGGQMSFTNLDVPSDFRQSLSGFG 1177
QY 61 QTFQPSGTLNHTQRTSSLVLTEDGHIETSDSNIPFKSPGTMDGLLHVSVISDT 120
DB 1178 QTFQPSGTLNHTQRTSSLVLTEDGHIETSDSNIPFKSPGTMDGLLHVSVISDT 1237
QY 121 SGRLILIDQVLRNORLPSFSNAQSLRLGGHFGGCTSNVLYORFSSPEVLDLTSNS 180
DB 1238 SGRLILIDQVLRNORLPSFSNAQSLRLGGHFGGCTSNVLYORFSSPEVLDLTSNS 1297
QY 181 TKDASLGGCSLNKPPFLMLFKSPKRNKGRIFNVNQL 218
DB 1298 LKRDVSLGGCSLNKPPFLMLFKSPKRNKGRIFNVNQL 1335

RESULT 12

ID AAB48456 standard; protein; 1724 AA.

XX AAB48456;
XX
XX 02-MAR-2001 (first entry)
XX
XX Human laminin 5 polypeptide, SEQ ID NO: 2.
XX
XX Human; laminin 5; vulnery; antiulcer; antiinflammatory; antidiabetic;
XX cell adhesion promoter; wound healing; ulcers; burn; skin graft;
XX periodontitis; gingivitis; Type I diabetes; angiogenesis regulation.
XX
XX Homo sapiens.
XX
XX PN WO200066731-A2.
XX
XX PD 09-NOV-2000.
XX
XX PF 28-APR-2000; 2000MO-US011459.
XX
XX PR 30-APR-1999; 99US-0131720P.
XX 21-AUG-1999; 99US-0149738P.
XX 24-SEP-1999; 99US-0155945P.
XX
XX PA (BIOS-) BIOSTATUM INC.
XX
XX PI Boutaud A;

XX DR WPI: 2000-687538/67.
XX DR N-PSDB; AAC83717.

XX PT Laminin 5-expressing cells, used to accelerate wound healing associated
XX with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,
XX PT burns, acute wounds and skin grafts.

XX PS Claim 3; Page 53-59; 232pp; English.

XX The present sequence is a laminin 5 chain polypeptide. Recombinant
XX laminin 5-expressing cells are used to accelerate wound healing,
XX especially diabetic foot ulcers, venous ulcers, pressure sores, skin
XX surgery, burns, acute wounds, skin grafts, corneal ulcerations, gastro-
XX intestinal ulcers, periodontitis, and gingivitis. They are also used to
XX improve the biocompatibility of medical devices, and to promote cell
XX adhesion to a surface. They can be used for the ex vivo treatment of Type
XX I diabetes. Laminin can also be used to regulate angiogenesis. The cell
XX line produces and secretes recombinant heterotrimeric laminin, whereas
XX prior art cell lines have been created that produce but do not secrete
XX only one or two chain laminins

XX SQ Sequence 1724 AA;

Query Match 76.0%; Score 850; DB 3; Length 1724;
Best Local Similarity 76.6%; Pred. No. 2.7e-91;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDVTVGTVKCSBDMKLVRTASFSRGGQMSFTNLDVPSDFRQSLSGFG 60
DB 1129 MKNLKKTSGVRLNDVTVGTVKCSBDMKLVRTASFSRGGQMSFTNLDVPSDFRQSLSGFG 1188
QY 61 QTFQPSGTLNHTQRTSSLVLTEDGHIETSDSNIPFKSPGTMDGLLHVSVISDT 120
DB 1189 QTFQPSGTLNHTQRTSSLVLTEDGHIETSDSNIPFKSPGTMDGLLHVSVISDT 1248
QY 121 SGRLILIDQVLRNORLPSFSNAQSLRLGGHFGGCTSNVLYORFSSPEVLDLTSNS 180
DB 1249 SGRLILIDQVLRNORLPSFSNAQSLRLGGHFGGCTSNVLYORFSSPEVLDLTSNS 1308
QY 181 TKDASLGGCSLNKPPFLMLFKSPKRNKGRIFNVNQL 218
DB 1309 LKRDVSLGGCSLNKPPFLMLFKSPKRNKGRIFNVNQL 1346

RESULT 13

ID ADE08094 standard; protein; 3332 AA.

XX ADE08094;
XX
XX 29-JAN-2004 (first entry)
XX
XX Novel protein (useful for identifying genetic disorders) #249.
XX
XX novel gene; novel protein; tissue marker; molecular weight marker;
XX chromosome marker; genetic disorder.
XX
XX Unidentified.
XX
XX PN WO2003054152-A2.
XX
XX PD 03-JUL-2003.
XX
XX PF 10-DEC-2002; 2002MO-US039555.
XX
XX PR 10-DEC-2001; 2001US-0339739P.
XX 11-DEC-2001; 2001US-0339453P.
XX 14-MAR-2002; 2002US-0365091P.
XX 14-MAR-2002; 2002US-0365841P.
XX 12-APR-2002; 2002US-0372381P.
XX 12-APR-2002; 2002US-0372615P.
XX 22-APR-2002; 2002US-00128558.

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PR 24-APR-2002; 2002US-0376045P.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX WPI; 2003-569235/53.
XX N-PSDB; ADB07183.
XX
XX PT New polynucleotides, useful for expressing recombinant proteins for
XX analysis, characterization or therapeutic use, or as markers for tissues
XX in which the corresponding protein is preferentially expressed.
XX
XX Claim 20; SEQ ID NO 1160; 1177pp; English.
XX
XX CC The invention comprises the amino acid and coding sequences of novel
XX proteins. The DNA and protein sequences of the invention are useful as:
XX markers for tissues in which the corresponding protein is preferentially
XX expressed; as molecular weight markers on gels; as chromosome markers or
XX tags; to identify chromosomes or to map related gene positions; and to
XX compare with endogenous DNA sequences in patients to identify potential
XX genetic disorders. The present amino acid sequence represents a protein
XX of the invention.
XX
XX SQ Sequence 3332 AA;
XX
XX Query Match 76.0%; Score 850; DB 7; Length 3332;
XX Best Local Similarity 76.6%; Pred. No. 7.4e-91;
XX Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;
XX
XX QY 1 MKNLKKTSGVRLNDVTGVTKKCEDMKLVRTASFSRGGQMSPTNLDVSTDRFQLSFGF 60
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX DB 2737 MKNLKKTSGVRLNDVTGVTKKCEDMKLVRTASFSRGGQLSFTDGLPTDHLQASFGF 2796
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX QY 61 QTFQPSGTLNMQTRTSSLLVTLDEGHIELSTDSNIPFKSGPTMDGLLHVSVISDT 120
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX DB 2797 QTFQPSGTLNMQTRTSSLLVTLDEGHIELSTDSNIPFKSGPTMDGLLHVSVISDT 2856
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX QY 121 SGLRLIIDQVLRNORLPSPNAOQSLRLGGHFGSGCTSNVYVORFSGSPETLDLASKS 180
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX DB 2857 SGLRLIIDQVLRNORLPSPNAOQSLRLGGHFGSGCTSNVYVORFSGSPETLDLASKS 2916
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX QY 181 TKKDAISLGGCSLNKPFLMLFKSPKPKNGRIFFNVQL 218
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX DB 2917 LKRDVSLGGCSLNKPFLMLFKSGTRFNKTKTRINQL 2954
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX
XX RESULT 14
XX AAG75103
XX ID AAG75103 standard; protein; 469 AA.
XX
XX AC AAG75103;
XX
XX DT 03-SEP-2001 (first entry)
XX
XX DE Human colon cancer antigen protein SEQ ID NO:5867.
XX
XX KM Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma; chromosome 18.
XX
XX OS Homo sapiens.
XX
XX PN MO200122920-A2.
XX
XX PD 05-APR-2001.
XX
XX PF 28-SEP-2000; 2000MO-US026524.
XX
XX PR 29-SEP-1999; 99US-0157137P.
XX PR 03-NOV-1999; 99US-0163280P.
XX
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PA (HUMA-) HUMAN GENOME SCT INC.
XX
XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
XX DR WPI; 2001-235357/24.
XX
XX DR N-PSDB; AAH34508.
XX
XX PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers.
XX
XX PS Claim 11; Page 7385-7387; 9803pp; English.
XX
XX CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where the
XX proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytoskeletal activity and can be used in gene therapy
XX and vaccine production. N and P may be used in the prevention, diagnosis
XX and treatment of diseases associated with inappropriate P expression. For
XX example, N and P may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of P by expressing inactive proteins or to
XX supplement the patient's own production of P. Additionally, N may be used
XX to produce the colon cancer-associated P, by inserting the nucleic acids
XX into a host cell and culturing the cell to express the proteins. N and P
XX can be used in the prevention, diagnosis and treatment of colorectal
XX carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
XX sequences used in the exemplification of the present invention. N.B.
XX Pages 666 to 682 and page 7053 of the sequence listing were missing at
XX CC time of publication, meaning no sequences are present for SEQ ID NO:1027
XX to 1052, 7921 and 7922
XX
XX SQ Sequence 469 AA;
XX
XX Query Match 60.8%; Score 680; DB 4; Length 469;
XX Best Local Similarity 72.2%; Pred. No. 8e-72;
XX Matches 135; Conservative 17; Mismatches 35; Indels 0; Gaps 0;
XX
XX QY 32 TASFSRGGQMSPTNLDVSTDRFQLSFGFQTFQPSGTLNMQTRTSSLLVTLDEGHIELS 91
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX DB 1 SASFSRGGQLSFTDGLPTDHLQASFGFQTFQPSGTLNMQTRTSSLLVTLDEGHIELS 60
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX QY 92 TSDSNIPFKSGPTMDGLLHVSVISDTSGRLIIDQVLRNORLPSPNAOQSLRLG 151
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX DB 61 TSDSNIPFKSGPTMDGLLHVSVISDTSGRLIIDQVLRNORLPSPNAOQSLRLG 120
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX QY 152 GGHFGSGCTSNVYVORFSGSPETLDLASKSTKDAISLGGCSLNKPFLMLFKSPKPKNGR 211
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX DB 121 GSNFGSGCTSNVYVORFSGSPETLDLASKSTKDAISLGGCSLNKPFLMLFKSGTRFNKTK 180
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX QY 212 IFNVQL 218
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX DB 181 TFRINQL 187
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX
XX RESULT 15
XX AAB48447
XX ID AAB48447 standard; protein; 1792 AA.
XX
XX AC AAB48447;
XX
XX DT 02-MAR-2001 (first entry)
XX
XX DE Mouse laminin 8 polypeptide, SEQ ID NO: 12.
XX
XX KM Mouse; laminin 8; neuroprotective; angiogenic; osteopathic;
XX antiarteriosclerotic; glycoprotein; mesenchymal tissue injury;
XX vascular tissue injury; neural injury; angiogenesis regulation.
XX
XX OS Mus musculus.
XX
XX PN MO200066732-A2.
XX
XX PR 09-NOV-2000.
XX
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XX 28-APR-2000; 2000WO-US011543.
PF
XX
PR 30-APR-1999; 99US-0131720P.
PR 21-AUG-1999; 99US-0149738P.
PR 24-SEP-1999; 99US-0155945P.
PR 11-FEB-2000; 2000US-0182012P.
XX
PA (BIOS-) BIOSTRATUM INC.
XX
PI Kortessmaa J, Tryggvason K;
XX
XX WPI; 2000-687539/67.
DR N-PDB; AAC3708.
XX
XX Purified laminin 8 protein, useful for research and therapeutic purposes
PT including peripheral nerve regeneration, treatment of degenerative muscle
PT disorders, angiogenesis regulation, and ex vivo cell therapy.
XX
PS Claim 5; Page 136-142; 245pp; English.
XX
CC The present sequence is a laminin 8 polypeptide chain. Laminins are a
CC family of heterotrimeric glycoproteins that function via binding
CC interactions with neighbouring cell receptors and by forming laminin
CC networks. They are signalling molecules which influence cellular
CC function. Laminin 8 is useful for treating injuries to tissue of
CC mesenchymal origin, such as bone, cartilage, tendon, and ligament.
CC treating injuries to vascular tissue, promoting cell attachment and
CC migration, ex vivo cell therapy, improving the biocompatibility of
CC medical devices, and preparing improved cell culture devices and media.
CC Laminin 8 is also useful for promoting re-endothelialisation at the site
CC of vascular injuries, improving the take of grafts, improving the
CC biocompatibility of medical devices, treating neural injuries (neural
CC regeneration), regulating angiogenesis, and promoting cell attachment and
CC migration
XX
SQ Sequence 1792 AA;

Query Match 18.2%; Score 204; DB 3; Length 1792;
Best Local Similarity 29.1%; Pred. No. 6.6e-14;
Matches 64; Conservative 35; Mismatches 99; Indels 22; Gaps 8;

QY 5 KKTSGVRLNDYGVTKKSGEDMKLVRTASPSRGQMSFTNLD-VPESTRFQLSPFGROT 63
DB 1180 KKPNNLEQETETLGVGCPEDSLISRAYFN--GQSFIASTQKISFPDPEGGFNRTL 1237
QY QPSGTLNHOVRTSLVLTLEDGHIIESTRDSNIPFKSPQYMDGLHH-VSVISDTSG 122
DB 1238 QPNGLLFYVTSGSVPFISLDNGVVDVK--GIKWMSTDKQYHDLPHFVVTISIDTR- 1294
QY 123 LRLIIDQVLRNRQRLPSFNSAQS-----LRIQ-----GHFECISNVLVORFSQ 169
DB 1295 YELVVDKSRRLGKN--PTKGAEGQVTEKKFYFGGSPISPOYANFTGCISNAVFTRLDR 1352
QY 170 SPEYLDLASKSTKDAISGCSLNKPPLMLFKSPKRFNK 209
DB 1353 DVEVEDFQRYSEKVHTSLYECPIESSPLFLHKKGNSSK 1392
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Search completed: February 22, 2005, 08:18:48
Job time : 41.1892 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:19:00 ; Search time 29.2165 Seconds
(without alignments)
2441.722 Million cell updates/sec

Title: US-10-817-423-6

Perfect score: 1118
Sequence: 1 MKNLKKTSGVRLNDTVGVTVT.....MLFKSPKRFKRIFFVNVQL 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/prodata/2/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/2/pubppa/PCTUS_PUBCOMB.pep:*
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12: /cgn2_6/prodata/2/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep:*
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18: /cgn2_6/prodata/2/pubppa/US11_NEW_PUB.pep:*
19: /cgn2_6/prodata/2/pubppa/US60_NEW_PUB.pep:*
20: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1118	100.0	1694	15	US-10-603-725-12
2	1118	100.0	1725	15	US-10-603-725-10
3	880	76.0	1693	15	US-10-603-725-4
4	850	76.0	1693	15	US-10-603-725-8
5	850	76.0	1713	14	US-10-171-311-113
6	850	76.0	1713	15	US-10-372-683-10
7	850	76.0	1713	15	US-10-603-725-6
8	850	76.0	1724	15	US-10-603-725-2
9	680	60.8	1469	14	US-10-106-698-5877
10	187	16.7	1581	16	US-10-408-765A-114
11	187	16.7	1816	14	US-10-299-058-2
12	187	16.7	1816	14	US-10-299-058-4
13	187	16.7	1816	15	US-10-372-683-4

14	187	16.7	1823	15	US-10-363-616-457	Sequence 457, App
15	186	16.6	3635	9	US-09-845-583-2	Sequence 2, Appl
16	186	16.6	3635	14	US-10-037-182-4	Sequence 4, Appl
17	186	16.6	3635	15	US-10-037-417-47	Sequence 47, Appl
18	186	16.6	3635	15	US-10-037-417-6	Sequence 6, Appl
19	176	15.7	3600	15	US-10-037-417-2	Sequence 2, Appl
20	176	15.7	3690	15	US-10-112-944-347	Sequence 347, App
21	175	15.7	49	9	US-09-925-299-1149	Sequence 1149, Ap
22	175	15.7	49	10	US-09-925-299-1149	Sequence 1149, Ap
23	174	15.6	463	15	US-10-264-048-3039	Sequence 3039, Ap
24	174	15.6	908	15	US-10-037-417-4	Sequence 4, Appl
25	174	15.6	953	9	US-09-845-583-4	Sequence 4, Appl
26	174	15.6	953	15	US-10-037-417-50	Sequence 50, Appl
27	174	15.6	1634	15	US-10-037-417-49	Sequence 49, Appl
28	174	15.6	1640	15	US-10-037-417-8	Sequence 8, Appl
29	174	15.6	1677	15	US-10-112-944-801	Sequence 801, App
30	174	15.6	3695	14	US-10-037-182-2	Sequence 2, Appl
31	174	15.6	3695	15	US-10-312-352-22	Sequence 22, Appl
32	174	15.6	3696	15	US-10-312-088-31	Sequence 31, Appl
33	174	15.6	3705	15	US-10-312-088-30	Sequence 30, Appl
34	173.5	15.5	3712	13	US-10-108-605-103	Sequence 103, App
35	173.5	15.5	3712	15	US-10-037-417-48	Sequence 48, Appl
36	173.5	15.5	3712	15	US-10-037-417-51	Sequence 51, Appl
37	151.5	13.6	365	9	US-09-925-299-1007	Sequence 1007, Ap
38	151.5	13.6	365	10	US-09-925-299-1007	Sequence 1007, Ap
39	134.5	12.0	3070	10	US-09-961-403-7	Sequence 7, Appl
40	128.5	11.5	2923	9	US-09-788-711A-4	Sequence 4, Appl
41	128.5	11.5	2923	10	US-09-916-849A-3	Sequence 3, Appl
42	128.5	11.5	2923	14	US-10-225-567A-524	Sequence 524, App
43	128.5	11.5	2923	14	US-10-174-677-29	Sequence 29, Appl
44	128.5	11.5	2923	15	US-10-120-801-53	Sequence 53, Appl
45	128.5	11.5	2923	15	US-10-292-798-932	Sequence 932, App

ALIGNMENTS

RESULT 1
US-10-603-725-12
; Sequence 12, Application US/10603725
; Generalization No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Bouland, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1694
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-603-725-12

Query Match 100.0%; Score 1118; DB 15; Length 1694;
Best Local Similarity 100.0%; Pred. No. 7e-109;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKNLKTSGVRLNDTVGVTVTKKCEBDMKLVRTASFRGGOMSPFTNIDVPSTDFOLSGFG	60
DB	1098	MKNLKTSGVRLNDTVGVTVTKKCEBDMKLVRTASFRGGOMSPFTNIDVPSTDFOLSGFG	1157
QY	61	QTFQPSGTLNHQTRTSSLLVTLLEDGHIESTDSNIPFKSPGYNDGLHHVSVISDT	120
DB	1158	QTFQPSGTLNHQTRTSSLLVTLLEDGHIESTDSNIPFKSPGYNDGLHHVSVISDT	1217
QY	121	SGRLIIDQVYRBNQRLPSFNAOOSLRIGGHPGCTSNVYVORFOSPEVLDLASKS	180
DB	1218	SGRLIIDQVYRBNQRLPSFNAOOSLRIGGHPGCTSNVYVORFOSPEVLDLASKS	1277
QY	181	TKKDAISLGGCSLNKPPFLMLFKSPKRFKRIFFVNVQL	218

Db 1278 TKKDAISLGCCSLNKPPFLMLFKSPKRFNKGRIFFNVNQL 1315

RESULT 2

US-10-603-725-10
; Sequence 10, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boutand, Arlet
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1725
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-603-725-10

Query Match 100.0%; Score 1118; DB 15; Length 1725;
Best Local Similarity 100.0%; Pred. No. 7,2e-109;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDVTGVTKKCSBDKLVRTASFSRGQMSFTNLDVPSIDRFQLSFGF 60
DB 1129 MKNLKKTSGVRLNDVTGVTKKCSBDKLVRTASFSRGQMSFTNLDVPSIDRFQLSFGF 1188
QY 61 QTFQPSGTLNMQTRTSSLLVLTLEDGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 120
DB 1189 QTFQPSGTLNMQTRTSSLLVLTLEDGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 1248
QY 121 SGLRLIIDQVLRNRQRLPSFSNAOQSLRLGGHFGGCSINVLVORFSSPEVLDLASKS 180
DB 1249 SGLRLIIDQVLRNRQRLPSFSNAOQSLRLGGHFGGCSINVLVORFSSPEVLDLASKS 1308
QY 181 TKKDAISLGCCSLNKPPFLMLFKSPKRFNKGRIFFNVNQL 218
DB 1309 TKKDAISLGCCSLNKPPFLMLFKSPKRFNKGRIFFNVNQL 1346

RESULT 3

US-10-603-725-4
; Sequence 4, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boutand, Arlet
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1693
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-725-4

Query Match 76.0%; Score 850; DB 15; Length 1693;
Best Local Similarity 76.6%; Pred. No. 2e-80;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDVTGVTKKCSBDKLVRTASFSRGQMSFTNLDVPSIDRFQLSFGF 60
DB 1098 MKNLKKTSGVRLNDVTGVTKKCSBDKLVRTASFSRGQMSFTNLDVPSIDRFQLSFGF 1157
QY 61 QTFQPSGTLNMQTRTSSLLVLTLEDGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 120
DB 1158 QTFQPSGTLNMQTRTSSLLVLTLEDGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 1217
QY 121 SGLRLIIDQVLRNRQRLPSFSNAOQSLRLGGHFGGCSINVLVORFSSPEVLDLASKS 180

Db 1218 SGLRLIIDQVLRNRQRLPSFSNAOQSLRLGGHFGGCSINVLVORFSSPEVLDLASKS 1277

QY 181 TKKDAISLGCCSLNKPPFLMLFKSPKRFNKGRIFFNVNQL 218

Db 1278 LKRDVSLGGCSLNKPPFLMLFKSPKRFNKGRIFFNVNQL 1315

RESULT 4

US-10-603-725-8
; Sequence 8, Application US/10603725
; Publication No. US20040014665A1
; GENERAL INFORMATION:
; APPLICANT: Boutand, Arlet
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/10/603,725
; CURRENT FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1693
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-725-8

Query Match 76.0%; Score 850; DB 15; Length 1693;
Best Local Similarity 76.6%; Pred. No. 2e-80;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKKTSGVRLNDVTGVTKKCSBDKLVRTASFSRGQMSFTNLDVPSIDRFQLSFGF 60
DB 1098 MKNLKKTSGVRLNDVTGVTKKCSBDKLVRTASFSRGQMSFTNLDVPSIDRFQLSFGF 1157
QY 61 QTFQPSGTLNMQTRTSSLLVLTLEDGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 120
DB 1158 QTFQPSGTLNMQTRTSSLLVLTLEDGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 1217
QY 121 SGLRLIIDQVLRNRQRLPSFSNAOQSLRLGGHFGGCSINVLVORFSSPEVLDLASKS 180
DB 1218 SGLRLIIDQVLRNRQRLPSFSNAOQSLRLGGHFGGCSINVLVORFSSPEVLDLASKS 1277
QY 181 TKKDAISLGCCSLNKPPFLMLFKSPKRFNKGRIFFNVNQL 218
DB 1278 LKRDVSLGGCSLNKPPFLMLFKSPKRFNKGRIFFNVNQL 1315

RESULT 5

US-10-171-311-113
; Sequence 113, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamackar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gamaavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 113
LENGTH: 1713
TYPE: PRT
ORGANISM: Homo sapiens
US-10-171-311-113

Query Match
Best Local Similarity 76.0%; Score 850; DB 14; Length 1713;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

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1118 MKNLKTSGVRLNDVGVTKKSEBWKLVRSASFSRGGQLSFTDGLPTDHLQASFGF 1177
1178 QTFQPSGILLDHQTRTNLQVTLLEDGYIELSTDSGGPIFKSPQTYMDGLLHVSVISDN 1237
121 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFECCISNVLVORFSQSPVYDLASKS 180
1238 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFECCISNVLVORFSQSPVYDLASKS 1297
181 TKDASLGGCSLNKPPFLMFKSPKRNKGRIFNVNQL 218
1298 LKRDVSLGGCSLNKPPFLMLKSGTRFNKTKTRINQL 1335

RESULT 6

US-10-372-683-10
Sequence 10, Application US/10372683
Publication No. US2004009171A1
GENERAL INFORMATION:

APPLICANT: GERRITSEN, MARY E.
APPLICANT: PALE JR., FRANKLIN V.
APPLICANT: WU, THOMAS D.
TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
FILE REFERENCE: P1928R1P1
CURRENT APPLICATION NUMBER: US/10/372,683
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 10/271,690
PRIOR FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: US 60/344,534
PRIOR FILING DATE: 2001-10-18
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 10
LENGTH: 1713
TYPE: PRT
ORGANISM: Homo sapien
US-10-372-683-10

Query Match
Best Local Similarity 76.0%; Score 850; DB 15; Length 1713;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

1 MKNLKTSGVRLNDVGVTKKSEBWKLVRTASFSRGGQMSFTNLDVPSDFRQLSFGF 60
1118 MKNLKTSGVRLNDVGVTKKSEBWKLVRSASFSRGGQLSFTDGLPTDHLQASFGF 1177
61 QTFQPSGILLDHQTRTNLQVTLLEDGYIELSTDSGGPIFKSPQTYMDGLLHVSVISDT 120
1178 QTFQPSGILLDHQTRTNLQVTLLEDGYIELSTDSGGPIFKSPQTYMDGLLHVSVISDN 1237
121 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFECCISNVLVORFSQSPVYDLASKS 180
1238 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFECCISNVLVORFSQSPVYDLASKS 1297
181 TKDASLGGCSLNKPPFLMFKSPKRNKGRIFNVNQL 218
1298 LKRDVSLGGCSLNKPPFLMLKSGTRFNKTKTRINQL 1335

RESULT 7

US-10-603-725-6
Sequence 6, Application US/10603725
Publication No. US20040014665A1
GENERAL INFORMATION:

APPLICANT: Boutland, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/10/603,725
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 1713
TYPE: PRT
ORGANISM: Homo sapiens
US-10-603-725-6

Query Match
Best Local Similarity 76.0%; Score 850; DB 15; Length 1713;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

1 MKNLKTSGVRLNDVGVTKKSEBWKLVRTASFSRGGQMSFTNLDVPSDFRQLSFGF 60
1118 MKNLKTSGVRLNDVGVTKKSEBWKLVRSASFSRGGQLSFTDGLPTDHLQASFGF 1177
61 QTFQPSGILLDHQTRTNLQVTLLEDGYIELSTDSGGPIFKSPQTYMDGLLHVSVISDT 120
1178 QTFQPSGILLDHQTRTNLQVTLLEDGYIELSTDSGGPIFKSPQTYMDGLLHVSVISDN 1237
121 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFECCISNVLVORFSQSPVYDLASKS 180
1238 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFECCISNVLVORFSQSPVYDLASKS 1297
181 TKDASLGGCSLNKPPFLMFKSPKRNKGRIFNVNQL 218
1298 LKRDVSLGGCSLNKPPFLMLKSGTRFNKTKTRINQL 1335

RESULT 8

US-10-603-725-2
Sequence 2, Application US/10603725
Publication No. US20040014665A1
GENERAL INFORMATION:

APPLICANT: Boutland, Ariel
TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/10/603,725
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1724
TYPE: PRT
ORGANISM: Homo sapiens
US-10-603-725-2

Query Match
Best Local Similarity 76.0%; Score 850; DB 15; Length 1724;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

1 MKNLKTSGVRLNDVGVTKKSEBWKLVRTASFSRGGQMSFTNLDVPSDFRQLSFGF 60
1129 MKNLKTSGVRLNDVGVTKKSEBWKLVRSASFSRGGQLSFTDGLPTDHLQASFGF 1188
61 QTFQPSGILLDHQTRTNLQVTLLEDGYIELSTDSGGPIFKSPQTYMDGLLHVSVISDT 120
1189 QTFQPSGILLDHQTRTNLQVTLLEDGYIELSTDSGGPIFKSPQTYMDGLLHVSVISDN 1248
121 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFECCISNVLVORFSQSPVYDLASKS 180
1249 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFECCISNVLVORFSQSPVYDLASKS 1308
181 TKDASLGGCSLNKPPFLMFKSPKRNKGRIFNVNQL 218

Db 1309 LKRDVSLGGCSLNKPPFLMLKNGSTFRNKTRINQL 1346

RESULT 9

US-10-106-698-5877
; Sequence 5877, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005PI
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 5877
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (47)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (65)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (436)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5877

Query Match 60.8%; Score 680; DB 14; Length 469;
Best Local Similarity 72.2%; Pred. No. 3.6e-63;
Matches 135; Conservative 17; Mismatches 35; Indels 0; Gaps 0;

QY 32 TASFSRGQMSFTNLVPSIDRQLSGRQTPQPSGTLNHOVRTSLVLTEDGHIELS 91
DB 1 SASFSRGKQLSFTDLGLPPTDHLQASFGFTQPSGILDHQVTRXLQVLTEDGYIELS 60
QY 92 TRDSNIPFESPGTYMDGLAHVSVISDTSGRLRLIDDQVLRNRQRLPFSNAQOSLRIG 151
DB 61 TSDSXGPIFSPQTYMDGLAHVSVISDNGRLRLIDDQVLRNRQRLPFSNAQOSLRIG 120
QY 152 GHEGECISNVLVQPSQSPVETDLASKSTYKQASLGGCSLNKPPFLMLFKSPRRNKGR 211
DB 121 GSNFEGCISNVFVQRLSLSPVETDLTNSMLKRDVSLGGCSLNKPPFLMLKSTFRNKTK 180
QY 212 IFNVNQL 218
DB 181 TFRINQL 187

RESULT 10

US-10-408-765A-154
; Sequence 154, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Bojin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.

; APPLICANT: Warnock, Dale B.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660089,465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154
; LENGTH: 1581
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-154

Query Match 16.7%; Score 187; DB 16; Length 1581;
Best Local Similarity 28.3%; Pred. No. 4.3e-10;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KXTSGVRLNDTVGYTKKCSBDWKLVRTPASFRGQMSFTNLD-VPSIDRFQLSFGQTF 63
DB 967 KDFNLBQETETLGVGYGCPEDSLISRAYFN--GQSFIAISIQKISFPDGFEGGFNFRLL 1024
QY 64 QPSGTLNMQRTSSLVLTEDGHIELSTRDSNIPFESPGTYMDGLAHVSVISDTSGRL 123
DB 1023 QPNGLLFYASGSDVFSISLNDGTVIMDVK--GIKVGSDVKQYMDGLSHF--VIVSVSPT 1080
QY 124 R--LLID-DQVLRNRQRLPFSNAQOSLR---LGG-----GHEGECISNVLVQPSQ 170
DB 1081 RYELIVDSRVGSKPTGKLEQDQASKKPFPGSPISAGYANVTGCSINAYFRVRD 1140
QY 171 PEVLDAKSTYKQASLGGCSLNKPPFLMLFKSPRRNK 209
DB 1141 VEVEDFQRYTEKVRHTSLVECPLESPLFLHKKGNLSK 1179

RESULT 11

US-10-299-058-2
; Sequence 2, Application US/10299058
; Publication No. US20030103975A1
; GENERAL INFORMATION:
; APPLICANT: JONES, JONATHAN C.R.
; APPLICANT: GONZALES, MEREDITH
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION
; FILE REFERENCE: 1720-1-002 CIP
; CURRENT APPLICATION NUMBER: US/10/299,058
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/706,235
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/163,199
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1816
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; OTHER INFORMATION: X in position 1112 = Arg/Pro
US-10-299-058-2

Query Match 16.7%; Score 187; DB 14; Length 1816;
Best Local Similarity 28.3%; Pred. No. 5.3e-10;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KXTSGVRLNDTVGYTKKCSBDWKLVRTPASFRGQMSFTNLD-VPSIDRFQLSFGQTF 63
DB 1202 KDFNLBQETETLGVGYGCPEDSLISRAYFN--GQSFIAISIQKISFPDGFEGGFNFRLL 1259
QY 64 QPSGTLNMQRTSSLVLTEDGHIELSTRDSNIPFESPGTYMDGLAHVSVISDTSGRL 123
DB 1260 QPNGLLFYASGSDVFSISLNDGTVIMDVK--GIKVGSDVKQYMDGLSHF--VIVSVSPT 1315
QY 124 R--LLID-DQVLRNRQRLPFSNAQOSLR---LGG-----GHEGECISNVLVQPSQ 170

Db 1316 RYELIYDKSRVSGKNPTKGI EGTQAS EKKFYFGSGSPISAQYANFTGCISNAFYTRVDRD 1375
 QY 171 PEVLDAKSTKCDASIGGCSLNKPPLMLFKSPKRFNK 209
 Db 1376 VEVEDFORYTEKVTSLYECPISSPLFLHKKGNLSK 1414

RESULT 12

US-10-299-058-4
 ; Sequence 4, Application US/10299058
 ; Publication No. US20030103975A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JONES, JONATHAN C.R.
 ; APPLICANT: GONZALES, MEREDITH
 ; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND ENDOTHELIALIZATION
 ; FILE REFERENCE: 1720-1-002 CIP
 ; CURRENT APPLICATION NUMBER: US/10/299,058
 ; CURRENT FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: 09/706,235
 ; PRIOR FILING DATE: 2000-11-03
 ; PRIOR APPLICATION NUMBER: 60/163,199
 ; PRIOR FILING DATE: 1999-11-03
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 1816
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; OTHER INFORMATION: X in position 1112 = R/P
 US-10-299-058-4

Query Match 16.7%; Score 187; DB 14; Length 1816;
 Best Local Similarity 28.3%; Pred. No. 5.3e-10;
 Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDYGVYTKKSEDMKLVRTASFSRGGMSFTNLD-VPTDRFOLSFGQTF 63
 Db 1202 KQFNLEGTETLVGVGCPEDSLISRRAYFN--GQSFASIOKISFPDGFEGGFNRTL 1259
 QY 64 QPSTGLNHTQRTSLVLTLEDGHIELSTRDSNIPFKSGTYMDGLHNVYSIDTSGL 123
 Db 1260 QPGLLFYASGSDVSIISDNGTVIMDK--GIKQSVKQYNDGLSH--VSSVSPT 1315
 QY 124 R--LLID-DQVLRNRQLPSPSNAQSLR---LGG-----GHFECISNVLVQRPQS 170
 Db 1316 RYELIYDKSRVSGKNPTKGI EGTQAS EKKFYFGSGSPISAQYANFTGCISNAFYTRVDRD 1375
 QY 171 PEVLDAKSTKCDASIGGCSLNKPPLMLFKSPKRFNK 209
 Db 1376 VEVEDFORYTEKVTSLYECPISSPLFLHKKGNLSK 1414

RESULT 13

US-10-372-683-4
 ; Sequence 4, Application US/10372683
 ; Publication No. US20040009171A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GERRITSEN, MARY E.
 ; APPLICANT: PEARL JR., FRANKLIN V.
 ; APPLICANT: WU, THOMAS D.
 ; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
 ; FILE REFERENCE: P1928R1P1
 ; CURRENT APPLICATION NUMBER: US/10/372,683
 ; CURRENT FILING DATE: 2003-02-21
 ; PRIOR APPLICATION NUMBER: US 10/271,690
 ; PRIOR FILING DATE: 2002-10-16
 ; PRIOR APPLICATION NUMBER: US 60/344,534
 ; PRIOR FILING DATE: 2001-10-18
 ; NUMBER OF SEQ ID NOS: 49
 ; SEQ ID NO 4
 ; LENGTH: 1816

; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-372-683-4

Query Match 16.7%; Score 187; DB 15; Length 1816;
 Best Local Similarity 28.3%; Pred. No. 5.3e-10;
 Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDYGVYTKKSEDMKLVRTASFSRGGMSFTNLD-VPTDRFOLSFGQTF 63
 Db 1202 KQFNLEGTETLVGVGCPEDSLISRRAYFN--GQSFASIOKISFPDGFEGGFNRTL 1259
 QY 64 QPSTGLNHTQRTSLVLTLEDGHIELSTRDSNIPFKSGTYMDGLHNVYSIDTSGL 123
 Db 1260 QPGLLFYASGSDVSIISDNGTVIMDK--GIKQSVKQYNDGLSH--VSSVSPT 1315
 QY 124 R--LLID-DQVLRNRQLPSPSNAQSLR---LGG-----GHFECISNVLVQRPQS 170
 Db 1316 RYELIYDKSRVSGKNPTKGI EGTQAS EKKFYFGSGSPISAQYANFTGCISNAFYTRVDRD 1375
 QY 171 PEVLDAKSTKCDASIGGCSLNKPPLMLFKSPKRFNK 209
 Db 1376 VEVEDFORYTEKVTSLYECPISSPLFLHKKGNLSK 1414

RESULT 14

US-10-363-616-457
 ; Sequence 457, Application US/10363616
 ; Publication No. US20040044181A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseg, Inc
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
 ; FILE REFERENCE: 21272-113 (793)
 ; CURRENT APPLICATION NUMBER: US/10/363,616
 ; CURRENT FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: 09/654,935
 ; PRIOR FILING DATE: 2000-09-01
 ; NUMBER OF SEQ ID NOS: 490
 ; SEQ ID NO 457
 ; LENGTH: 1823
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-363-616-457

Query Match 16.7%; Score 187; DB 15; Length 1823;
 Best Local Similarity 28.3%; Pred. No. 5.3e-10;
 Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDYGVYTKKSEDMKLVRTASFSRGGMSFTNLD-VPTDRFOLSFGQTF 63
 Db 1209 KQFNLEGTETLVGVGCPEDSLISRRAYFN--GQSFASIOKISFPDGFEGGFNRTL 1266
 QY 64 QPSTGLNHTQRTSLVLTLEDGHIELSTRDSNIPFKSGTYMDGLHNVYSIDTSGL 123
 Db 1267 QPGLLFYASGSDVSIISDNGTVIMDK--GIKQSVKQYNDGLSH--VSSVSPT 1322
 QY 124 R--LLID-DQVLRNRQLPSPSNAQSLR---LGG-----GHFECISNVLVQRPQS 170
 Db 1323 RYELIYDKSRVSGKNPTKGI EGTQAS EKKFYFGSGSPISAQYANFTGCISNAFYTRVDRD 1382
 QY 171 PEVLDAKSTKCDASIGGCSLNKPPLMLFKSPKRFNK 209
 Db 1383 VEVEDFORYTEKVTSLYECPISSPLFLHKKGNLSK 1421

RESULT 15

US-09-845-583-2
 ; Sequence 2, Application US/09845583
 ; Patent No. US20020142934A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burgeson, Robert
 ; APPLICANT: Brumken, William Joseph
 ; APPLICANT: Champliand, Marie-France

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:13:40 ; Search time 10.1795 Seconds
(without alignments)
1598.653 Million cell updates/sec

Title: US-10-817-423-6

Perfect score: 1118
Sequence: 1 MNKLKKTSGVRLNDTVGVLT.....MLEKSPKRFNRKGRIFNVNQL 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/aa/5A COMB pep:*
- 2: /cgn2_6/prodata/1/aa/5E COMB pep:*
- 3: /cgn2_6/prodata/1/aa/6A COMB pep:*
- 4: /cgn2_6/prodata/1/aa/6B COMB pep:*
- 5: /cgn2_6/prodata/1/aa/6C COMB pep:*
- 6: /cgn2_6/prodata/1/aa/backfile1 pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	1694	US-09-560-385A-12	Sequence 12, Appl
2	1118	100.0	1725	US-09-560-385A-10	Sequence 10, Appl
3	850	76.0	1693	US-09-560-385A-4	Sequence 4, Appl
4	850	76.0	1693	US-09-560-385A-8	Sequence 8, Appl
5	850	76.0	1713	US-08-600-982-24	Sequence 24, Appl
6	850	76.0	1713	US-09-560-385A-6	Sequence 6, Appl
7	850	76.0	1713	US-09-538-092-1359	Sequence 1359, Ap
8	850	76.0	1713	PCT-US94-10261A-24	Sequence 24, Appl
9	850	76.0	1724	US-09-560-385A-2	Sequence 2, Appl
10	204	18.2	1792	US-09-561-818A-12	Sequence 12, Appl
11	204	18.2	1816	US-09-561-818A-10	Sequence 10, Appl
12	187	16.7	1792	US-09-561-818A-4	Sequence 4, Appl
13	187	16.7	1800	US-09-561-818A-8	Sequence 8, Appl
14	187	16.7	1816	US-09-561-818A-2	Sequence 2, Appl
15	187	16.7	1824	US-09-561-818A-6	Sequence 6, Appl
16	186	16.6	3635	US-09-845-583A-2	Sequence 2, Appl
17	174	15.6	953	US-09-845-583A-4	Sequence 4, Appl
18	174	15.6	3647	US-09-949-016-10932	Sequence 10932, A
19	144.5	12.9	3084	US-09-562-702A-12	Sequence 12, Appl
20	144.5	12.9	3106	US-09-562-702A-10	Sequence 10, Appl
21	137.5	12.3	1130	5444158-2	Patent No. 5444158
22	137.5	12.3	1130	5444158-2	Patent No. 5444158
23	134.5	12.0	1130	US-08-460-309-2	Sequence 2, Appl
24	134.5	12.0	1130	US-08-125-077-2	Sequence 2, Appl
25	134.5	12.0	3070	US-09-961-403-7	Sequence 7, Appl
26	134.5	12.0	3088	US-09-562-702A-8	Sequence 8, Appl
27	134.5	12.0	3089	US-09-562-702A-4	Sequence 4, Appl

28	134.5	12.0	3110	US-09-562-702A-2	Sequence 2, Appl
29	134.5	12.0	3110	US-09-562-702A-6	Sequence 6, Appl
30	134.5	12.0	3110	US-09-561-7098-7	Sequence 7, Appl
31	134.5	12.0	3110	US-09-917-254-86	Sequence 86, Appl
32	134.5	12.0	3110	US-09-949-016-5937	Sequence 5937, Ap
33	134.5	12.0	3111	US-08-460-309-4	Sequence 4, Appl
34	134.5	12.0	3111	US-08-125-077-4	Sequence 4, Appl
35	101.5	9.1	3075	US-08-460-309-5	Sequence 5, Appl
36	101.5	9.1	3075	US-08-125-077-5	Sequence 5, Appl
37	98.5	8.8	21	US-08-445-135-7	Sequence 7, Appl
38	94.5	8.5	675	5258288-1	Patent No. 5258288
39	94.5	8.5	675	5258288-1	Patent No. 5258288
40	91	8.1	212	US-09-270-767-43408	Sequence 43408, A
41	89.5	8.0	1381	US-08-826-134-4	Sequence 4, Appl
42	84.5	7.6	1384	US-09-949-016-7814	Sequence 7814, Ap
43	84	7.5	814	US-09-486-072-1	Sequence 1, Appl
44	83.5	7.5	1331	US-09-949-016-6861	Sequence 6861, Ap
45	82	7.3	271	US-08-956-012-3	Sequence 3, Appl

ALIGNMENTS

```
RESULT 1
US-09-560-385A-12
; Sequence 12, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Bouland, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1694
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-560-385A-12

Query Match      100.0%; Score 1118; DB 4; Length 1694;
Best Local Similarity 100.0%; Pred. No. 56-124;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLKKTSGVRLNDTVGVLTAKCEDEWKLVRITASFSRGGQMSFTNLDVPSDRPQLSFGF 60
DB 1098 MNKLKKTSGVRLNDTVGVLTAKCEDEWKLVRITASFSRGGQMSFTNLDVPSDRPQLSFGF 1157
QY 61 QTRPQSGTLLNHQTRTSSLLVLTLEDGHIELSTDSNIPFKSPGTWMDGLLHVSVISDT 120
DB 1158 QTRPQSGTLLNHQTRTSSLLVLTLEDGHIELSTDSNIPFKSPGTWMDGLLHVSVISDT 1217
QY 121 SGRLRLIDDOVLARNRQLPFSNAOOSLRIGGHPFECISNVVYORFOSPEVYDLASKS 180
DB 1218 SGRLRLIDDOVLARNRQLPFSNAOOSLRIGGHPFECISNVVYORFOSPEVYDLASKS 1277
QY 181 TKTDASLGGCSLKNPPLMLFKSPKRNKRIRFNVNQL 218
DB 1278 TKTDASLGGCSLKNPPLMLFKSPKRNKRIRFNVNQL 1315

RESULT 2
US-09-560-385A-10
; Sequence 10, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Bouland, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 36
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 1725
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-560-385A-10

Query Match 100.0%; Score 1118; DB 4; Length 1725;
Best Local Similarity 100.0%; Pred. No. 5, 2e-124;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKNLKTSGVRLNDVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVPSIDRFQLSFGF 60
DB 1129 MKNLKTSGVRLNDVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVPSIDRFQLSFGF 1188
QY 61 QTFQPSGTLNHOQRTSSLLVTLBEGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 120
DB 1189 QTFQPSGTLNHOQRTSSLLVTLBEGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 1248
QY 121 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFEFGCISNVLVORFSQSPETVLDLASKS 180
DB 1249 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFEFGCISNVLVORFSQSPETVLDLASKS 1308
QY 181 TKKDAISLGGCSLNKPPFLMFKSPKRFNKGRIFNNQL 218
DB 1309 TKKDAISLGGCSLNKPPFLMFKSPKRFNKGRIFNNQL 1346

RESULT 3
US-09-560-385A-4
Sequence 4, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Boutand, Ariel
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560, 385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1693
TYPE: PRT
ORGANISM: Homo sapiens
US-09-560-385A-4

Query Match 76.0%; Score 850; DB 4; Length 1693;
Best Local Similarity 76.6%; Pred. No. 6, 5e-92;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKTSGVRLNDVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVPSIDRFQLSFGF 60
DB 1098 MKNLKTSGVRLNDVGVTKKCSBDMKLVRSASFSGQLSTDLGLPTDHLQASFGF 1157
QY 61 QTFQPSGTLNHOQRTSSLLVTLBEGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 120
DB 1158 QTFQPSGTLNHOQRTSSLLVTLBEGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 1217
QY 121 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFEFGCISNVLVORFSQSPETVLDLASKS 180
DB 1218 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFEFGCISNVLVORFSQSPETVLDLASKS 1277
QY 181 TKKDAISLGGCSLNKPPFLMFKSPKRFNKGRIFNNQL 218
DB 1278 LKRDVSLGGCSLNKPPFLMFKSPKRFNKGRIFNNQL 1315

RESULT 4
US-09-560-385A-8
Sequence 8, Application US/09560385A
Patent No. 6703363
GENERAL INFORMATION:
APPLICANT: Boutand, Ariel

TITLE OF INVENTION: Recombinant Laminin 5
FILE REFERENCE: 99-274-C
CURRENT APPLICATION NUMBER: US/09/560, 385A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 1693
TYPE: PRT
ORGANISM: Homo sapiens
US-09-560-385A-8

Query Match 76.0%; Score 850; DB 4; Length 1693;
Best Local Similarity 76.6%; Pred. No. 6, 5e-92;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKNLKTSGVRLNDVGVTKKCSBDMKLVRTASFSRGQMSFTNLDVPSIDRFQLSFGF 60
DB 1098 MKNLKTSGVRLNDVGVTKKCSBDMKLVRSASFSGQLSTDLGLPTDHLQASFGF 1157
QY 61 QTFQPSGTLNHOQRTSSLLVTLBEGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 120
DB 1158 QTFQPSGTLNHOQRTSSLLVTLBEGHIELSTDSNIPFKSPGYMDGLHHVSVISDT 1217
QY 121 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFEFGCISNVLVORFSQSPETVLDLASKS 180
DB 1218 SGRLIIDQVLRNRQLPSFSNAQSLRLGGHFEFGCISNVLVORFSQSPETVLDLASKS 1277
QY 181 TKKDAISLGGCSLNKPPFLMFKSPKRFNKGRIFNNQL 218
DB 1278 LKRDVSLGGCSLNKPPFLMFKSPKRFNKGRIFNNQL 1315

RESULT 5
US-08-600-982-24
Sequence 24, Application US/08600982
Patent No. 6120991
GENERAL INFORMATION:
APPLICANT: Carter, William G.
APPLICANT: Gail, Susanna A.
APPLICANT: Ryan, Maureen C.
TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Christensen, O'Connor, Johnson, and Kindness
STREET: 1420 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101-8100
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,982
FILING DATE: 02-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B170 protein as translated from sequence

DESCRIPTION: OF FIGURES 15A-15F, and as shown also in FIGURES
; DESCRIPTION: 19A-19R
; US-08-600-982-24

Query Match 76.0%; Score 850; DB 3; Length 1713;
Best Local Similarity 76.6%; Pred. No. 6.6e-92;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKRLKTSGVRLNDVGVTKKCEBDMKLVRTASFSRGGQMSFTNLDVPSDFOLSPGF 60
DB 1118 MKRLKTSGVRLNDVGVTKKCEBDMKLVRSASFSRGGQLSFTDGLPPTDHLQASFGF 1177

QY 61 QTFQPSGTLNHOQRTSSLLVLTLEDGHIELSTRDSNIPFKSPGYMDGLHHVSVISDT 120
DB 1178 QTFQPSGTLNHOQRTSSLLVLTLEDGHIELSTRDSNIPFKSPGYMDGLHHVSVISDN 1237

QY 121 SGLRLIIDQVLRNORLPSFSNAQSLRLGGHFGFCISNVLVORPSQSPVYLDLASKS 180
DB 1238 SGLRLIIDQVLRNORLPSFSNAQSLRLGGHFGFCISNVLVORPSQSPVYLDLTSNS 1297

QY 181 TKKDAISGGCSLNKPPFLMFKSPKRNKGRINNVOL 218
DB 1298 LKRDVSLGGCSLNKPPFLMFKSPKRNKGRINNVOL 1335

RESULT 6
US-09-560-385A-6
; Sequence 6, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Bontand, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560.385A
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1713
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-560-385A-6

Query Match 76.0%; Score 850; DB 4; Length 1713;
Best Local Similarity 76.6%; Pred. No. 6.6e-92;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKRLKTSGVRLNDVGVTKKCEBDMKLVRTASFSRGGQMSFTNLDVPSDFOLSPGF 60
DB 1118 MKRLKTSGVRLNDVGVTKKCEBDMKLVRSASFSRGGQLSFTDGLPPTDHLQASFGF 1177

QY 61 QTFQPSGTLNHOQRTSSLLVLTLEDGHIELSTRDSNIPFKSPGYMDGLHHVSVISDT 120
DB 1178 QTFQPSGTLNHOQRTSSLLVLTLEDGHIELSTRDSNIPFKSPGYMDGLHHVSVISDN 1237

QY 121 SGLRLIIDQVLRNORLPSFSNAQSLRLGGHFGFCISNVLVORPSQSPVYLDLASKS 180
DB 1238 SGLRLIIDQVLRNORLPSFSNAQSLRLGGHFGFCISNVLVORPSQSPVYLDLTSNS 1297

QY 181 TKKDAISGGCSLNKPPFLMFKSPKRNKGRINNVOL 218
DB 1298 LKRDVSLGGCSLNKPPFLMFKSPKRNKGRINNVOL 1335

RESULT 7
US-09-538-092-1359
; Sequence 1359, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSegFormatter Version 0.9
; SEQ ID NO 1359
; LENGTH: 1713
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number Q16787
; US-09-538-092-1359

Query Match 76.0%; Score 850; DB 4; Length 1713;
Best Local Similarity 76.6%; Pred. No. 6.6e-92;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKRLKTSGVRLNDVGVTKKCEBDMKLVRTASFSRGGQMSFTNLDVPSDFOLSPGF 60
DB 1118 MKRLKTSGVRLNDVGVTKKCEBDMKLVRSASFSRGGQLSFTDGLPPTDHLQASFGF 1177

QY 61 QTFQPSGTLNHOQRTSSLLVLTLEDGHIELSTRDSNIPFKSPGYMDGLHHVSVISDT 120
DB 1178 QTFQPSGTLNHOQRTSSLLVLTLEDGHIELSTRDSNIPFKSPGYMDGLHHVSVISDN 1237

QY 121 SGLRLIIDQVLRNORLPSFSNAQSLRLGGHFGFCISNVLVORPSQSPVYLDLASKS 180
DB 1238 SGLRLIIDQVLRNORLPSFSNAQSLRLGGHFGFCISNVLVORPSQSPVYLDLTSNS 1297

QY 181 TKKDAISGGCSLNKPPFLMFKSPKRNKGRINNVOL 218
DB 1298 LKRDVSLGGCSLNKPPFLMFKSPKRNKGRINNVOL 1335

RESULT 8
PCT-US94-10261A-24
; Sequence 24, Application PC/TUS9410261A
; GENERAL INFORMATION:
; APPLICANT: Carter, William G.
; APPLICANT: Gil, Susanna A.
; APPLICANT: Ryan, Maureen C.
; TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Christensen, O'Connor, Johnson, and Kindness
; STREET: 1420 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-8100
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10261A
; FILING DATE: 02-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K.
; REGISTRATION NUMBER: 26,997
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-8100
; TELEFAX: (206) 224-0779
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 1713 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: E170 protein as translated from sequence of
; DESCRIPTION: FIGURES 15A-15P, and as shown also in FIGURES 19A-19R
; PCT-US94-10261A-24

```

```

Query Match          76.0%; Score 850; DB 5; Length 1713;
Best Local Similarity 76.6%; Pred. No. 6.6e-92;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

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```

QY 1 MKRLKTSGVRLNDVGVYTKKSEBWKLVRTASFSRGQMSFTNLDVPSDRFQLSFGF 60
DB 1118 MKRLKTSGVRLNDVGVYTKKSEBWKLVRSASFSRGQLSTDTGLPPTDHLQASFGF 1177
QY 61 QTFPQSGTLNHQRTSSLVLTLEDGHIESTRDSNIPFKSPGYMDGLHHVYSIDPT 120
DB 1178 QTFPQSGTLNHQRTSSLVLTLEDGHIESTRDSNIPFKSPGYMDGLHHVYSIDN 1237
QY 121 SGRLRLIDQVLRNRQLPSFSNAQOSLRIGGCHFGECISNVLVQRFSSQSPVLDLASKS 180
DB 1238 SGRLRLIDQVLRNRQLPSFSNAQOSLRIGGCHFGECISNVLVQRLSLSPVLDLTSNS 1297
QY 181 TKKDAISLGGCSLNKPPLMLFKSPKPKNGRIINNVQL 218
DB 1298 LKRDVSLGGCSLNKPPLMLKSGTRFNKTKTRINQL 1335

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RESULT 9

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US-09-560-385A-2
; Sequence 2, Application US/09560385A
; Patent No. 6703363
; GENERAL INFORMATION:
; APPLICANT: Bouland, Ariel
; TITLE OF INVENTION: Recombinant Laminin 5
; FILE REFERENCE: 99-274-C
; CURRENT APPLICATION NUMBER: US/09/560,385A
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1724
; TYPE: PRP
; ORGANISM: Homo sapiens
; US-09-560-385A-2

```

```

Query Match          76.0%; Score 850; DB 4; Length 1724;
Best Local Similarity 76.6%; Pred. No. 6.7e-92;
Matches 167; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

```

```

QY 1 MKRLKTSGVRLNDVGVYTKKSEBWKLVRTASFSRGQMSFTNLDVPSDRFQLSFGF 60
DB 1129 MKRLKTSGVRLNDVGVYTKKSEBWKLVRSASFSRGQLSTDTGLPPTDHLQASFGF 1188
QY 61 QTFPQSGTLNHQRTSSLVLTLEDGHIESTRDSNIPFKSPGYMDGLHHVYSIDPT 120
DB 1189 QTFPQSGTLNHQRTSSLVLTLEDGHIESTRDSNIPFKSPGYMDGLHHVYSIDN 1248
QY 121 SGRLRLIDQVLRNRQLPSFSNAQOSLRIGGCHFGECISNVLVQRFSSQSPVLDLASKS 180
DB 1249 SGRLRLIDQVLRNRQLPSFSNAQOSLRIGGCHFGECISNVLVQRLSLSPVLDLTSNS 1308
QY 181 TKKDAISLGGCSLNKPPLMLFKSPKPKNGRIINNVQL 218
DB 1309 LKRDVSLGGCSLNKPPLMLKSGTRFNKTKTRINQL 1346

```

```

RESULT 10
US-09-561-818A-12
; Sequence 12, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:

```

```

; APPLICANT: Kortessmaa, Jarkko
; APPLICANT: Trygvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1792
; TYPE: PRP
; ORGANISM: Mus musculus
; US-09-561-818A-12

```

```

Query Match          18.2%; Score 204; DB 4; Length 1792;
Best Local Similarity 29.1%; Pred. No. 1.8e-14;
Matches 64; Conservative 35; Mismatches 99; Indels 22; Gaps 8;

```

```

QY 5 KKTSGVRLNDVGVYTKKSEBWKLVRTASFSRGQMSFTNLDVPSDRFQLSFGFOTF 63
DB 1180 KDFMILRQETELGVYGCPEBDSLISRRAVFN--GQSFIAIIOKISFPDGFEGGFNFTL 1237
QY 64 QPSGTLNHQRTSSLVLTLEDGHIESTRDSNIPFKSPGYMDGLHH--VSVISDPSG 122
DB 1238 QPSGTLNHQRTSSLVLTLEDGHIESTRDSNIPFKSPGYMDGLHH--VSVISDPSG 1294
QY 123 LRLRLIDQVLRNRQLPSFSNAQOS-----LRLGG-----GHFGECISNVLVQRFSSQ 169
DB 1295 YELVVDKRLRQKN--PTKGRABQRTQTEKKPFYFGSGSPISPOYANFTGICISNAVYTRDR 1352
QY 170 SPEVLDLASKSTYKDAISLGGCSLNKPPLMLFKSPKPKNGRIINNVQL 209
DB 1353 DVEVEDPQRYSEKVTSLYECPIESSPLFLHKKGKNSK 1392

```

RESULT 11

```

US-09-561-818A-10
; Sequence 10, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarkko
; APPLICANT: Trygvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1816
; TYPE: PRP
; ORGANISM: Mus musculus
; US-09-561-818A-10

```

```

Query Match          18.2%; Score 204; DB 4; Length 1816;
Best Local Similarity 29.1%; Pred. No. 1.9e-14;
Matches 64; Conservative 35; Mismatches 99; Indels 22; Gaps 8;

```

```

QY 5 KKTSGVRLNDVGVYTKKSEBWKLVRTASFSRGQMSFTNLDVPSDRFQLSFGFOTF 63
DB 1204 KDFMILRQETELGVYGCPEBDSLISRRAVFN--GQSFIAIIOKISFPDGFEGGFNFTL 1261
QY 64 QPSGTLNHQRTSSLVLTLEDGHIESTRDSNIPFKSPGYMDGLHH--VSVISDPSG 122
DB 1262 QPSGTLNHQRTSSLVLTLEDGHIESTRDSNIPFKSPGYMDGLHH--VSVISDPSG 1318
QY 123 LRLRLIDQVLRNRQLPSFSNAQOS-----LRLGG-----GHFGECISNVLVQRFSSQ 169
DB 1319 YELVVDKRLRQKN--PTKGRABQRTQTEKKPFYFGSGSPISPOYANFTGICISNAVYTRDR 1376
QY 170 SPEVLDLASKSTYKDAISLGGCSLNKPPLMLFKSPKPKNGRIINNVQL 209
DB 1377 DVEVEDPQRYSEKVTSLYECPIESSPLFLHKKGKNSK 1416

```


RESULT 12

US-09-561-818A-4
; Sequence 4, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortteesmaa, Jarkko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1792
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-4

Query Match 16.7%; Score 187, DB 4; Length 1792;
Best Local Similarity 28.3%; Pred. No. 2e-12;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDYGVTKKCEBDMKLVRTASFSRGGMSFTNLD-VPESTRFQSLFQGFQTF 63
DB 1178 KQPNLLBQETELGVGCEPDSLSIRAYFN--GQSFASIQKISFFDFEGGFNRTL 1235
QY 64 QPSCGLLNHQTSSLLVTLDEGHIELSTRDSNIPFKSPGTWMDGLLHVSVISDTSGL 123
DB 1236 QPFGLLFYASGSDVBSISLNDGTVMYDK--GIKQVSVKQYNDGLSHF--VISSVSPT 1291
QY 124 R--LLID-DQVLRNORLPSPSNAQOSLR---LGG-----GHFEGCISNVLVORFSQS 170
DB 1292 RYELIYDKSRVSGSKNFKGIETQASBKKEFYGGSPISAQVNFQTCISNAFTVDRD 1351
QY 171 PEVLIDASKSTKQDASLGGCSLNKPPPLMLFKSPKPKFNK 209
DB 1352 VEVEDFORYTEKHTSLYECPIESSPLFLHKKGKMLSK 1390

RESULT 13

US-09-561-818A-8
; Sequence 8, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortteesmaa, Jarkko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1800
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-8

Query Match 16.7%; Score 187, DB 4; Length 1800;
Best Local Similarity 28.3%; Pred. No. 2e-12;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDYGVTKKCEBDMKLVRTASFSRGGMSFTNLD-VPESTRFQSLFQGFQTF 63
DB 1178 KQPNLLBQETELGVGCEPDSLSIRAYFN--GQSFASIQKISFFDFEGGFNRTL 1235
QY 64 QPSCGLLNHQTSSLLVTLDEGHIELSTRDSNIPFKSPGTWMDGLLHVSVISDTSGL 123
DB 1236 QPFGLLFYASGSDVBSISLNDGTVMYDK--GIKQVSVKQYNDGLSHF--VISSVSPT 1291

QY 124 R--LLID-DQVLRNORLPSPSNAQOSLR---LGG-----GHFEGCISNVLVORFSQS 170
DB 1292 RYELIYDKSRVSGSKNFKGIETQASBKKEFYGGSPISAQVNFQTCISNAFTVDRD 1351
QY 171 PEVLIDASKSTKQDASLGGCSLNKPPPLMLFKSPKPKFNK 209
DB 1352 VEVEDFORYTEKHTSLYECPIESSPLFLHKKGKMLSK 1390

RESULT 14

US-09-561-818A-2
; Sequence 2, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortteesmaa, Jarkko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-2

Query Match 16.7%; Score 187, DB 4; Length 1816;
Best Local Similarity 28.3%; Pred. No. 2e-12;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDYGVTKKCEBDMKLVRTASFSRGGMSFTNLD-VPESTRFQSLFQGFQTF 63
DB 1202 KQPNLLBQETELGVGCEPDSLSIRAYFN--GQSFASIQKISFFDFEGGFNRTL 1259
QY 64 QPSCGLLNHQTSSLLVTLDEGHIELSTRDSNIPFKSPGTWMDGLLHVSVISDTSGL 123
DB 1260 QPFGLLFYASGSDVBSISLNDGTVMYDK--GIKQVSVKQYNDGLSHF--VISSVSPT 1315
QY 124 R--LLID-DQVLRNORLPSPSNAQOSLR---LGG-----GHFEGCISNVLVORFSQS 170
DB 1316 RYELIYDKSRVSGSKNFKGIETQASBKKEFYGGSPISAQVNFQTCISNAFTVDRD 1375
QY 171 PEVLIDASKSTKQDASLGGCSLNKPPPLMLFKSPKPKFNK 209
DB 1376 VEVEDFORYTEKHTSLYECPIESSPLFLHKKGKMLSK 1414

RESULT 15

US-09-561-818A-6
; Sequence 6, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortteesmaa, Jarkko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1824
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-6

Query Match 16.7%; Score 187, DB 4; Length 1824;
Best Local Similarity 28.3%; Pred. No. 2e-12;
Matches 62; Conservative 34; Mismatches 103; Indels 20; Gaps 8;

QY 5 KKTSGVRLNDYGVTKKCEBDMKLVRTASFSRGGMSFTNLD-VPESTRFQSLFQGFQTF 63

```
Db      1202 KDFNLLEQETETLVGVGCGPEBDSLISRAYFN--GQSFIASIOKISFFDGFEGGFNFRFL 1259
Qy      64  OPSGTLNQHOTRTSSLLVTLBEDGHELSTRDSNIPIFKSPGTYMDGLLHVSVISDTSGL 123
Db      1260 QPENGILFYAAGSDVPSISLDNGTVIMDYK--GIKVQYVDKQYNDGLSHF--VISVSPT 1315
Qy      124  R--LLID-DQVLRNRQRLPSPFSAQQLR---LGG-----GHFEGCISNVLVQRFSSQS 170
Db      1316 RYELIYDKSRVGSKNPTKGIEQTVQASEKKFYFGGSPISAQYANFTGCISNAYFTRVDRD 1375
Qy      171  PEVLDAASKSTYKDAALGGCSLNKPPFLMLFKSPKRPNK 209
Db      1376 VEVEDFQRYTEKVTSLYECPIESSPLFLHKKGKNLSK 1414
```

Search completed: February 22, 2005, 08:40:56
Job time : 11.1795 secs